Package 'aides'

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Type Package

Title Additive Information & Details of Evidence Synthesis

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Description A supportive collection of functions for pooled analysis of aggregate data. The current version supports users to test assumptions before relevant analysis of bias from study size and sequential analysis such as mentioned by Wetterslev, J., Jakobsen, J. C., & Gluud, C. (2017) <doi:10.1186/s12874-017-0315-7>.

License GPL (>= 3)

Depends R (>= 4.2.0)

Imports boot, graphics, grDevices, meta, stats, utils

Suggests bookdown, DiagrammeR, knitr, rmarkdown, testthat (>= 3.0.0)

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R topics documented:

`aides-package` *aides: Additive Information & Details of Evidence Synthesis*

Description

aides, an R package, has been proposed to be a useful collection of functions designed to offer supplementary information and intricacies in data synthesis and evidence evaluation. Essentially, package *aides* serves as an aiding toolkit for pooled analysis of aggregated data, crafted with a vision to support a more inclusive and informed approach to evidence-based decision-making; and it is developed with values on flexibility, ease of use, and comprehensibility. Package *aides* will be updated with advances of methodology of data synthesis and evidence evaluation. The initial goals are to simplify analysis process for both professionals and public users, and to support them in navigating the complexities of synthesized evidence. Long-term goal of package *aides* is to support knowledge translation and decision-making based on the obtained information with comprehensive understanding of the evidence.

Package *aides* is currently is developed using **R version 4.2.2 (2022-10-31 ucrt)**. Extra imported packages are as follows:

- *boot* (version 1.3-28)
- *metafor* (version 4.4-0)
- *meta* (version 7.0-0)

Details

Current version consists of eight functions, including four functions for examining fundamental assumptions before test of small-study effects (i.e. function `PlotDistrSS`, `TestDisparity`, `PlotDisparity`, and `TestDiscordance`) and four functions for performing sequential-method-related analyses (i.e. `DoSA`, `DoOSA`, `PlotOSA`, and `PlotPower`).

`DoOSA` *Observed sequential analysis.*

Description

DoOSA() is a function for conducting observed sequential analysis.

Usage

```
DoOSA(
  data = NULL,
  source = NULL,
  time = NULL,
  n = NULL,
  es = NULL,
  se = NULL,
  r1 = NULL,
  m1 = NULL,
  sd1 = NULL,
  n1 = NULL,
  r2 = NULL,
  m2 = NULL,
  sd2 = NULL,
  n2 = NULL,
  group = c("Group 1", "Group 2"),
  ref = 2,
  prefer = "small",
  measure = "ES",
  model = "random",
  method = "DL",
  pooling = "IV",
  trnsfrm = "logit",
  poolProp = "IV",
  alpha = 0.05,
  beta = 0.2,
  anchor = NULL,
  adjust = "D2",
  plot = FALSE,
  SAP = FALSE
)
```

Arguments

data	DATAFRAME consists of relevant information.
source	CHARACTER for labeling the included data sets.
time	NUMERIC values of time sequence.
n	INTEGER values of sample sizes.
es	NUMERIC values of effect sizes.
se	NUMERIC values of standard errors for the effect sizes.
r1	INTEGER values of observed events in group 1 in the included data.
m1	NUMERIC values of estimated means in group 1 in the included data.
sd1	NUMERIC values of standard deviations in group 1 in the included data.
n1	INTEGER values of sample sizes in group 1 in the included data.

r2	INTEGER values of observed events in group 2 in the included data.
m2	NUMERIC values of estimated means in group 2 in the included data.
sd2	NUMERIC values of standard deviations in group 2 in the included data.
n2	INTEGER values of sample sizes in group 2 in the included data.
group	CHARACTER for labeling two groups.
ref	NUMERIC values of 1 or 2 for indicating group 1 or 2 as reference.
prefer	CHARACTER of "small" and "large" for indicating which direction is beneficial effect in statistic test.
measure	CHARACTER for indicating which statistic measure should be used.
model	CHARACTER of "random" and "fixed" for indicating whether to use random-effects model or fixed-effect model.
method	CHARACTER for indicating which estimator should be used in random-effects model. In addition to the default "DL" method, the current version also supports "REML" and "PM" methods for calculating heterogeneity estimator.
pooling	CHARACTER for indicating which method has to be used for pooling binary data. Current version consists of "IV" and "MH" for binary data pooling.
trnsfrm	CHARACTER for indicating which method for transforming pooled proportion. Current version supports "none", "logit", "log", "arcsine", and "DAT" for the transformation.
poolProp	CHARACTER for indicating which method has to be used for pooling proportion. Current version supports "IV" and "GLMM" for the data pooling.
alpha	NUMERIC value between 0 to 1 for indicating the assumed type I error.
beta	NUMERIC value between 0 to 1 for indicating the assumed type II error.
anchor	NUMERIC value for indicating the presumed meaningful effect based on anchor-based approach.
adjust	CHARACTER for indicating how to adjust optimal information size. Current version consists of "none", "D2", "I2", "CHL", "CHM", and "CHH" for the adjustment.
plot	LOGIC value for indicating whether to illustrate alpha-spending monitoring plot.
SAP	LOGIC value for indicating whether to show sequential-adjusted power.

Details

1. Basic information for the function **DoOSA()**: **DoOSA()** supports observed sequential analysis of aggregate data synthesis based on head-to-head comparison using either binary or continuous data in each group. Minimum information for the function **DoOSA()** encompasses a data set of study-level data, and time sequence. Operative points of using function **DoOSA()** are listed below:

1.1. Parameter `data` should be used for assigning a data set.

1.2. Study-level data have to be assigned according to outcome type:

1.2.1. **For dichotomous outcome**: Parameter `n1` and `n2` should be defined with parameter `r1` and `r2`.

1.2.2. **For continuous outcome**: parameter `n1` and `n2` should be defined with parameter `m1`, `sd1`, `m2`, `sd2`.

1.3. Parameter `source` and `time` are required for doing observed sequential analysis. Other parameters are auxiliary.

1. Default in the function **DoOSA()** Certain defaults have been elucidated in the introductory section about the parameters, but some of them need to be elaborated upon due to their complexity.

2.1. Default on the parameter `measure` is `"ES"` that automatically uses risk ratio ("RR") for binary outcome and mean difference ("MD") for continuous outcome respectively. Argument `"OR"` and `"SMD"` can be used for the parameter `measure` when original analysis pools data based on odds ratio or standardized mean difference.

2.2. Default on the parameter `method` is `"DL"` for applying DerSimonian-Laird heterogeneity estimator in the original pooled analysis. Other eligible arguments for the parameter are `"REML"` for restricted maximum-likelihood estimator, `"PM"` for Paule-Mandel estimator, `"ML"` for maximum-likelihood estimator, `"HS"` for Hunter-Schmidt estimator, `"SJ"` for Sidik-Jonkman estimator, `"HE"` for Hedges estimator, and `"EB"` for empirical Bayes estimator.

2.3. Default on the parameter `pooling` is `"IV"` for applying inverse variance weighting method. Other commonly-used and eligible arguments for the parameter are `"MH"` for Mantel-Haenszel method and `"Peto"` for pooling data using Peto method. The arguments `"MH"` and `"Peto"` are exclusively available for binary outcomes, while the argument `"IV"` will be automatically applied in the case of continuous outcomes.

2.4. Default on the parameter `adjust` is `"D2"` for adjusting optimal information size (OIS) based on diversity (D-squared statistics). Other eligible arguments for the parameter are `"None"` for the OIS without adjustment, `"I2"` for adjusted OIS based on I-squared statistics, `"CHL"` for adjusted OIS based on low heterogeneity by multiplying 1.33, `"CHM"` for adjusted OIS by multiplying 2 due to moderate heterogeneity, and `"CHL"` for adjusted OIS by multiplying 4 due to high heterogeneity.

Value

DoOSA() returns a summary on the result of sequential analysis, and can be stored as an object in `DoOSA` class. Explanations of returned information are listed as follows:

`studies`	Numbers of studies included in the sequential analysis.
`AIS`	Acquired information size refers to the total sample size in the sequential analysis.
`alpha`	A numeric value of type I error for the sequential analysis.
`beta`	A numeric value of type II error for the sequential analysis.
`OES`	A numeric value of observed effect size of meta-analysis.
`variance`	A numeric value of variance of meta-analysis.
`diversity`	A numeric value to show diversity in the pooled analysis.
`AF`	A numeric value of adjustment factor.
`OIS.org`	A numeric value for optimal information size without adjustment.
`OIS.adj`	A numeric value for optimal information size with adjustment.

frctn	A vector of fraction of each study included in the sequential analysis.
weight	A vector of weight of each study included in the sequential analysis.
es.cum	A vector of cumulative effect size in the sequential analysis.
se.cum	A vector of standard error for the cumulative effect size in the sequential analysis.
zval.cum	A vector of cumulative z-value in the sequential analysis.
asb	A data frame of alpha-spending values for each study.
aslb	A numeric value for lower alpha-spending boundary.
asub	A numeric value for upper alpha-spending boundary.

Author(s)

Enoch Kang

References

Jennison, C., & Turnbull, B. W. (2005). Meta-analyses and adaptive group sequential designs in the clinical development process. **Journal of biopharmaceutical statistics**, *15(4)*, 537–558. https://doi.org/10.1081/BIP-200062273.

Revicki, D., Hays, R. D., Cella, D., & Sloan, J. (2008). Recommended methods for determining responsiveness and minimally important differences for patient-reported outcomes. **Journal of clinical epidemiology**, *61(2)*, 102-109. https://doi.org/10.1016/j.jclinepi.2007.03.012.

Wetterslev, J., Jakobsen, J. C., & Gluud, C. (2017). Trial sequential analysis in systematic reviews with meta-analysis. **BMC medical research methodology**, *17(1)*, 1-18.

NCSS Statistical Software (2023). **Group-sequential analysis for two proportions**. In *PASS Documentation*. Available online: https://www.ncss.com/wp-content/themes/ncss/pdf/Procedures/NCSS/Group-Sequential_Analysis_for_Two_Proportions.pdf

See Also

DoSA, PlotOSA, PlotPower

Examples

```
## Not run:
# 1. Import a dataset of study by Fleiss (1993)
library(meta)
data("Fleiss1993bin")

# 2. Perform observed sequential analysis
output <- DoOSA(Fleiss1993bin, study, year,
                r1 = d.asp, n1 = n.asp,
                r2 = d.plac, n2 = n.plac,
                measure = "RR",
                group = c("Aspirin", "Control"))

## End(Not run)
```

DoSA *Sequential analysis.*

Description

DoSA() is a function for conducting sequential analysis.

Usage

```
DoSA(
  data = NULL,
  source = NULL,
  time = NULL,
  n = NULL,
  es = NULL,
  se = NULL,
  r1 = NULL,
  m1 = NULL,
  sd1 = NULL,
  n1 = NULL,
  r2 = NULL,
  m2 = NULL,
  sd2 = NULL,
  n2 = NULL,
  group = c("Group 1", "Group 2"),
  ref = 2,
  prefer = "small",
  measure = "ES",
  model = "random",
  method = "DL",
  pooling = "IV",
  trnsfrm = "logit",
  poolProp = "IV",
  alpha = 0.05,
  beta = 0.2,
  PES = NULL,
  RRR = NULL,
  PV = "post-hoc",
  adjust = "D2",
  plot = FALSE,
  id = FALSE,
  invert = FALSE,
  smooth = FALSE,
  SAP = FALSE,
  BSB = FALSE
)
```

Arguments

data	DATAFRAME consists of relevant information.
source	CHARACTER for labeling the included data sets.
time	NUMERIC values of time sequence.
n	INTEGER values of sample sizes.
es	NUMERIC values of effect sizes.
se	NUMERIC values of standard errors for the effect sizes.
r1	INTEGER values of observed events in group 1 in the included data.
m1	NUMERIC values of estimated means in group 1 in the included data.
sd1	NUMERIC values of standard deviations in group 1 in the included data.
n1	INTEGER values of sample sizes in group 1 in the included data.
r2	INTEGER values of observed events in group 2 in the included data.
m2	NUMERIC values of estimated means in group 2 in the included data.
sd2	NUMERIC values of standard deviations in group 2 in the included data.
n2	INTEGER values of sample sizes in group 2 in the included data.
group	CHARACTER for labeling two groups.
ref	NUMERIC values of 1 or 2 for indicating group 1 or 2 as reference.
prefer	CHARACTER of "small" and "large" for indicating which direction is beneficial effect in statistic test.
measure	CHARACTER for indicating which statistic measure should be used.
model	CHARACTER of "random" and "fixed" for indicating whether to use random-effects model or fixed-effect model.
method	CHARACTER for indicating which estimator should be used in random-effects model. In addition to the default "DL" method, the current version also supports "REML" and "PM" methods for calculating heterogeneity estimator.
pooling	CHARACTER for indicating which method has to be used for pooling binary data. Besides, current version also supports "MH" and "Peto" for binary data pooling.
trnsfrm	CHARACTER for indicating which method for transforming pooled proportion. Current version supports "none", "logit", "log", "arcsine", and "DAT" for the transformation.
poolProp	CHARACTER for indicating which method has to be used for pooling proportion. Current version supports "IV" and "GLMM" for the data pooling.
alpha	NUMERIC value between 0 to 1 for indicating the assumed type I error.
beta	NUMERIC value between 0 to 1 for indicating the assumed type II error.
PES	NUMERIC value for indicating the presumed meaningful effect size.
RRR	NUMERIC value between 0 and 1 for indicating the presumed relative risk reduction. This parameter only works for dichotomous outcome by replacing parameter PES.

PV	NUMERIC value for indicating the presumed variance of the meaningful effect size. Current version allows a numeric value, "post-hoc", and "PES" based on different considerations.
adjust	CHARACTER for indicating how to adjust optimal information size. Current version consists of "none", "D2", "I2", "CHL", "CHM", and "CHH" for the adjustment.
plot	LOGIC value for indicating whether to illustrate alpha-spending monitoring plot.
id	LOGIC value for indicating whether to label each data source.
invert	LOGIC value for indicating whether to invert plot.
smooth	LOGIC value for indicating whether to smooth error boundaries.
SAP	LOGIC value for indicating whether to show sequential-adjusted power.
BSB	LOGIC value for indicating whether to illustrate beta-spending boundaries.

Details

1. Basic information for the function **DoSA()**: **DoSA()** supports sequential analysis of aggregate data synthesis based on head-to-head comparison using either binary or continuous data in each group. Minimum information for the function **DoSA()** encompasses a data set of study-level data, and information for analysis settings in terms of time sequence, presumed meaningful effect size, and presumed variance of the meaningful effect size. Operative points of using function **DoSA()** are listed below:

1.1. Parameter `data` should be used for assigning a data set. 1.2. Study-level data have to be assigned according to outcome type: 1.2.1. **For dichotomous outcome**: Parameter `n1` and `n2` should be defined with parameter `r1` and `r2`. 1.2.2. **For continuous outcome**: parameter `n1` and `n2` should be defined with parameter `m1`, `sd1`, `m2`, `sd2`. 1.3. Parameter `source`, `time`, `PES`, and `PV` are required for conducting sequential analysis. Other parameters are auxiliary.

1. Default in the function **DoSA()** Certain defaults have been elucidated in the introductory section about the parameters, but some of them need to be elaborated upon due to their complexity.

2.1. Default on the parameter `measure` is `"ES"` that automatically uses risk ratio ("RR") for binary outcome and mean difference ("MD") for continuous outcome respectively. Argument `"OR"` and `"SMD"` can be used for the parameter `measure` when original analysis pools data based on odds ratio or standardized mean difference.

2.2. Default on the parameter `method` is `"DL"` for applying DerSimonian-Laird heterogeneity estimator in the original pooled analysis. Other eligible arguments for the parameter are `"REML"` for restricted maximum-likelihood estimator, `"PM"` for Paule-Mandel estimator, `"ML"` for maximum-likelihood estimator, `"HS"` for Hunter-Schmidt estimator, `"SJ"` for Sidik-Jonkman estimator, `"HE"` for Hedges estimator, and `"EB"` for empirical Bayes estimator.

2.3. Default on the parameter `pooling` is `"IV"` for applying inverse variance weighting method. Other commonly-used and eligible arguments for the parameter are `"MH"` for Mantel-Haenszel method and `"Peto"` for pooling data using Peto method. The arguments `"MH"` and `"Peto"` are exclusively available for binary outcomes, while the argument `"IV"` will be automatically applied in the case of continuous outcomes.

2.4. Default on the parameter adjust is "D2" for adjusting required information size (RIS) based on diversity (D-squared statistics). Other eligible arguments for the parameter are "None" for the RIS without adjustment, "I2" for adjusted RIS based on I-squared statistics, "CHL" for adjusted RIS based on low heterogeneity by multiplying 1.33, "CHM" for adjusted RIS by multiplying 2 due to moderate heterogeneity, and "CHL" for adjusted RIS by multiplying 4 due to high heterogeneity.

Value

DoSA() returns a summary on the result of sequential analysis, and can be stored as an object in DoSA class. Explanations of returned information are listed as follows:

studies	Numbers of studies included in the sequential analysis.
AIS	Acquired information size refers to the total sample size in the sequential analysis.
alpha	A numeric value of type I error for the sequential analysis.
beta	A numeric value of type II error for the sequential analysis.
PES	A numeric value of presumed meaningful effect size for the sequential analysis.
RRR	A numeric value of relative risk reduction.
variance	A numeric value of presumed variance of the meaningful effect size for the sequential analysis.
diversity	A numeric value to show diversity in the pooled analysis.
AF	A numeric value of adjustment factor.
RIS.org	A numeric value for required information size without adjustment.
RIS.adj	A numeric value for adjusted required information size.
frctn	A vector of fraction of each study included in the sequential analysis.
weight	A vector of weight of each study included in the sequential analysis.
es.cum	A vector of cumulative effect size in the sequential analysis.
se.cum	A vector of standard error for the cumulative effect size in the sequential analysis.
zval.cum	A vector of cumulative z-value in the sequential analysis.
asb	A data frame of alpha-spending values for each study.
aslb	A numeric value for lower alpha-spending boundary.
asub	A numeric value for upper alpha-spending boundary.

Author(s)

Enoch Kang

References

Jennison, C., & Turnbull, B. W. (2005). Meta-analyses and adaptive group sequential designs in the clinical development process. **Journal of biopharmaceutical statistics**, *15(4)*, 537–558. https://doi.org/10.1081/BIP-200062273.

Wetterslev, J., Jakobsen, J. C., & Gluud, C. (2017). Trial sequential analysis in systematic reviews with meta-analysis. **BMC medical research methodology**, *17(1)*, 1-18.

NCSS Statistical Software (2023). **Group-sequential analysis for two proportions**. In *PASS Documentation*. Available online: https://www.ncss.com/wp-content/themes/ncss/pdf/Procedures/NCSS/Group-Sequential_Analysis_for_Two_Proportions.pdf

See Also

DoOSA, PlotOSA, PlotPower

Examples

```
## Not run:
# 1. Import a dataset of study by Fleiss (1993)
library(meta)
data("Fleiss1993bin")

# 2. Perform observed sequential analysis
output <- DoSA(Fleiss1993bin, study, year,
               r1 = d.asp, n1 = n.asp,
               r2 = d.plac, n2 = n.plac,
               measure = "RR",
               PES = 0.05,
               RRR = 0.2,
               group = c("Aspirin", "Control"))

## End(Not run)
```

PlotDisparity *Illustrate disparity plot.*

Description

PlotDisparity() is a function for illustrating graphics of disparities in sample size analysis.

Usage

```
PlotDisparity(
  object,
  which = NULL,
  lgcTtl = TRUE,
  lgcTtlX = TRUE,
```

```
  lgcTtlY = TRUE,
  lgcLgnd = TRUE,
  lgcDtls = FALSE,
  lgcLblZn = TRUE,
  txtLbl = NULL,
  szFntTtl = NULL,
  szFntTtlX = NULL,
  szFntTtlY = NULL,
  szFntAxsX = NULL,
  szFntEC = NULL,
  szFntAxsY = NULL,
  szFntLgnd = NULL,
  szFntLbl = NULL,
  szFntLblEC = NULL,
  szPnt = NULL,
  szPntEC = NULL,
  szPntNEC = NULL,
  typPltCV = NULL,
  typPnt = NULL,
  typPntEC = NULL,
  typPntNEC = NULL,
  typLn0 = NULL,
  typLnEC = NULL,
  clrTtl = NULL,
  clrTtlX = NULL,
  clrTtlY = NULL,
  clrAxsX = NULL,
  clrAxsY = NULL,
  clrLgnd = NULL,
  clrVrtnL = NULL,
  clrVrtnM = NULL,
  clrVrtnH = NULL,
  clrLblZn = NULL,
  clrLbl = NULL,
  clrLblEC = NULL,
  clrPnt = NULL,
  clrPntEC = NULL,
  clrPntNEC = NULL,
  clrLn0 = NULL,
  clrLnEC = NULL,
  clrLnCV = NULL,
  anglAxsX = NULL,
  anglLbl = NULL,
  sort = NULL
)
```

Arguments

object	OBJECT of the disparity test output in **disparity** class.

which	CHARACTER for indicating type of disparity plot. Current version consists of five plots, including disparity plot of variability and outliers based on: (1) coefficient of variance ("CV"), (2) IQR-outlier ("IQR"), (3) Z-outlier ("Z"), (4) GESD-outlier ("GESD"), (5) MAD-outlier ("MAD").
lgcTtl	LOGIC value for indicating whether to show main title.
lgcTtlX	LOGIC value for indicating whether to show title on axis X.
lgcTtlY	LOGIC value for indicating whether to show title on axis Y.
lgcLgnd	LOGIC value for indicating whether to show legend.
lgcDtls	LOGIC value for indicating whether to show full information of the disparity test rather than plot-related information.
lgcLblZn	LOGIC value for indicating whether to show labels of variability zone.
txtLbl	CHARACTER for indicating numeric information of each study disparity plot (outlier). Current version provides options for no label (NULL), numbers of cases ("n"), numbers of excessive cases ("n.excessive"), and proportion of excessive cases ("prop.excessive").
szFntTtl	NUMERIC value for indicating font size of main title.
szFntTtlX	NUMERIC value for indicating font size of title on axis X.
szFntTtlY	NUMERIC value for indicating font size of title on axis Y.
szFntAxsX	NUMERIC value(s) for indicating font size of study label(s).
szFntEC	NUMERIC value(s) for indicating font size of study label(s) for those studies with excessive case.
szFntAxsY	NUMERIC value for indicating font size of scale on axis Y.
szFntLgnd	NUMERIC value for indicating font size of legend.
szFntLbl	NUMERIC value(s) for indicating font size of label(s) for observed value(s).
szFntLblEC	NUMERIC value(s) for indicating font size of label(s) for observed value(s) with excessive case.
szPnt	NUMERIC value(s) for indicating size(s) of observed point(s).
szPntEC	NUMERIC value for indicating size of observed point(s) with excessive cases.
szPntNEC	NUMERIC value for indicating size of observed point(s) without excessive cases.
typPltCV	CHARACTER for indicating sub-type of disparity plot for showing variability. Current version provides two sub-types: "half" and "full" plot.
typPnt	NUMERIC value(s) for indicating type(s) of observed point(s).
typPntEC	NUMERIC value for indicating type of observed point(s). with excessive cases.
typPntNEC	NUMERIC value for indicating type of observed point(s). without excessive cases.
typLn0	NUMERIC value for indicating type of horizontal line for no excessive case.
typLnEC	NUMERIC value for indicating type of vertical line(s) for excessive case(s).
clrTtl	CHARACTER of a color name for main title.
clrTtlX	CHARACTER of a color name for title on axis X.

clrTtlY	CHARACTER of a color name for title on axis Y.
clrAxsX	CHARACTER of color name(s) for study label.
clrAxsY	CHARACTER of a color name for scale on axis Y.
clrLgnd	CHARACTER of a color name for legend.
clrVrtnL	CHARACTER of a color name for low variability zone.
clrVrtnM	CHARACTER of a color name for moderate variability zone.
clrVrtnH	CHARACTER of a color name for high variability zone.
clrLblZn	CHARACTER of color name(s) for variability zone(s).
clrLbl	CHARACTER of color name(s) for observed value(s).
clrLblEC	CHARACTER of color name(s) for observed value(s) of studies with excessive cases.
clrPnt	CHARACTER of color name(s) for every observed point.
clrPntEC	CHARACTER of a color name for proportion of excessive cases.
clrPntNEC	CHARACTER of a color name for observed point without excessive case.
clrLn0	CHARACTER of a color name for horizontal line of no excessive case.
clrLnEC	CHARACTER of color name for vertical line(s) of excessive case(s).
clrLnCV	CHARACTER of color name for line of the association between standard deviation and cases.
anglAxsX	NUMERIC value between 0 and 360 for indicating angle of study labels on x axis on the disparity plot (outlier).
anglLbl	NUMERIC value between 0 and 360 for indicating angle of observed values on the disparity plot (outlier).
sort	CHARACTER of data sorting reference for disparity plot. Currentversion consists of "time", "size", and "excessive" for displaying observations on disparity plot of outlier(s).

Value

PlotDisparity() returns a disparity plot.

Author(s)

Enoch Kang

References

Shapiro, S. S., & Wilk, M. B. (1965). An analysis of variance test for normality (complete samples). **Biometrika**, *52(3)*, 591-611.

Rosner, B. (1983). Percentage Points for a Generalized ESD Many-Outlier Procedure. **Technometrics**, *25(2)*, 165-172.

Rousseeuw, P. J. & Croux C. (1993). Alternatives to the Median Absolute Deviation, **Journal of the American Statistical Association**, *88(424)*, 1273-1283. http://dx.doi.org/10.1080/01621459.1993.10476408

Hendricks, W. A., & Robey, K. W. (1936). The sampling distribution of the coefficient of variation. **The Annals of Mathematical Statistics**, *7(3)*, 129-132.

Sokal, R. R., & Braumann, C. A. (1980). Significance tests for coefficients of variation and variability profiles. **Systematic Biology**, *29(1)*, 50-66.

See Also

TestDisparity

`PlotDistrSS` *Illustrate distribution of study sizes.*

Description

PlotDistrSS() is a function for illustrating graphics of distribution of study sizes.

Usage

```
PlotDistrSS(n, data = NULL, study = NULL, time = NULL, method = "default")
```

Arguments

`n`	NUMERIC values for sample size (n) of each study.
`data`	DATA FRAME consists of three columns for study label, study year, and sample size.
`study`	CHARACTER for study labels.
`time`	NUMERIC values of time sequence.
`method`	CHARACTER for indicating which method should be used for testing normality.

Value

PlotDistrSS() returns a plot of distribution of sample sizes.

Author(s)

Enoch Kang

References

Rosenblatt, M. (1956). Remarks on Some Nonparametric Estimates of a Density Function. **The Annals of Mathematical Statistics**, *27(3)*, 832–837. doi:10.1214/aoms/1177728190.

Parzen, E. (1962). On Estimation of a Probability Density Function and Mode. **The Annals of Mathematical Statistics**, *33(3)*, 1065–1076. doi:10.1214/aoms/1177704472. JSTOR 2237880.

See Also

TestDisparity, PlotDisparity

PlotOSA *Illustrate observed sequential plot.*

Description

PlotOSA() is a function for plotting observed sequential analysis.

Usage

```
PlotOSA(
  object = NULL,
  sclAxsX = "sample",
  txtTtl = NULL,
  group = NULL,
  lgcZone = FALSE,
  lgcLblStdy = FALSE,
  lgcSAP = FALSE,
  lgcInvert = FALSE,
  lgcSmooth = FALSE,
  szFntTtl = 1.8,
  szFntTtlX = 1.2,
  szFntTtlY = NULL,
  szFntAxsX = 0.8,
  szFntAxsY = 0.8,
  szFntLgnd = 0.7,
  szFntLblY = 1.2,
  szFntStdy = 0.8,
  szFntOIS = 0.8,
  szFntAIS = 0.8,
  szPntStdy = 1,
  szPntASB = 0.8,
  szLn0 = 1,
  szLnSig = 1,
  szLnZCum = 2,
  szLnASB = 1,
  szLnOIS = 1,
  typPntStdy = NULL,
  typPntASB = NULL,
  typLn0 = 1,
  typLnSig = 2,
  typLnZCum = 1,
  typLnASB = 3,
  typLnOIS = 2,
  clrTtl = "black",
  clrTtlX = "black",
  clrTtlY = "black",
  clrAxsX = "black",
```

```
  clrAxsY = "black",
  clrLgnd = "black",
  clrLblY = "black",
  clrLblStdy = "black",
  clrLblOIS = "black",
  clrLblAIS = "black",
  clrPntStdy = "gray25",
  clrPntASB = "none",
  clrLn0 = "gray25",
  clrLnSig = "gray",
  clrLnZCum = "blue4",
  clrLnASB = "red4",
  clrLnOIS = "red4",
  anglStdy = 30,
  BSB = FALSE
)
```

Arguments

object	OBJECT in **DoOSA** class that is an output of observed sequential analysis using function DoOSA().
sclAxsX	CHARACTER for indicating unit of scale on axis X.
txtTtl	CHARACTER for user-defined main title on the observed sequential analysis plot.
group	CHARACTER for labeling two groups.
lgcZone	LOGIC value for indicating whether to show zones.
lgcLblStdy	LOGIC value for indicating whether to label each data source.
lgcSAP	LOGIC value for indicating whether to show sequential-adjusted power.
lgcInvert	LOGIC value for indicating whether to invert plot.
lgcSmooth	LOGIC value for indicating whether to smooth error boundaries.
szFntTtl	NUMERIC value for indicating font size of main title.
szFntTtlX	NUMERIC value for indicating font size of title on axis X.
szFntTtlY	NUMERIC value for indicating font size of title on axis Y.
szFntAxsX	NUMERIC value for indicating font size of scale on axis X.
szFntAxsY	NUMERIC value for indicating font size of scale on axis Y.
szFntLgnd	NUMERIC value for indicating font size of legend.
szFntLblY	NUMERIC value for indicating font size of the label of "Cumulative z-score" on axis Y.
szFntStdy	NUMERIC value(s) for indicating font size(s) of the label(s) of each data source.
szFntOIS	NUMERIC value for indicating font size of the label of optimal information size.
szFntAIS	NUMERIC value for indicating font size of the label of acquired information size.

szPntStdy	NUMERIC value(s) for indicating size(s) of observed point(s).
szPntASB	NUMERIC value for indicating size of point(s) on alpha-spending boundaries.
szLn0	NUMERIC value for indicating width of null line.
szLnSig	NUMERIC value for indicating width of line for statistical significance.
szLnZCum	NUMERIC value for indicating width of line for cumulative z-score.
szLnASB	NUMERIC value for indicating width of line for alpha-spending boundaries.
szLnOIS	NUMERIC value for indicating width of line for optimal information size.
typPntStdy	NUMERIC value(s) between 1 to 5 for indicating type(s) of observed point(s). Symbols in the current version includes circle, square, diamond, triangle point-up, and triangle point down.
typPntASB	NUMERIC value between 1 to 5 for indicating type of point(s) on alpha-spending boundaries. Symbols in the current version includes circle, square, diamond, triangle point-up, and triangle point down.
typLn0	NUMERIC value for indicating type of null line.
typLnSig	NUMERIC value for indicating type of line for statistical significance.
typLnZCum	NUMERIC value for indicating type of line for cumulative z-score.
typLnASB	NUMERIC value for indicating type of line for alpha-spending boundaries.
typLnOIS	NUMERIC value for indicating type of line for optimal information size.
clrTtl	CHARACTER of a color name for main title.
clrTtlX	CHARACTER of a color name for title on axis X.
clrTtlY	CHARACTER of a color name for title on axis Y.
clrAxsX	CHARACTER of a color name for scale on axis X.
clrAxsY	CHARACTER of a color name for scale on axis Y.
clrLgnd	CHARACTER of a color name for legend.
clrLblY	CHARACTER of a color name for the label "Cumulative z-score" on axis Y.
clrLblStdy	CHARACTER of color name(s) for the label(s) of each data source.
clrLblOIS	CHARACTER of a color name for the label of optimal information size.
clrLblAIS	CHARACTER of a color name for the label of acquired information size.
clrPntStdy	CHARACTER of color name(s) for observed point(s) of data source.
clrPntASB	CHARACTER of a color name for point(s) on the alpha-spending boundaries.
clrLn0	CHARACTER of a color name for null line.
clrLnSig	CHARACTER of a color name for line of statistical significance.
clrLnZCum	CHARACTER of a color name for line of cumulative z-score.
clrLnASB	CHARACTER of a color name for line of alpha-spending boundaries.
clrLnOIS	CHARACTER of a color name for line of optimal information size.
anglStdy	NUMERIC value between 0 and 360 for indicating angle of data source.
BSB	LOGIC value for indicating whether to illustrate beta-spending boundaries.

Value

PlotOSA() returns a plot of observed sequential analysis.

Author(s)

Enoch Kang

References

Jennison, C., & Turnbull, B. W. (2005). Meta-analyses and adaptive group sequential designs in the clinical development process. **Journal of biopharmaceutical statistics**, *15(4)*, 537–558. https://doi.org/10.1081/BIP-200062273.

Wetterslev, J., Jakobsen, J. C., & Gluud, C. (2017). Trial sequential analysis in systematic reviews with meta-analysis. **BMC medical research methodology**, *17(1)*, 1-18.

NCSS Statistical Software (2023). **Group-sequential analysis for two proportions**. In *PASS Documentation*. Available online: https://www.ncss.com/wp-content/themes/ncss/pdf/Procedures/NCSS/Group-Sequential_Analysis_for_Two_Proportions.pdf

See Also

DoSA, DoOSA, PlotPower

Examples

```
## Not run:
# 1. Import a dataset of study by Fleiss (1993)
library(meta)
data("Fleiss1993bin")

# 2. Perform observed sequential analysis
 output <- DoOSA(Fleiss1993bin, study, year,
                 r1 = d.asp, n1 = n.asp,
                 r2 = d.plac, n2 = n.plac,
                 measure = "RR",
                 group = c("Aspirin", "Control"),
                 plot = TRUE)

# 3. Illustrate plot of observed sequential analysis
 PlotOSA(output)

## End(Not run)
```

PlotPower *Illustrate statistical power plot of observed sequential analysis.*

Description

PlotPower() is a function for plotting power of observed sequential analysis.

Usage

```
PlotPower(
  object = NULL,
  txtTtl = NULL,
  lgcPwrO = FALSE,
  lgcLblStdy = FALSE,
  szFntTtl = 1.8,
  szFntTtlX = 1.2,
  szFntTtlY = 1.2,
  szFntAxsX = 0.8,
  szFntAxsY = 0.8,
  szFntLgnd = 0.8,
  szFntStdy = 0.6,
  szPntPwrO = 0.8,
  szPntPwrS = 0.8,
  szLnPwrCtf = 1,
  szLnPwrO = 1.2,
  szLnPwrP = 1.2,
  szLnPwrS = 1.2,
  typPntPwrO = 2,
  typPntPwrS = 2,
  typLnPwrCtf = 2,
  typLnPwrO = 1,
  typLnPwrP = 2,
  typLnPwrS = 1,
  clrTtl = "black",
  clrTtlX = "black",
  clrTtlY = "black",
  clrAxsX = "black",
  clrAxsY = "black",
  clrLgnd = "gray25",
  clrLblStdy = "gray25",
  clrPntPwrO = "gray75",
  clrPntPwrS = "green4",
  clrLnPwrCtf = "gray75",
  clrLnPwrO = "gray75",
  clrLnPwrP = c("firebrick", "blue4"),
  clrLnPwrS = "green4",
  anglStdy = 90
```

)

Arguments

object	OBJECT in **DoOSA** class that is an output of observed sequential analysis using function DoOSA().
txtTtl	CHARACTER for user-defined main title on the power plot of observed sequential analysis.
lgcPwrO	LOGIC value for indicating whether to show original observed power without sequential adjustment.
lgcLblStdy	LOGIC value for indicating whether to label each data source.
szFntTtl	NUMERIC value for indicating font size of main title.
szFntTtlX	NUMERIC value for indicating font size of title on axis X.
szFntTtlY	NUMERIC value for indicating font size of title on axis Y.
szFntAxsX	NUMERIC value for indicating font size of scale on axis X.
szFntAxsY	NUMERIC value for indicating font size of scale on axis Y.
szFntLgnd	NUMERIC value for indicating font size of legend.
szFntStdy	NUMERIC value(s) for indicating font size(s) of the label(s) of each data source.
szPntPwrO	NUMERIC value for indicating size of observed point(s) of statistical power without sequential adjustment.
szPntPwrS	NUMERIC value for indicating size of observed point(s) of statistical power after sequential adjustment.
szLnPwrCtf	NUMERIC value for indicating width of line for assumed power.
szLnPwrO	NUMERIC value for indicating width of line for observed power without sequential adjustment.
szLnPwrP	NUMERIC value for indicating width of line for predicted or expected power after sequential adjustment.
szLnPwrS	NUMERIC value for indicating width of line for observed power after sequential adjustment.
typPntPwrO	NUMERIC value(s) between 1 to 5 for indicating type(s) of observed point(s) without sequential adjustment. Symbols in the current version includes circle, square, diamond, triangle point-up, and triangle point down.
typPntPwrS	NUMERIC value between 1 to 5 for indicating type of point(s) after sequential adjustment. Symbols in the current version includes circle, square, diamond, triangle point-up, and triangle point down.
typLnPwrCtf	NUMERIC value for indicating type of assumed power.
typLnPwrO	NUMERIC value for indicating type of line for observed power without sequential adjustment.
typLnPwrP	NUMERIC value for indicating type of line for predicted or expected power after sequential adjustment.
typLnPwrS	NUMERIC value for indicating type of line for observed power after sequential adjustment.

clrTtl	CHARACTER of a color name for main title.
clrTtlX	CHARACTER of a color name for title on axis X.
clrTtlY	CHARACTER of a color name for title on axis Y.
clrAxsX	CHARACTER of a color name for scale on axis X.
clrAxsY	CHARACTER of a color name for scale on axis Y.
clrLgnd	CHARACTER of a color name for legend.
clrLblStdy	CHARACTER of color name(s) for the label(s) of each data source.
clrPntPwr0	CHARACTER of color name(s) for observed point(s) of power without sequential adjustment..
clrPntPwrS	CHARACTER of a color name for observed point(s) of power after sequential adjustment.
clrLnPwrCtf	CHARACTER of a color name for assumed power.
clrLnPwr0	CHARACTER of a color name for line of observed power without sequential adjustment.
clrLnPwrP	CHARACTER of a color name for line of predicted or expected power after sequential adjustment.
clrLnPwrS	CHARACTER of a color name for line of observed power after sequential adjustment.
anglStdy	NUMERIC value between 0 and 360 for indicating angle of data source.

Value

PlotPower() returns a plot of statistical power of observed sequential analysis.

Author(s)

Enoch Kang

References

Harrer, M., Cuijpers, P., Furukawa, T.A., & Ebert, D.D. (2021). *Doing Meta-Analysis with R: A Hands-On Guide*. Boca Raton, FL and London: Chapman & Hall/CRC Press. ISBN 978-0-367-61007-4.

Jennison, C., & Turnbull, B. W. (2005). Meta-analyses and adaptive group sequential designs in the clinical development process. **Journal of biopharmaceutical statistics**, *15(4)*, 537–558. https://doi.org/10.1081/BIP-200062273.

Wetterslev, J., Jakobsen, J. C., & Gluud, C. (2017). Trial sequential analysis in systematic reviews with meta-analysis. **BMC medical research methodology**, *17(1)*, 1-18.

See Also

DoSA, DoOSA, PlotOSA

Examples

```
## Not run:
# 1. Import a dataset of study by Fleiss (1993)
library(meta)
data("Fleiss1993bin")

# 2. Perform observed sequential analysis
 output <- DoOSA(Fleiss1993bin, study, year,
                 r1 = d.asp, n1 = n.asp,
                 r2 = d.plac, n2 = n.plac,
                 measure = "RR",
                 group = c("Aspirin", "Control"),
                 plot = TRUE)

# 3. Illustrate statistical power plot of observed sequential analysis
 PlotPower(output)

## End(Not run)
```

`TestDiscordance` *Test assumption of discordance between theoretical and observed study scale.*

Description

TestDiscordance() is a function for discordance in rank of study size analysis.

Usage

```
TestDiscordance(
  n,
  se,
  data,
  study = NULL,
  method = "prop",
  coval = 0.2,
  tot = 0,
  plot = FALSE,
  color = "lightpink"
)
```

Arguments

`n`	NUMERIC values for sample size (n) of each study.
`se`	NUMERIC values for standard error of each study.
`data`	DATA FRAME consists of three columns for study label, sample size, and standard error.

study	CHARACTER for study label of each study.
method	CHARACTER of "rank" or "prop" for indicating which method should be used.
coval	NUMERIC value of cutoff point ranged from 0 to 1 in order to detecting of discordance between theoretical and observed study scale.
tot	NUMERIC value of tolerate discordance in ranks between theoretical and observed study scale. The numeric value should be ranged from 0 to 1 / 4 number of studies.
plot	LOGIC value for indicating whether to illustrate discordance plot.
color	CHARACTER of a color name for emphasizing the studies with discordance in ranks between theoretical and observed study size.

Value

TestDiscordance() returns a summary of result of discordance in rank of study size.

Author(s)

Enoch Kang

References

Howell, D. C. (2012). **Statistical methods for psychology (7th ed.)**. Belmont, CA: Thomson. Available online: https://labs.la.utexas.edu/gilden/files/2016/05/Statistics-Text.pdf.

See Also

TestDisparity

Examples

```
## Not run:
# 1. Import a dataset of study by Fleiss (1993)
library(meta)
data("Fleiss1993bin")
data <- Fleiss1993bin

# 2. Calculate total sample size and standard error of each study
data$n  <- data$n.asp + data$n.plac
data$se <- sqrt((1 / data$d.asp) - (1 / data$n.asp) + (1 / data$d.plac) - (1 / data$n.plac))

# 3. Test discordance in ranks between theoretical and observed study size.
output <- TestDiscordance(n = n, se = se, study = study, data = data)

# 4. Illustrate discordance plot
TestDiscordance(n = n, se = se, study = study, data = data, plot = TRUE)

## End(Not run)
```

`TestDisparity` *Test assumption of disparities in sample size.*

Description

TestDisparity() is a function for disparities in sample size analysis.

Usage

```
TestDisparity(
  n,
  data = NULL,
  study = NULL,
  time = NULL,
  outlier = NULL,
  ctf = 0.2,
  vrblty = NULL,
  ctfLwr = 0.1,
  ctfUpr = 0.3,
  rplctns = 1000,
  plot = FALSE,
  sort = NULL,
  color = "firebrick3"
)
```

Arguments

`n`	NUMERIC values for sample size (n) of each study.
`data`	DATA FRAME consists of columns for study label, study year, and sample size.
`study`	CHARACTER for study labels.
`time`	NUMERIC values of time sequence.
`outlier`	CHARACTER for method of outlier detection. Current version consists of four methods, and three of them can be used for normal distribution. The rest one method can be used for data with non-normal distribution. For normal distribution data, outlier detection can be performed using 1.5 interquartile range method ("IQR"), z score method ("Z"), and generalized extreme studentized deviate method ("GESD"). For data with non-normal distribution, package *aides* detects outliers using median absolute deviation method ("MAD"). Parameter `outlier` with argument "Default" automatically takes "GESD" or "MAD" based on data distribution.
`ctf`	NUMERIC value of cutoff point for proportion of excessive cases in outlier-based disparity test, and the value should be larger than 0.
`vrblty`	CHARACTER for method of variability detection. Current version consists of two methods in terms of coefficient of variation (CV) and robust CV (RCV) using MAD. For normal distribution data, variability detection can be performed

	common CV method, and MAD based RCV could be used for data with non-normal distribution. Default argument for parameter `vrblty` is "CV" in order to detect variability.
`ctfLwr`	NUMERIC value of cutoff value for lower boundary of variability that should be larger than 0.
`ctfUpr`	NUMERIC value of cutoff value for upper boundary of variability that should be larger than `ctfLwr`.
`rplctns`	INTEGER value of bootstrap replications for obtaining probability of variability-based disparity test, and the integer must be equal or larger than 1,000.
`plot`	LOGIC value for indicating whether to illustrate proportion of excessive cases plot.
`sort`	CHARACTER of data sorting reference for disparity plot. Current version consists of "time", "size", and "excessive" for displaying observations on disparity plot of outlier(s).
`color`	CHARACTER of a color name for emphasizing the significant disparities in sample size.

Value

TestDisparity() returns a summary of result regarding disparities in sample size, and can be stored as an object in `disparity` class. Explanations of returned information are listed as follows:

`disparity`	String to return the overall judgement of disparity test.
`w.normality`	A numeric value of statistics of normality test to show whether sample sizes among studies are distributed normally.
`p.normality`	A numeric value of p-value of normality test to show whether sample sizes among studies are distributed normally.
`outlier.method`	String shows outlier detection method used in disparity test.
`vrblty.method`	String shows variability detection method used in disparity test.
`outlier`	A data frame to show details of identified outliers (studies).
`prop.outlier`	A numeric value to show proportion of outliers among all studies.
`n.excessive`	A numeric value of excessive cases among all samples.
`p.prop.outlier`	A numeric value of p-value of disparity outlier test.
`lci.prop.outlier`	A numeric value for lower limit of 95% confidence interval of disparity outlier test.
`uci.prop.outlier`	A numeric value for upper limit of 95% confidence interval of disparity outlier test.
`variability`	A numeric value to show variability among all studies.
`p.variability`	A numeric value of p-value of disparity variability test.
`lci.variability`	A numeric value for lower limit of 95% confidence interval of disparity variability test.

`uci.variability`
: A numeric value for lower limit of 95% confidence interval of disparity variability test.

Author(s)

Enoch Kang

References

Shapiro, S. S., & Wilk, M. B. (1965). An analysis of variance test for normality (complete samples). **Biometrika**, *52(3)*, 591-611.

Rosner, B. (1983). Percentage Points for a Generalized ESD Many-Outlier Procedure. **Technometrics**, *25(2)*, 165-172.

Leys, C., Ley, C., Klein, O., Bernard, P., & Licata, L. (2013). Detecting outliers: Do not use standard deviation around the mean, use absolute deviation around the median. **Journal of experimental social psychology**, *49(4)*, 764-766.

Rousseeuw, P. J. & Croux C. (1993). Alternatives to the Median Absolute Deviation, **Journal of the American Statistical Association**, *88(424)*, 1273-1283. http://dx.doi.org/10.1080/01621459.1993.10476408

Hendricks, W. A., & Robey, K. W. (1936). The sampling distribution of the coefficient of variation. **The Annals of Mathematical Statistics**, *7(3)*, 129-132.

Sokal, R. R., & Braumann, C. A. (1980). Significance tests for coefficients of variation and variability profiles. **Systematic Biology**, *29(1)*, 50-66.

See Also

`TestDiscordance`, `PlotDisparity`

Examples

```
## Not run:
# 1. Import a dataset of study by Olkin (1995)
library(meta)
data("Olkin1995")
data <- Olkin1995

# 2. Calculate total sample size and standard error of each study
data$n  <- data$n.exp + data$n.cont

# 3. Test disparities in sample sizes
output <- TestDisparity(n, data, author, year)

# 4. Illustrate disparity plot
TestDisparity(n, data, author, year, plot = TRUE)

## End(Not run)
```

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