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Description Network meta-analysis tools based on contrast-based approach using the multivariate meta-analysis and meta-regression models (Noma et al. (2023) <Forthcoming>). Standard analysis tools for network meta-analysis and meta-regression (e.g., synthesis analysis, ranking analysis, and creating league table) are available by simple commands. For inconsistency analyses, the local and global inconsistency tests based on the Higgins’ design-by-treatment interaction model can be applied. Also, the side-splitting and the Jackson’s random inconsistency model are available. Standard graphical tools for network meta-analysis (e.g., network plot, ranked forest plot, and transitivity analysis) can also be utilized. For the synthesis analyses, the Noma-Hamura’s improved REML (restricted maximum likelihood)-based methods (Noma et al. (2023) <doi:10.1002/jrsm.1652> <doi:10.1002/jrsm.1651>) are adopted as the default methods.

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- NMA-package: The 'NMA' package.

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**Description**

Network meta-analysis tools based on contrast-based approach using the multivariate meta-analysis and meta-regression models (Noma et al., 2023c). Standard analysis tools for network meta-analysis and meta-regression (e.g., synthesis analysis, ranking analysis, and creating league table) are available by simple commands. For inconsistency analyses, the local and global inconsistency tests based on the Higgins’ design-by-treatment interaction model can be applied. Also, the side-splitting and the Jackson’s random inconsistency model are available. Standard graphical tools for network meta-analysis (e.g., network plot, ranked forest plot, and transitivity analysis) can also be utilized. For the synthesis analyses, the Noma-Hamura’s improved REML (restricted maximum likelihood)-based methods (Noma et al., 2023ab) are adopted as the default methods.
antidiabetic

References


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**Phung et al. (2010)’s network meta-analysis data**

**Description**


- **id**: Study ID
- **t**: Treatment (Placebo, AGI, DPP-4 inhibitor, Glinine, GLP-1 analog, Sulfonylurea, Thiazolidinedione)
- **y**: Mean of the change in HbA1c
- **sd**: Standard deviation of the change in HbA1c
- **n**: Sample size

**Usage**

data(antidiabetic)
**Format**

An arm-based dataset with 20 studies

**References**


**diabetes**

*Elliott and Mayer (2007)’s network meta-analysis data*

**Description**


- **study:** Study ID
- **trt:** Treatment (Diuretic, ACEI (ACE inhibitor), ARB, Beta blocker, CCB (Calcium-channel blocker), Placebo)
- **n:** Sample size
- **d:** Number of events (occurrence of diabetes)

**Usage**

data(diabetes)

**Format**

An arm-based dataset with 22 studies

**References**

Higgins' global inconsistency test

Description

Higgins' global inconsistency test based on the design-by-treatment interaction model. REML-based Wald test for the all possible design-by-treatment interactions on the network is performed.

Usage

global.ict(x)

Arguments

x Output object of setup

Value

Results of the global inconsistency test are presented.

• coding: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
• reference: Reference treatment category.
• number of studies: Number of studies.
• designs: Study designs (combinations of treatments of individual trials) on the network.
• Coefficients of the design-by-treatment interaction model: Regression coefficients estimates and their SEs, 95% confidence intervals and P-values.
• Between-studies SD: Between-studies SD estimate.
• Between-studies COR: Between-studies correlation coefficient estimate (=0.50).
• X2-statistic: Chi-squared statistic of the global inconsistency test.
• df: Degree of freedom.
• P-value: P-value of the global inconsistency test.

References


Examples

data(heartfailure)

hf2 <- setup(study=study,trt=trt,d=d,n=n,measure="OR",ref="Placebo",data=heartfailure)
global.ict(hf2)

Description

A network meta-analysis data from Sciarretta et al. (2011) that compared 7 antihypertensive drug classes and placebo for occurrence of heart failure.

- study: Study ID
- trial: Trial name
- trt: Treatment (AB (Alpha blocker), ACE (ACE inhibitor), ARB, BB (Beta blocker), CCB (Calcium-channel blocker), CT (conventional treatments), Diuretic (DD), Placebo)
- n: Sample size
- d: Number of events (occurrence of heart failure)
- pubyear: Publication year
- SBP: Mean of baseline systolic blood pressure (mmHg)
- DBP: Mean of diastolic systolic blood pressure (mmHg)

Usage

data(heartfailure)

Format

An arm-based dataset with 26 studies

References

**local.ict**

*Local inconsistency tests for all closed loops on the network*

**Description**

Local inconsistency tests for all closed loops on the network are performed. Higgins’ inconsistency test (Generalized Bucher’s test) that assesses the design-by-treatment interactions on the triangle loops are performed and their results are presented.

**Usage**

```r
local.ict(x)
```

**Arguments**

- **x**: Output object of `setup`.

**Value**

Results of the local inconsistency tests for all closed loops on the network are presented.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **reference**: Reference treatment category.
- **N**: Number of studies.
- **tau**: Between-studies SD estimate.
- **X2-statistic**: Chi-squared statistics of the generalized Bucher’s test.
- **df**: Degree of freedom.
- **P-value**: P-value of the generalized Bucher’s test.

**References**


**Examples**

```r
data(heartfailure)
hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
local.ict(hf2)
```
Description

Generating a networkplot. The sizes of the nodes and edges are proportional to the corresponding sample sizes of direct comparisons.

Usage

```r
netplot(x, text=TRUE, col="black", bg="blue", base.lwd=1, base.cex=1)
```

Arguments

- `x`: Output object of `setup`
- `text`: A logical value that specify whether the treatment labels are added
- `col`: Outer circumferential color of the nodes (default: black)
- `bg`: Color of the node (default: blue)
- `base.lwd`: A parameter adjusting edge widths (default: 1)
- `base.cex`: A parameter adjusting node sizes (default: 1)

Value

A networkplot is generated.

Examples

```r
data(heartfailure)
hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
netplot(hf2)  # default color and sizes
netplot(hf2, base.lwd=1.5, base.cex=1.5)  # change the sizes
netplot(hf2, col="red", bg="red")  # change the color
netplot(hf2, text=FALSE)  # without texts
```
Network meta-analysis based on contrast-based approach using the multivariate meta-analysis model

Description

Network meta-analysis based on contrast-based approach using the multivariate random-effects meta-analysis model. The synthesis results and prediction intervals based on the consistency assumption are provided. The ordinary REML method and its improved higher order asymptotic methods (Noma-Hamura methods) are available.

Usage

nma(x, eform=FALSE, method="NH")

Arguments

x Output object of setup
eform A logical value that specify whether the outcome should be transformed by exponential function (default: FALSE)

Value

Results of the network meta-analysis using the multivariate meta-analysis model.

- coding: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- reference: Reference treatment category.
- number of studies: The number of synthesized studies.
- method: The estimation and prediction methods.
- Coef. (vs. treat1): Estimates, their SEs, Wald-type 95% confidence intervals, and P-values for the grand mean parameter vector.
- tau (Between-studies_SD) estimate: Between-studies SD (tau) estimate.
- tau2 (Between-studies_variance) estimate: Between-studies variance (tau^2) estimate.
- Multivariate H2-statistic: Jackson’s multivariate H2-statistic.
- Multivariate I2-statistic: Jackson’s multivariate I2-statistic.
- Test for Heterogeneity: Multivariate Q-statistic and P-value of the test for heterogeneity.
- 95%PI: 95% prediction intervals.
References


Examples

```r
data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
hf3 <- setup(study=study, trt=trt, d=d, n=n, measure="RR", ref="Placebo", data=heartfailure)
hf4 <- setup(study=study, trt=trt, d=d, n=n, measure="RD", ref="Placebo", data=heartfailure)

nma(hf2, eform=TRUE)
nma(hf3, eform=TRUE)
nma(hf4)
```

---

**nmaforest**

*Generating a ranked forest plot for the synthesis results of network meta-analysis*

Description

A ranked forest plot for the synthesis results of network meta-analysis is generated based on the *forestplot* package by simple command. Details of the forestplot is customized by using the output objects of *obj.forest* function; see also help(*obj.forest*).

Usage

```r
nmaforest(x, method="NH", col.plot="black", digits=3, ascending=TRUE)
```

Arguments

- `x`: Output object of setup
col.plot  | Color of the confidence interval plot (default: black)
digits   | Number of decimal places
ascending | Type of order. Default is ascending order, but it can be changed to descending order changing to FALSE.

Value

A ranked forest plot for the synthesis results of network meta-analysis is generated.

Examples

data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
nmaforest(hf2) # Default setting
nmaforest(hf2, col.plot="blue") # Change the color
nmaforest(hf2, ascending=FALSE) # Change to the descending order

nmafunnel  

Comparison-adjusted funnel plot

Description

A comparison-adjusted funnel plot for the studies involving treatment 1 (reference treatment specified in setup) is generated.

Usage

nmafunnel(x, method="NH", legends="topright")

Arguments

x  | Output object of setup
legends | Location of the legend on the plot (default: topright)

Value

Comparison-adjusted funnel plot for the studies involving treatment 1 (reference treatment specified in setup) is presented.

• coding: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
• summary: design: design of studies, N: number of the corresponding studies, n: total sample size.
References


Examples

```r
data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
hf4 <- setup(study=study, trt=trt, d=d, n=n, measure="RD", ref="Placebo", data=heartfailure)

nmafunnel(hf2, legends="bottomright")
nmafunnel(hf4)
```

Generating a league table

Description

A league table is generated for all possible pairs of the treatments. The league table can be outputted as a CSV file through setting `out.csv="filename"`.

Usage

```
nmaleague(x, method="NH", eform=FALSE, digits=3, PI=FALSE, out.csv=NULL)
```

Arguments

- **x**: Output object of `setup`.
- **eform**: A logical value that specify whether the outcome should be transformed by exponential function (default: `FALSE`)
- **digits**: Number of decimal places
- **PI**: A logical value that specify whether the inference or prediction results are provided
- **out.csv**: A character object that specify a filename if the user wants to output the league table as a CSV file (e.g., `out.csv="out_league.csv"`).

Value

A league table is generated.
References


Examples

data(smoking)

smk2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="A", data=smoking)
nmaleague(smk2) # default setting
nmaleague(smk2, eform=TRUE) # transformed to exponential-scale
nmaleague(smk2, eform=TRUE, digits=2) # digits can be changed
nmaleague(smk2, eform=TRUE, PI=TRUE) # prediction intervals

---

**nmaQ**  
*Multivariate Q-statistic and its factorization*

**Description**

Multivariate Q-statistic and its factorized versions (within and between designs) are presented. P-values of the corresponding Q-tests are also presented.

**Usage**

nmaQ(x)

**Arguments**

- **x**  
  Output object of setup

**Value**

Multivariate Q-statistic and its factorized ones (within and between designs) are presented.

- *coding*: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- *number of studies*: The number of synthesized studies.
Within designs (individual designs): Q-statistics for individual designs and their P-values.

- Q-statistics: Multivariate Q-statistics and its factorized ones (within and between designs), and their P-values.

References


Examples

data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
nmaQ(hf2)

nmarank

Calculating ranking statistics of network meta-analysis

Description

Ranking statistics of network meta-analysis such as SUCRA, MEANRANK, and probability of ranking are calculated by parametric bootstrap.

Usage

nmarank(x, B=20000, method="NH", ascending=TRUE)

Arguments

- **x**: Output object of setup
- **B**: Number of parametric bootstrap resampling (default: 20000)
- **ascending**: A logical value that specify whether the ranking is defined by ascending or descending order.
Value

Results of the ranking statistics of network meta-analysis are provided. Also, ranking probability plots are generated.

- **SUCRA**: SUCRA estimates of individual treatment by parametric bootstrap.
- **MEANRANK**: Mean rank estimates of individual treatment by parametric bootstrap.
- **Probability of ranking**: Probability of ranking (best, 2nd, 3rd,..., worst) estimates of individual treatment by parametric bootstrap.

References


Examples

data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
nmarank(hf2)
nmarank(hf2, ascending=FALSE)

---

**nmareg**

*Network meta-regression based on contrast-based approach*

Description

Network meta-regression based on contrast-based approach using the multivariate meta-regression model. Effect modifications by study-level covariates (specified in the `setup` function) can be assessed. In many network meta-analysis, some treatment contrasts involve only 1 or 2 (or 0) direct comparisons, and the regression coefficients of the corresponding outcomes cannot be validly estimated (non-identifiable). Thus, the `nmareg` function can specify a subset of outcome variables to be modelled by the regression model (to be assessed the effect modifications) by `treats`. Currently, the parameter estimation is performed by the ordinary REML method.

Usage

`nmareg(x, z, treats)`

Arguments

- **x**: Output object of `setup`.
- **z**: Covariate name vector.
- **treats**: A vector that specifies treatments to be assessed effect modifications that correspond to the elements of outcome vectors `y` in `x` (please specify the treatment numbers of coding; multiple outcomes can be specified jointly, as a vector).
Results of the network meta-regression analysis are presented.

- **Coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **Covariates**: Covariate that specified in setup.
- **Outcome evaluated the effect modifications**: Treatment contrasts that the effect modifications are evaluated.
- **Coefficients**: Estimates, their SEs, Wald-type 95% confidence intervals, and P-values for the regression parameters (cons: intercept, beta: regression coefficient for the explanatory variable).
- **Between-studies_SD**: Between-studies SD (tau) estimate.
- **Between-studies_COR**: Between-studies correlation coefficient (should be 0.50).

### References


### Examples

```r
data(heartfailure)

hf2 <- setup(study=study,trt=trt,d=d,n=n,z=c(SBP,DBP,pubyear),measure="OR", ref="Placebo",data=heartfailure)
nmaweight(hf2,z=SBP,treats=3)
nmaweight(hf2,z=c(SBP,DBP),treats=c(3,4,6))
```

### Description

Contribution weight matrices to assess how individual studies influence the synthesized results are presented. Jackson et al. (2017) and Noma et al. (2017) showed the contribution rates are estimated by the factorized information, and the contribution weight matrices are calculated through the factorized information.
**Usage**

\[ \text{nmaweight}(x) \]

**Arguments**

- **x**: Output object of `setup`

**Value**

Contribution weight matrices for the consistency model are presented. Also, a heatmap for the contribution matrix of overall evidence is presented.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **Contribution of direct and indirect information**: Contribution rates of direct and indirect evidence for individual treatment pairs.
- **Contribution weights: Direct comparison**: Contribution weight matrix for direct evidence.
- **Contribution weights: Indirect comparison (BoS)**: Contribution weight matrix for indirect evidence (BoS; borrowing of strength of Jackson et al. (2017)).
- **Contribution weights: Overall evidence**: Contribution weight matrix for overall evidence.

**References**


**Examples**

```r
data(smoking)
smk2 <- setup(study=study,trt=trt,d=d,n=n,measure="OR",ref="A",data=smoking)
nmaweight(smk2)
```

**Description**

Numerical objects of ranked forest plot for the synthesis results of network meta-analysis are generated. These objects can be used to make a customized forest plot using `forestplot` function of `forestplot` package.
Usage

```r
obj.forest(x, method="NH", digits=3, ascending=TRUE)
```

Arguments

- **x**: Output object of `setup`
- **digits**: Number of decimal places
- **ascending**: Type of order. Default is ascending order, but it can be changed to descending order changing to `FALSE`.

Value

Numerical objects of ranked forest plot is generated. They can be used for `forestplot` function of `forestplot` package to make a customized ranked forest plot.

- **labeltext**: A matrix that presents the label text table of the forestplot.
- **coef**: A matrix that presents the point estimates and confidence limits.
- **boxsize**: A vector that indicates the boxsizes.

Examples

```r
data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)

obj.forest(hf2)
```

Description

Pairwise meta-analyses for all treatment pairs with direct comparisons on the network are performed. The synthesis analyses are performed by `rma` and `regtest` in `metafor` package.

Usage

```r
pairwise(x, method="REML")
```

Arguments

- **x**: Output object of `setup`
- **method**: Method of the estimation of pairwise meta-analysis. All possible options of `rma` function in `metafor` package is available (default: REML).
**Value**

Results of the meta-analyses for all possible treatment pairs are presented.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **measure**: Outcome measure.
- **Summary effect measures**: N (number of studies), summary estimates, 95% confidence intervals, and P-values for all possible pairs.
- **Heterogeneity measures**: N (number of studies), tau2 (heterogeneity variance) estimate, I2-statistic, and H2-statistic.
- **Egger test**: N (number of studies), P-value of the Egger test for assessing publication bias.

**References**


**Examples**

```r
data(heartfailure)

hf2 <- setup(study=study,trt=trt,d=d,n=n,measure="OR",ref="Placebo",data=heartfailure)
pairwise(hf2)
```

---

**random.icm**

*Jackson's random inconsistency model*

**Description**

Jackson’s random inconsistency model for modelling the design-by-treatment interactions. Model-based testing results for heterogeneity and inconsistency (design-by-treatment interactions) and the I2-statistics are presented.

**Usage**

`random.icm(x)`
Arguments

x Output object of setup

Value

Results of the analysis of Jackson’s random inconsistency model and I2-statistics are presented.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **reference**: Reference treatment category.
- **number of studies**: Number of studies.
- **number of designs**: Number of designs.
- **designs**: Study designs (combinations of treatments of individual trials) on the network.
- **Coef. (vs. treat 1)**: Regression coefficients estimates and their SEs, 95% confidence intervals and P-values.
- **Between-studies_SD**: Between-studies SD estimate.
- **Between-designs_SD**: Between-designs SD estimate.
- **Likelihood ratio tests for the variance components**: Results of the likelihood ratio tests for comparing (1) the fixed- and random-effects models without inconsistency effects (heterogeneity), (2) the random-effects models with and without inconsistency effects (inconsistency), and (3) the fixed-effect model without inconsistency effects and the random-effects model with inconsistency effects (heterogeneity + inconsistency).
- **Heterogeneity and inconsistency statistics**: R-statistics and I2-statistics for comparing (1) the fixed- and random-effects models without inconsistency effects (heterogeneity), (2) the random-effects models with and without inconsistency effects (inconsistency), and (3) the fixed-effect model without inconsistency effects and the random-effects model with inconsistency effects (heterogeneity + inconsistency).

References


Examples

data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, measure="OR", ref="Placebo", data=heartfailure)
random.icm(hf2)

rdc

Rounding a numerical value

Description

A function that returns a rounded value as a character.

Usage

rdc(a, digits)

Arguments

a
A numerical value to be rounded

digits
Number of decimal places

Value

The rounded value is returned as a character.

Examples

rdc(2.412, 3)
rdc(2.41, 3)
rdc(2.4, 3)
rdc(2, 3)

rdc(-2.41, 3)
rdc(-2.4, 3)
rdc(-2, 3)

rdc(0, 3)
Description

A setup function to generate R objects that can be used for network meta-analysis. Users should prepare arm-level datasets, and the setup function transforms the arm-level data to the contrast-based summary statistics. Both of dichotomous and continuous outcomes can be treated. The type of outcome variable can be specified by the measure. If the measure is specified as OR, RR or RD, the outcome should be dichotomous, and d and n are needed to compute the summary statistics. Besides, if the measure is specified as MD or SMD, the outcome should be continuous, and m, s and n are needed to compute the summary statistics. Also, if the measure is specified as HR, the outcome should be survival (time-to-event), and d and n are needed to compute the summary statistics. Note HR corresponds to rate-ratio in ordinary sense and this option corresponds to the person-time analysis; hazard ratio accords to rate-ratio if the survival time distribution is exponential distribution. Several covariates can be involved as z for network meta-regression analysis (nmareg) and transitivity analysis (transitivity).

Usage

setup(study, trt, d, n, m, s, z, measure, ref, data)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>Study ID</td>
</tr>
<tr>
<td>trt</td>
<td>Treatment variable. It can be formed as both of numbered treatment (=1,2,...) and characters (e.g., &quot;Placebo&quot;, &quot;ARB&quot;, &quot;Beta blocker&quot;).</td>
</tr>
<tr>
<td>d</td>
<td>Number of events (for dichotomous outcome and survival outcome).</td>
</tr>
<tr>
<td>n</td>
<td>Sample size (for dichotomous and continuous outcome) or total person-time at risk (for survival outcome).</td>
</tr>
<tr>
<td>m</td>
<td>Mean of the outcome variable (for continuous outcome).</td>
</tr>
<tr>
<td>s</td>
<td>Standard deviation of the outcome variable (for continuous outcome).</td>
</tr>
<tr>
<td>z</td>
<td>Covariate name vector to be used for network meta-regression analysis or transitivity analysis (optional).</td>
</tr>
<tr>
<td>measure</td>
<td>Outcome measure (can be OR (odds ratio), RR (risk ratio), and RD (risk difference) for dichotomous outcome, MD (mean difference) and SMD (standardized mean difference) for continuous outcome, and HR (hazard ratio) for survival outcome.</td>
</tr>
<tr>
<td>ref</td>
<td>Reference treatment category that should be involved in trt.</td>
</tr>
<tr>
<td>data</td>
<td>A data frame that involves the arm-based data.</td>
</tr>
</tbody>
</table>
Value

Contrast-based summary statistics are generated.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **reference**: Reference treatment category.
- **measure**: Outcome measure.
- **covariate**: Covariate name(s).
- **N**: The number of study.
- **p**: The dimension of the contrast-based statistics.
- **df**: The degree of freedom.
- **study**: The ID variable that specifies studies.
- **trt**: The original vector that specifies treatment categories.
- **treat**: A numerical vector that specifies treatment categories based on the coding table.
- **d**: The original vector that specifies number of events.
- **n**: The original vector that specifies sample sizes.
- **m**: The original vector that specifies means.
- **s**: The original vector that specifies standard deviations.
- **Z**: The data frame that specifies covariates matrix (design matrix).
- **y**: Contrast-based summary estimates.
- **S**: Vectored within-study covariance matrix.

References


Examples

data(heartfailure)

hf2 <- setup(study=study,trt=trt,d=d,n=n,measure="OR",ref="Placebo",data=heartfailure)
hf3 <- setup(study=study,trt=trt,d=d,n=n,measure="RR",ref="Placebo",data=heartfailure)
hf4 <- setup(study=study,trt=trt,d=d,n=n,measure="RD",ref="Placebo",data=heartfailure)

hf5 <- setup(study=study,trt=trt,d=d,n=n,z=c(SBP,DBP,pubyear),measure="OR",ref="Placebo",data=heartfailure)

data(antidiabetic)

ad2 <- setup(study=id,trt=t,m=y,s=sd,n=n,measure="MD",ref="Placebo",data=antidiabetic)
ad3 <- setup(study=id,trt=t,m=y,s=sd,n=n,measure="SMD",ref="Placebo",data=antidiabetic)
sidesplit

Sidesplitting for quantifying direct and indirect evidence for all possible treatment pairs and the inconsistency test

Description

Noma’s sidesplitting for quantifying direct and indirect evidence for all possible treatment pairs based on network meta-regression and the inconsistency tests are performed. For the bias correction that causes the involvement of multi-arm trials, we adopted the adjustment method of Noma et al. (2017) and Noma (2023).

Usage

sidesplit(x)

Arguments

x

Output object of setup

Value

Results of the sidesplitting for all possible treatment pairs are presented.

- coding: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- reference: Reference treatment category.
- Direct evidence: Summary estimates, SEs, 95% confidence intervals, and P-values for the direct evidence.
- Indirect evidence: Summary estimates, SEs, 95% confidence intervals, and P-values for the indirect evidence.
- Difference: Differences of the summary estimates of direct and indirect evidence, and their inconsistency tests.

References


Examples

data(smoking)

smk2 <- setup(study=study,trt=trt,d=d,n=n,measure="OR",ref="A",data=smoking)

sidesplit(smk2)
**Smoking cessation data**

**Description**

A network meta-analysis data for smoking cessation from Lu and Ades (2006) and Higgins et al. (2012).

- **study**: Study ID.
- **trt**: A character variable that indicates the type of intervention, A: No contact, B: Self help, C: Individual counselling, D: Group counselling.
- **n**: Number of participants of the intervention.
- **d**: Number of successes of the intervention.

**Usage**

data(smoking)

**Format**

An arm-based dataset with 24 studies.

**References**


**Description**

To check transitivity on the network, summary statistics of a certain covariate among different study designs are presented. Also, a summary plot for these statistics is presented.

**Usage**

transitivity(x, z, gcol="blue", yrange)
Arguments

- **x**: Output object of setup
- **z**: Covariate name for assessing transitivity (must be involved in covariate of the output object of setup)
- **gcol**: Color of the plot
- **yrange**: Range of y-axis of the plot

Value

Summary statistics of the covariate among different study designs and its summary plot are presented.

- **coding**: A table that presents the correspondence between the numerical code and treatment categories (the reference category is coded as 1).
- **covariate**: Covariate that specified in setup.

References


Examples

data(heartfailure)

hf2 <- setup(study=study, trt=trt, d=d, n=n, z=c(SBP, DBP, pubyear), measure="OR", ref="Placebo", data=heartfailure)

transitivity(hf2, SBP)
transitivity(hf2, DBP)
transitivity(hf2, pubyear)
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