Package: metainc (via r-universe)

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Title Assessment of Inconsistency in Meta-Analysis using Decision Thresholds

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Description Assessment of inconsistency in meta-analysis by calculating the Decision Inconsistency index (DI) and the Across-Studies Inconsistency (ASI) index. These indices quantify inconsistency taking into account outcome-level decision thresholds.

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metainc-package   *'metainc': Brief overview of methods and general hints*

Description

Assessment of inconsistency in meta-analysis by calculating the Decision Inconsistency index (DI) and the Across-Studies Inconsistency (ASI) index. These indices quantify inconsistency taking into account outcome-level decision thresholds.

Details

The following possibilities are available in **'metainc'**:

- Generating or extracting samples of effect sizes from primary studies included in a meta-analysis ([getsamples](#))

- Calculating the Decision Inconsistency and Across-Studies Inconsistency index ([inc](#))

In addition, the following methods for sensitivity and subset analysis are available:

- Sensitivity analysis based on the baseline risk ([sens_br](#))

- Sensitivity analysis based on decision thresholds ([sens_dt](#))

- Leave-one-out analysis ([sens_inf](#))

- Subset analysis ([subset.inc](#))

Type help(package = "metainc") for a listing of R functions available in **'metainc'**.

Type citation("metainc") on how to cite **'metainc'** in publications.

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Cohen J. (1998). "Statistical Power Analysis in the Behavioral Sciences", 2nd edition ed. Hillsdale (NJ): Lawrence Erlbaum Associates, Inc.

Schunemann HJ, Higgins JPT, Vist GE, et al. (2019). "Completing 'Summary of findings' tables and grading the certainty of the evidence." *Cochrane Handbook for Systematic Reviews of Interventions*, 375–402.

Schunemann HJ, Vist GE, Higgins JPT, et al. (2019). "Interpreting results and drawing conclusions." *Cochrane Handbook for Systematic Reviews of Interventions*, 403–431.

Skoetz N, Goldkuhle M, van Dalen EC, et al. (2020). "GRADE guidelines 27: how to calculate absolute effects for time-to-event outcomes in summary of findings tables and Evidence Profiles." *Journal of Clinical Epidemiology*, **118**, 124–131.

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anticoagulation	*Sampled odds ratios from meta-analysis on the association between parenteral anticoagulation and mortality in patients with cancer*

Description

Matrix with sampled odds ratios from meta-analysis on the association between parenteral anticoagulation and mortality in patients with cancer (Akl et al., 2017).

Format

A matrix with 5000 sampled odds ratios (rows) for 18 studies (columns) following a Bayesian meta-analysis.

Details

Data from Akl et al. (2017) and displaying results presented as odds ratios. Each column corresponds to a different primary study.

Source

Akl, E. A., Kahale, L. A., Hakoum, M. B., Matar, C. F., Sperati, F., Barba, M., et al. (2017). "Parenteral anticoagulation in ambulatory patients with cancer." *Cochrane Database of Systematic Reviews*, **9**: CD006652.

See Also

inc, anticoagulation_df

Examples

```
data(anticoagulation)

# Since the results are already presented as odds ratios, we need
# to indicate that effects have not been transformed to log odds
# ratios yet (\code{transf = FALSE}).
dis1 <- inc(anticoagulation, br = 0.504, dt1 = 16, sm = "OR",
  transf = FALSE)
dis1

# Alternatively, we may simply apply the \code{inc()} function to
# log odds ratios.
```

```
data(anticoagulation)
dis2 <- inc(log(anticoagulation), br = 0.504, dt1 = 16, sm = "OR")
dis2
```

---

anticoagulation_df   *Meta-analysis on the association between parenteral anticoagulation*
                            and mortality in patients with cancer

---

Description

Data set from meta-analysis on the association between parenteral anticoagulation and mortality in
patients with cancer (Akl et al., 2017). For each primary study, results are expressed as a log odds
ratio.

Details

Data frame containing, for each primary study of the meta-analysis from Akl et al. (2017):

1. number of events (variables rA and rB) and total number of participants (nA and nB) for each
   group,

2. effect sizes [ln OR] (yi),

3. respective variances (vi),

4. risk of bias assessment (RoB).

Source

Akl, E. A., Kahale, L. A., Hakoum, M. B., Matar, C. F., Sperati, F., Barba, M., et al. (2017).
"Parenteral anticoagulation in ambulatory patients with cancer." *Cochrane Database of Systematic
Reviews*, **9**: CD006652.

See Also

inc, anticoagulation

Examples

```
data(anticoagulation_df)
m1 <- meta::metagen(yi, sqrt(vi), sm = "OR", data = anticoagulation_df,
  studlab = LETTERS[1:18])
set.seed(1090) # Make sampled effect sizes reproducible
sample1 <- getsamples(m1)
dis1 <- inc(sample1, dt1 = 16, dt2 = 31, dt3 = 60, br = 0.504, sm = "OR")
dis1

if(requireNamespace("metafor")){
# Same sampled effect sizes using R package 'metafor' (must be installed)
m2 <- metafor::rma(anticoagulation_df, measure = "OR", slab = LETTERS[1:18])
set.seed(1090) # Make sampled effect sizes reproducible
```

```
sample2 <- getsamples(m2)
dis2 <- inc(sample2, dt1 = 16, dt2 = 31, dt3 = 60, br = 0.504, sm = "OR")
dis2

all.equal(sample1, sample2) # Only difference: package name
}
```

---

getsamples   *Generate or extract samples of effect sizes from primary studies*

Description

Obtains a matrix containing sampled effect sizes from primary studies of a meta-analysis.

Usage

```
getsamples(
  obj,
  param = NULL,
  package = NULL,
  n.samples = 10000,
  sm,
  transf = TRUE
)
```

Arguments

obj	Meta-analysis object (see Details).
param	Parameters for effect sizes (see Details).
package	Character string with name of R package used to create the meta-analysis object obj.
n.samples	Number of samples per study if meta-analysis had been performed with R package **'meta'** or rma from R package **'metafor'**.
sm	A character string indicating the summary measure used in primary studies.
transf	A logical indicating whether effect sizes are transformed or on the original scale. If transf = TRUE (default), effect estimates are expected to be on the log scale (for example, log odds ratios instead of odds ratios for sm = "OR").

Details

Creates a matrix with sampled effect sizes of primary studies (number of rows equal to the number of samples, number of columns equal to the number of studies in the meta-analysis).

Main input to this function is argument obj containing a meta-analysis object created with bugs from R package **'R2OpenBUGS'**, jags from **'R2jags'**, jags.samples from **'rjags'**, brm from **'brms'**, rma from **'metafor'**, or metabin, metacont or metagen from **'meta'**.

Argument param corresponds to the effect size measures of the primary studies (for R packages
'R2OpenBUGS', **'R2jags'**, and **'rjags'**) or to the name of the column that contains the unique
identification of each primary study in the data frame containing the results of primary studies used
for meta-analysis (**'brms'** package). This argument is not required if the meta-analysis has been
performed using R package **'meta'** or **'metafor'**.

Information of the R package used to conduct the meta-analysis can be provided in argument
package. The value of package can be 'R2OpenBUGS', 'R2jags', 'rjags', 'meta', 'metafor' or
'brms'. This information is not required for an object created with **'meta'**, **'metafor'** or **'brms'**.

Argument n.samples contains the number of samples per study for meta-analyses created with
'meta' or **'metafor'**. Default is 10000 samples.

Summary measure used in primary studies (argument sm) can be either "OR" (odds ratio), "RR" (risk
ratio), "HR" (hazard ratio), "RD" (risk difference), "MD" (mean difference), "SMD" (standardised
mean difference), "GEN_ratio" (generic ratio) or "GEN_diff" (generic difference). Does not need
to be provided if the meta-analysis was performed with **'meta'** or **'metafor'**.

Value

A matrix containing sampled effect sizes (rows) for primary study (columns).

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>

Examples

```
# Example with an object obtained using the 'R2OpenBUGS' package ("es",
# whose simulations on the effect sizes of primary studies are those
# of the "delta" parameter). If the object had been obtained using a
# different package, all remaining arguments would be the same and only
# the "package" argument would have a different input.

# In this example, argument \code{transf = TRUE} (default), as sampled
# effect sizes are log odds ratios.

load(url("https://raw.github.com/BernardoSousaPinto/metainc_extra_files/main/es.Rdata"))

sample <- getsamples(es, param = "delta", package = "R2OpenBUGS", sm = "OR")
sample


# Example using a dataset providing effect sizes for primary studies (yi)
# and respective variances (vi). A frequentist meta-analysis using the 'meta'
# package is conducted.

data("anticoagulation_df")
m1 <- meta::metagen(yi, sqrt(vi), sm = "OR", data = anticoagulation_df,
  studlab = LETTERS[1:18])
set.seed(1090) # Make sampled effect sizes reproducible
sample1 <- getsamples(m1)
sample1
```

```
if(requireNamespace("metafor")){
# Same samples of effect sizes using R package 'metafor' (must be installed)

m2 <- metafor::rma(anticoagulation_df, measure = "OR", slab = LETTERS[1:18])
set.seed(1090) # Make sampled effect sizes reproducible
sample2 <- getsamples(m2)
sample2

all.equal(sample1, sample2) # Only difference: package name
}
```

---

inc   *Decision Inconsistency and Across-Studies Inconsistency index*

Description

Calculates the Decision Inconsistency (DI) and Across-Studies Inconsistency (ASI) indices.

Usage

```
inc(
  x,
  dt1,
  dt2 = NULL,
  dt3 = NULL,
  sm,
  br = NULL,
  utility = NULL,
  scale = 1000,
  transf = TRUE,
  transf.dt = FALSE
)

## S3 method for class 'inc'
print(x, digits = 1, ...)

## S3 method for class 'inc'
summary(object, ...)

## S3 method for class 'summary.inc'
print(x, digits = 1, ...)
```

Arguments

x   An R object created with [getsamples](#) or a matrix containing the sampled effect
             sizes of primary studies.

dt1	A single numeric defining the decision threshold to distinguish (i) meaningful from trivial effects, if arguments dt2 and dt3 are not provided, (ii) negative / harmful from trivial effects, if only argument dt2 is also provided, or (iii) small from trivial effects if arguments dt2 and dt3 are provided.
dt2	A single numeric defining the decision threshold to distinguish (i) positive / beneficial from trivial effects if argument dt3 is not provided, or (ii) moderate from small effects if argument dt3 is provided.
dt3	A single numeric defining the decision threshold to distinguish large from moderate effects.
sm	A character string indicating the summary measure used in primary studies (see Details).
br	Baseline risk (only considered for odds, risk or hazard ratio).
utility	Utility value.
scale	The number of people per which absolute decision thresholds are provided (default: 1000, i.e., absolute decision threshold values are defined per 1000 persons). Only considered if br is not missing.
transf	A logical indicating whether the values of an effect size matrix (argument x) are to be transformed. By default transf = TRUE, it is assumed that the matrix contains, e.g., log odds ratios instead of odds ratios.
transf.dt	A logical indicating whether relative decision thresholds are transformed or on the original scale. If transf.dt = FALSE (default), relative decision thresholds are expected to be on the natural scale (e.g., odds ratios instead of log odds ratios for sm = "OR"). Note, the GRADE working group recommends to use absolute instead of relative decision thresholds.
digits	Minimal number of significant digits to print percentages, see print.default.
...	Additional arguments (ignored)
object	R object of class inc.

Details

Calculates the Decision Inconsistency index (DI) and the Across-Studies Inconsistency index (ASI) for a meta-analysis. The following possibilities are considered depending on the type of effect size measures:

- Effect size measure corresponding to a ratio (sm = "OR", "RR" or "HR") with the DI and the ASI being calculated based on absolute effects: This requires the specification of a baseline risk (i.e., br must be defined). The decision threshold values (dt1, dt2 and dt3 must be provided as absolute effects (i.e., number of additional or diminished events per N people. By default, it is assumed that these threshold values are provided per 1000 people. However, this can be changed using the scale argument).

- Effect size measure corresponding to a ratio (sm = "OR", "RR", "HR" or "GEN_ratio") with the DI and the ASI being calculated based on relative effect size measures: The sampled effect sizes of primary studies are directly compared with decision thresholds (dt1, dt2, dt3) also expressed as relative effect sizes. This is the adopted approach when no information is provided on the baseline risk (br).

- Effect size measure corresponding to a difference (sm = "MD", "SMD", "RD" or "GEN_diff"): The sampled effect sizes of primary studies are directly compared with decision thresholds (dt1, dt2, dt3) also expressed as differences.

Of note, when dealing with relative effect size measures, judgements based on absolute effects tend to be considered more important for decision making. The formulae for calculating absolute effects based on relative effect size measures are those used by the GRADE approach (see references below).

Ideally, arguments dt1, dt2 and dt3 should be provided. If only one decision threshold is available, it is either possible to provide (i) only dt1, or (ii) both dt1 and dt2 (if the threshold distinguishing clinically relevant benefits vs trivial effects is different from that distinguishing clinically relevant harms vs trivial effects).

Argument sm must be "OR" (odds ratio), "RR" (risk ratio), "HR" (hazard ratio), "MD" (mean difference), "SMD" (standardised mean difference), "RD" (risk difference), "GEN_diff" (generic difference), or "GEN_ratio" (generic ratio).

The baseline risk (br) must be a numeric value between 0 and 1. It can be provided when sm = "OR", "RR" or '"HR". The baseline risk is also known as assumed comparator risk (i.e., the risk that the outcome of interest occurs in the comparison intervention).

Value

An object of class inc, for which some standard methods are available, see metainc-package. Some of the components include:

DI   A percentage corresponding to the Decision Inconsistency index. The higher / closer to 100% the value, the higher the inconsistency.

ASI   A percentage corresponding to the Across-Studies Inconsistency index. The higher / closer to 100% the value, the higher the across-studies inconsistency.

class_distribution

A data frame containing the proportion of samples indicating (if three decision thresholds had been provided):

- Large positive effects (effect sizes higher than dt3): "large (higher)" row;
- Moderate positive effects (efect sizes between dt2 and dt3): "moderate (higher)" row;
- Small positive effects (effect sizes between dt1 and dt2): "small (higher)" row;
- Non meaningful effects (effect sizes between -dt1 and dt1): "not meaningful" row;
- Small negative effects (effect sizes between -dt1 and -dt2): "small (lower)" row;
- Moderate negative effects (effect sizes between -dt2 and -dt3): "moderate (lower)" row;
- Large negative effects (effect sizes lower than -dt3): "large (lower)" row.

prop_over_null   A numeric value indicating the proportion of samples with a value higher than the value representing no difference between the groups.

Author(s)

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References

Cohen J. (1998). "Statistical Power Analysis in the Behavioral Sciences", 2nd edition ed. Hillsdale (NJ): Lawrence Erlbaum Associates, Inc.

Schunemann HJ, Higgins JPT, Vist GE, et al. (2019). "Completing 'Summary of findings' tables and grading the certainty of the evidence." *Cochrane Handbook for Systematic Reviews of Interventions*, 375–402.

Schunemann HJ, Vist GE, Higgins JPT, et al. (2019). "Interpreting results and drawing conclusions." *Cochrane Handbook for Systematic Reviews of Interventions*, 403–431.

Skoetz N, Goldkuhle M, van Dalen EC, et al. (2020). "GRADE guidelines 27: how to calculate absolute effects for time-to-event outcomes in summary of findings tables and Evidence Profiles." *Journal of Clinical Epidemiology*, **118**, 124–131.

Examples

```
# Example with effect sizes measures expressed as ratios and with
# calculation of the Decision Inconsistency index and the Across-Studies
# Inconsistency index based on absolute effects:

data(anticoagulation)
inc_anticoagulation <-
  inc(anticoagulation, dt1 = 16, dt2 = 31, dt3 = 60, br = 0.5, sm = "OR",
      transf = FALSE)
inc_anticoagulation

# Same result
inc_anticoagulation <-
  inc(log(anticoagulation), dt1 = 16, dt2 = 31, dt3 = 60,
    br = 0.5, sm = "OR")
inc_anticoagulation

# Example with calculation of the Decision Inconsistency index and the
# Across-Studies Inconsistency index based on effect size measures expressed
# as mean differences:

data(montelukast)
inc_montelukast <- inc(montelukast, dt1 = 0.2, dt2 = 0.4, dt3 = 0.6, sm = "md")
inc_montelukast
```

---

montelukast · *Sampled effect sizes (mean differences) from Krishnamoorthy et al. (2020)*

Description

Matrix with sampled effect sizes (mean differences) from a meta-analysis by Krishnamoorthy et al. (2020).

Format

A matrix with 5000 sampled mean differences (rows) for 9 studies (columns) following a Bayesian meta-analysis.

Details

Data from Krishnamoorthy et al. (2020) (Figure 7), displaying results presented as mean differences. Each column corresponds to a different primary study.

Source

Krishnamoorthy, M., Mohd Noor, N., Mat Lazim, N., & Abdullah, B. (2020). "Efficacy of montelukast in allergic rhinitis treatment: a systematic review and meta-analysis." *Drugs*, **80**, 1381–1851.

See Also

inc

Examples

```
data(montelukast)
inc(montelukast, dt1 = 0.2, dt2 = 0.4, dt3 = 0.6, sm = "MD")
```

---

or2rr	*Calculate risk ratios from odds ratios and baseline risk*

Description

Calculate risk ratios from odds ratios and baseline risk.

Usage

```
or2rr(or, br)
```

Arguments

or	Odds ratio(s).
br	Baseline risk (also known as assumed comparator risk), i.e., risk that the outcome of interest would occur in the comparator intervention. It must be expressed as a value between 0 and 1.

Details

Converts odds ratios (OR) into risk ratios (RR) using the formula available in Schunemann et al. (2019), Chapter 15:

RR = OR / (1 - br x (1 - OR)),

with br corresponding to the baseline risk (the assumed comparator risk; i.e., the risk that the outcome of interest would occur in the comparison intervention).

Value

A vector or matrix with risk ratios.

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Schunemann HJ, Vist GE, Higgins JPT, et al. (2019). "Interpreting results and drawing conclusions." *Cochrane Handbook for Systematic Reviews of Interventions*, 403–431.

Examples

```
data(anticoagulation)
RRs <- or2rr(anticoagulation, br = 0.5)
head(RRs)
```

---

sens_br   *Sensitivity analysis (based on the baseline risk) for the Decision In-*
                                 consistency and Across-Studies Inconsistency index

---

Description

Sensitivity analysis on the Decision Inconsistency index and the Across-Studies Inconsistency index based on a range of baseline risks. It is applicable only to meta-analyses with a binary outcome (effect size measures expressed as risk ratios, odds ratios or hazard ratios).

Usage

```
sens_br(x, br1, br2, dt1, dt2 = NULL, dt3 = NULL, sm, by = 0.01, scale = 1000)

## S3 method for class 'sens_br'
plot(
  x,
  ylim1 = c(0, 100),
  ylim2 = c(0, 100),
  ylab1 = "DI index (%)",
```

```
    ylab2 = "ASI index (%)",
    ...
)
```

Arguments

x	An R object created with getsamples or a matrix containing sampled effect sizes of primary studies. Note, log transformed effect sizes must be provided (e.g., log odds ratios instead of odds ratios).
br1	Smallest baseline risk considered.
br2	Largest baseline risk considered.
dt1	A single numeric defining the decision threshold to distinguish (i) meaningful from trivial effects, if arguments dt2 and dt3 are not provided, or (ii) small from trivial effects if arguments dt2 and dt3 are provided.
dt2	A single numeric defining the decision threshold to distinguish moderate from small effects provided.
dt3	A single numeric defining the decision threshold to distinguish large from moderate effects.
sm	A character string indicating the summary measure used in primary studies (either sm = "OR", sm = "RR" or sm = "HR").
by	Increment of the sequence from br1 to br2.
scale	The number of people per which absolute decision thresholds are provided (default: 1000, i.e., absolute decision threshold values are defined per 1000 people).
ylim1	The y limits (min, max) of the plot showing the Decision Inconsistency index.
ylim2	The y limits (min, max) of the plot showing the Across-Studies Inconsistency index.
ylab1	A label for the y-axis (Decision Inconsistency index).
ylab2	A label for the y-axis (Across-Studies Inconsistency index).
...	Additional graphical arguments (ignored).

Details

Computes the Decision Inconsistency index (DI) and the Across-Studies Inconsistency index (ASI) across a range of baseline risks. It can only be applied for meta-analyses with binary outcome data (effect size measures expressed as (log) risk ratios, odds ratios or hazard ratios), with the DI and the ASI being calculated based on absolute effects. As a result, the decision threshold values (dt1, dt2, dt3) must be provided as absolute effects. By default, it is assumed that threshold values are provided as numbers of events per 1000 persons (scale = 1000).

Value

A data frame containing

br	Baseline risk
ASI	Decision Inconsistency index at baseline risk
DI	Across-Studies Inconsistency index at baseline risk

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Schunemann HJ, Higgins JPT, Vist GE, et al. (2019). "Completing 'Summary of findings' tables and grading the certainty of the evidence." *Cochrane Handbook for Systematic Reviews of Interventions*, 375–402.

Skoetz N, Goldkuhle M, van Dalen EC, et al. (2020). "GRADE guidelines 27: how to calculate absolute effects for time-to-event outcomes in summary of findings tables and Evidence Profiles." *Journal of Clinical Epidemiology*, **118**, 124–131.

Examples

```
data(anticoagulation)
dis <- sens_br(log(anticoagulation),  br1 = 0.3, br2 = 0.7, dt1 = 20,
  sm = "OR", by = 0.1)
dis
plot(dis, ylim1 = c(0, 100), ylim2 = c(0, 50))
```

---

sens_dt	*Sensitivity analysis (based on decision thresholds) for the Decision Inconsistency and Across-Studies Inconsistency index*

Description

Sensitivity analysis on the Decision Inconsistency index and the Across-Studies Inconsistency index based on a range of decision thresholds distinguishing meaningful versus trivial effects. It is applicable only to meta-analyses with binary outcome data (effect size measures expressed as risk ratios, odds ratios or hazard ratios).

Usage

```
sens_dt(x, br = NULL, min1, max1, min2, max2, sm, by = 1, scale = 1000)

heatplot(x, limits1 = NULL, limits2 = NULL, ...)
```

Arguments

x	An R object created with [getsamples](#) or a matrix containing the samples of the effect sizes of primary studies. Note that log-transformed effect sizes must be provided (e.g., log odds ratios instead of odds ratios).
br	Baseline risk.
min1	A single numeric defining the lowest value for the lower decision threshold. Must be lower than max1, min2 and max2.

max1	A single numeric defining the highest value for the lower decision threshold. Must be higher than min1, but lower than min2 and max2.
min2	A single numeric defining the lowest value for the higher decision threshold. Must be higher than min1 and max1, but lower than max2.
max2	A single numeric defining the highest value for the higher decision threshold. Must be higher than min1, max1 and min2.
sm	A character string indicating the summary measure used in primary studies (either sm = "OR", sm = "RR" or sm = "HR").
by	Increment of the sequences from min1 to max1 and min2 to max2.
scale	The number of people per which absolute decision thresholds are provided (default: 1000, i.e., absolute decision threshold values are defined per 1000 people).
limits1	Limits for the colour range in the heatplot showing the Decision Inconsistency index.
limits2	Limits for the colour range in the heatplot showing the Across-Studies Inconsistency index.
...	Additional graphical arguments (ignored).

Details

Computes the Decision Inconsistency index (DI) and the Across-Studies Inconsistency index (ASI) across a range of decision thresholds distinguishing meaningful vs trivial effects. This function can only be applied to dichotomous outcomes expressed as (log-) odds ratio, risk ratio and hazard ratio. Graphical representations can be obtained using the heatplot function.

Value

A data frame containing

dt1	Lower decision threshold
dt2	Higher decision threshold
ASI	Decision Inconsistency index for each combination of decision thresholds
DI	Across-Studies Inconsistency index for each combination of decision thresholds

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>, Guido Schwarzer <guido.schwarzer@uniklinik-freiburg.de>

References

Schunemann HJ, Higgins JPT, Vist GE, et al. (2019). "Completing 'Summary of findings' tables and grading the certainty of the evidence." *Cochrane Handbook for Systematic Reviews of Interventions*, 375–402.

Skoetz N, Goldkuhle M, van Dalen EC, et al. (2020). "GRADE guidelines 27: how to calculate absolute effects for time-to-event outcomes in summary of findings tables and Evidence Profiles." *Journal of Clinical Epidemiology*, **118**, 124–131.

Examples

```
data(anticoagulation)
dis <- sens_dt(log(anticoagulation),
  br = 0.5, min1 = -20, max1 = -10, min2 = 10, max2 = 20, sm = "or")
#
head(dis)
summary(dis$DI)
summary(dis$ASI)

heatplot(dis)
```

---

sens_inf   *Decision Inconsistency index for individual studies and leave-one out*
                                     sensitivity analysis for inconsistency measures

---

Description

Computation of the Decision Inconsistency index for each individual primary study and leave-one-out sensitivity analysis for the Decision Inconsistency index and the Across-Studies Inconsistency index.

Usage

```
sens_inf(x)

## S3 method for class 'sens_inf'
print(x, ...)

## S3 method for class 'sens_inf'
summary(object, ...)

## S3 method for class 'summary.sens_inf'
print(x, ...)
```

Arguments

x	An R object of class [inc](#).
...	Additional arguments (ignored).
object	An R object of class sens_inf.

Details

Computes the Decision Inconsistency index (DI) for each individual primary study and performs a leave-one-out sensitivity analysis for the DI and for the Across-Studies Inconsistency index. This function takes, as its single argument, an object of the class [inc](#).

Value

This function generates:

di_stud   A data frame containing the Decision Inconsistency index for each individual primary study.

di_asi_sens A data frame containing results of a leave-one-out sensitivity analysis for the Decision Inconsistency index and the Across-Studies Inconsistency index.

Author(s)

Bernardo Sousa-Pinto <bernardo@med.up.pt>

Examples

```
data(anticoagulation)
inc_anticoagulation <-
  inc(log(anticoagulation), dt1 = 16, dt2 = 31, dt3 = 60,
    br = 0.5, sm = "OR")
sens <- sens_inf(inc_anticoagulation)
sens
```

---

subset.inc   *Decision Inconsistency index and Across-Studies Inconsistency index in subsets of studies*

Description

Computation of the Decision Inconsistency index and the Across-Studies Inconsistency index for specific subsets of studies (allowing for subgroup analysis).

Usage

```
## S3 method for class 'inc'
subset(x, data, subset, ...)
```

Arguments

x   An object created with inc.

data   A data frame with the same number of primary studies as those included in the meta-analysis and containing the variables based on which subset analysis is to be performed.

subset   A logical vector to select studies for subset analysis.

...   Additional arguments (ignored).

Details

Computes the Decision Inconsistency index and the Across-Studies Inconsistency index for a subset (subgroup) of studies.

Value

An object of class `inc`.

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Examples

```
data(anticoagulation)
inc_anticoagulation <-
  inc(anticoagulation, dt1 = 16, dt2 = 31, dt3 = 60,
    br = 0.5, sm = "OR", transf = FALSE)
inc_anticoagulation

# Example with subset analysis restricted to studies with a low risk of bias:
data(anticoagulation_df)
subset1_anticoagulation <-
  subset(inc_anticoagulation, anticoagulation_df, RoB == "Low")
subset1_anticoagulation

# Example with subset analysis excluding studies with a high risk of bias
# (resulting in the same subset of studies as no study has "Moderate" RoB):
subset2_anticoagulation <-
  subset(inc_anticoagulation, anticoagulation_df, RoB != "High")
subset2_anticoagulation
```

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