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**Description**

Prediction Intervals for Random-Effects Meta-Analysis

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**Usage**

\[
\text{cima}(y, \text{se}, v = \text{NULL}, \alpha = 0.05, \text{method} = \text{c("boot", "DL", "HK", "SJ", "KR", "APX", "PL", "BC")}, B = 25000, \text{parallel} = \text{FALSE}, \text{seed} = \text{NULL}, \text{maxit1} = 1e+05, \text{eps} = 10^\text{-10}, \text{lower} = 0, \text{upper} = 1000, \text{maxit2} = 1000, \text{tol} = .\text{Machine}\$\text{double}\$.\text{eps}\text{^0.25}, \text{rnd} = \text{NULL}, \text{maxiter} = 100)
\]
Arguments

\textbf{y} \hspace{1cm} \text{the effect size estimates vector}
\textbf{se} \hspace{1cm} \text{the within studies standard errors vector}
\textbf{v} \hspace{1cm} \text{the within studies variance estimates vector}
\textbf{alpha} \hspace{1cm} \text{the alpha level of the prediction interval}
\textbf{method} \hspace{1cm} \text{the calculation method for the prediction interval (default = "boot").}
  
  - \textbf{boot}: A parametric bootstrap confidence interval (Nagashima et al., 2018).
  - \textbf{DL}: A Wald-type t-distribution confidence interval (the DerSimonian & Laird estimator for }\tau^2\text{ with an approximate variance estimator for the average effect, } (1/\sum \hat{w}_i)^{-1}, df = K - 1).\text{)
  - \textbf{HK}: A Wald-type t-distribution confidence interval (the REML estimator for }\tau^2\text{ with the Hartung (1999)’s variance estimator [the Hartung and Knapp (2001)’s estimator] for the average effect, } df = K - 1).\text{)
  - \textbf{SJ}: A Wald-type t-distribution confidence interval (the REML estimator for }\tau^2\text{ with the Sidik and Jonkman (2006)’s bias corrected SE estimator for the average effect, } df = K - 1).\text{)
  - \textbf{KR}: Partlett–Riley (2017) confidence interval / (the REML estimator for }\tau^2\text{ with the Kenward and Roger (1997)’s approach for the average effect, } df = \nu).\text{)
  - \textbf{APX}: A Wald-type t-distribution confidence interval / (the REML estimator for }\tau^2\text{ with an approximate variance estimator for the average effect, } df = K - 1).\text{)
  - \textbf{PL}: Profile likelihood confidence interval (Hardy & Thompson, 1996).
  - \textbf{BC}: Profile likelihood confidence interval with Bartlett-type correction (Noma, 2011).

\textbf{B} \hspace{1cm} \text{the number of bootstrap samples}
\textbf{parallel} \hspace{1cm} \text{the number of threads used in parallel computing, or FALSE that means single threading}
\textbf{seed} \hspace{1cm} \text{set the value of random seed}
\textbf{maxit1} \hspace{1cm} \text{the maximum number of iteration for the exact distribution function of } Q\text{)
\textbf{eps} \hspace{1cm} \text{the desired level of accuracy for the exact distribution function of } Q\text{)
\textbf{lower} \hspace{1cm} \text{the lower limit of random numbers of } \tau^2\text{)
\textbf{upper} \hspace{1cm} \text{the lower upper of random numbers of } \tau^2\text{)
\textbf{maxit2} \hspace{1cm} \text{the maximum number of iteration for numerical inversions}
\textbf{tol} \hspace{1cm} \text{the desired level of accuracy for numerical inversions}
\textbf{rnd} \hspace{1cm} \text{a vector of random numbers from the exact distribution of } \tau^2\text{)
\textbf{maxiter} \hspace{1cm} \text{the maximum number of iteration for REML estimation}

Details

Excellent reviews of heterogeneity variance estimation have been published (e.g., Veroniki, et al., 2018).
Value

- K: the number of studies.
- muhat: the average treatment effect estimate $\hat{\mu}$.
- lci, uci: the lower and upper confidence limits $\hat{\mu}_l$ and $\hat{\mu}_u$.
- tau2h: the estimate for $\tau^2$.
- i2h: the estimate for $I^2$.
- nuc: degrees of freedom for the confidence interval.
- vmuhat: the variance estimate for $\hat{\mu}$.

References


See Also

pima

Examples

data(sbp, package = "pimeta")
set.seed(20161102)

# Nagashima-Noma-Furukawa confidence interval
pimeta::cima(sbp$sy, sbp$sigmak, seed = 3141592)

# A Wald-type t-distribution confidence interval
# An approximate variance estimator & DerSimonian-Laird estimator for tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "DL")

# A Wald-type t-distribution confidence interval
# The Hartung variance estimator & REML estimator for tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "HK")

# A Wald-type t-distribution confidence interval
# The Sidik-Jonkman variance estimator & REML estimator for tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "SJ")

# A Wald-type t-distribution confidence interval
# The Kenward-Roger approach & REML estimator for tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "KR")

# A Wald-type t-distribution confidence interval
# An approximate variance estimator & REML estimator for tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "APX")

# Profile likelihood confidence interval
# Maximum likelihood estimators of variance for the average effect & tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "PL")

# Profile likelihood confidence interval with a Bartlett-type correction
# Maximum likelihood estimators of variance for the average effect & tau^2
pimeta::cima(sbp$y, sbp$sigmak, method = "BC")

convert_bin

Converting binary data

description

Converting binary outcome data to the effect size estimates and the within studies standard errors vector

Usage

convert_bin(m1, n1, m2, n2, type = c("logOR", "logRR", "RD"))

Arguments

m1 the number of successes in treatment group 1
n1 the number of patients in treatment group 1
m2 the number of successes in treatment group 2
n2 the number of patients in treatment group 2

type the outcome measure for binary outcome data (default = "logOR").

• logOR: logarithmic odds ratio, which is defined by \[ \log \left( \frac{m_1+0.5}{n_1-m_1+0.5} \right) \frac{n_2-m_2+0.5}{m_2+0.5}, \]
• logRR: logarithmic relative risk, which is defined by \[ \log \left( \frac{m_1+0.5}{n_1+0.5} \right) \frac{n_2+0.5}{m_2+0.5}. \]
• RD: risk difference, which is defined by \[ \frac{m_1}{n_1} - \frac{m_2}{n_2}. \]
Details

This function implements methods for logarithmic odds ratio, logarithmic relative risk, and risk difference described in Hartung & Knapp (2001).

Value

- \( y \): the effect size estimates vector.
- \( se \): the within studies standard errors vector.

References


Examples

```r
m1 <- c(15,12,29,44,14,14,19,10,17,38,19,21)
n1 <- c(16,16,34,56,22,54,17,58,14,26,44,29,38)
m2 <- c(9,18,31,6,17,7,23,3,6,12,22,19)
n2 <- c(16,16,34,56,22,55,15,58,15,27,45,30,38)
dat <- pimeta::convert_bin(m1, n1, m2, n2, type = "logOR")
pimeta::pima(dat$y, dat$se)
```

hyp Hypertension data

Description

The hypertension data (Wang et al., 2005) included 7 studies comparing the treatment effect of anti-hypertensive treatment versus control on reducing diastolic blood pressure (DBP) in patients with hypertension. Negative estimates indicate the reduction of DBP in the anti-hypertensive treatment group.

Usage

```r
data(hyp)
```

Format

A data frame with 10 rows and 2 variables

Details

- \( y \): Standardized mean difference
- \( se \): Standard error
- \( label \): Labels for each study
References


---

**i2h**

$I^2$ heterogeneity measure

Description

Returns the estimator for (Higgins & Thompson, 2002).

Usage

```r
i2h(se, tau2h)
```

Arguments

- `se`: the within studies standard errors vector
- `tau2h`: the estimate of $\tau^2$

Value

- `i2h`: the estimate for $I^2$.

References


Examples

```r
data(sbp, package = "pimeta")
tau2h <- pimeta::tau2h(sbp$y, sbp$sigmak)
pimeta::i2h(sbp$sigmak, tau2h$tau2h)
```
The pain data (Riley et al., 2011; Hauser et al., 2009) included 22 studies comparing the treatment effect of antidepressants on reducing pain in patients with fibromyalgia syndrome. The treatment effects were summarized using standardized mean differences on a visual analog scale for pain between the antidepressant group and control group. Negative estimates indicate the reduction of pain in the antidepressant group.

Usage
data(pain)

Format
A data frame with 22 rows and 2 variables

Details
- y: Standardized mean difference
- sigmak: Standard error

References


This function can estimate prediction intervals (PIs) as follows: A parametric bootstrap PI based on confidence distribution (Nagashima et al., 2018). A parametric bootstrap confidence interval is also calculated based on the same sampling method for bootstrap PI. The Higgins–Thompson–Spiegelhalter (2009) prediction interval. The Partlett–Riley (2017) prediction intervals.
Usage

pima(y, se, v = NULL, alpha = 0.05, method = c("boot", "HTS", "HK", "SJ", "KR", "CL", "APX"), B = 25000, parallel = FALSE, seed = NULL, maxit1 = 1e+05, eps = 10^(-10), lower = 0, upper = 1000, maxit2 = 1000, tol = .Machine$double.eps*0.25, rnd = NULL, maxiter = 100)

Arguments

y
the effect size estimates vector

se
the within studies standard error estimates vector

v
the within studies variance estimates vector

alpha
the calculation level of the prediction interval

method
the calculation method for the prediction interval (default = "boot").

- boot: A parametric bootstrap prediction interval (Nagashima et al., 2018).
- HTS: the Higgins–Thompson–Spiegelhalter (2009) prediction interval / (the DerSimonian & Laird estimator for $\tau^2$ with an approximate variance estimator for the average effect, $(1/\sum \hat{w}_i)^{-1}, df = K - 2$).
- SJ: Partlett–Riley (2017) prediction interval / (the REML estimator for $\tau^2$ with the Sidik and Jonkman (2006)’s bias corrected variance estimator for the average effect, $df = K - 2$).
- KR: Partlett–Riley (2017) prediction interval / (the REML estimator for $\tau^2$ with the Kenward and Roger (1997)’s approach for the average effect, $df = \nu - 1$).
- APX: Partlett–Riley (2017) prediction interval / (the REML estimator for $\tau^2$ with an approximate variance estimator for the average effect, $df = K - 2$).

B
the number of bootstrap samples

parallel
the number of threads used in parallel computing, or FALSE that means single threading

seed
set the value of random seed

maxit1
the maximum number of iteration for the exact distribution function of $Q$

eps
the desired level of accuracy for the exact distribution function of $Q$

lower
the lower limit of random numbers of $\tau^2$

upper
the upper limit of random numbers of $\tau^2$

maxit2
the maximum number of iteration for numerical inversions

tol
the desired level of accuracy for numerical inversions

rnd
a vector of random numbers from the exact distribution of $\tau^2$

maxiter
the maximum number of iteration for REML estimation
Details

The functions bootPI, pima_boot, pima_hts, htsdl, pima_htsreml, htsreml are deprecated, and integrated to the pima function.

Value

- $K$: the number of studies.
- $\muhat$: the average treatment effect estimate $\hat{\mu}$.
- $lci$, $uci$: the lower and upper confidence limits $\hat{\mu}_l$ and $\hat{\mu}_u$.
- $lpi$, $upi$: the lower and upper prediction limits $\hat{c}_l$ and $\hat{c}_u$.
- $tau2h$: the estimate for $\tau^2$.
- $i2h$: the estimate for $I^2$.
- $nup$: degrees of freedom for the prediction interval.
- $nuc$: degrees of freedom for the confidence interval.
- $vmuhat$: the variance estimate for $\hat{\mu}$.

References


See Also

print.pima, plot.pima, cima.
Examples

data(sbp, package = "pimeta")

# Nagashima-Noma-Furukawa prediction interval
# is sufficiently accurate when I^2 >= 10% and K >= 3
pimeta::pima(sbp$y, sbp$sigmak, seed = 3141592, parallel = 4)

# Higgins-Thompson-Spiegelhalter prediction interval and
# Partlett-Riley prediction intervals
# are accurate when I^2 > 30% and K > 25
pimeta::pima(sbp$y, sbp$sigmak, method = "HTS")
pimeta::pima(sbp$y, sbp$sigmak, method = "HK")
pimeta::pima(sbp$y, sbp$sigmak, method = "SJ")
pimeta::pima(sbp$y, sbp$sigmak, method = "KR")
pimeta::pima(sbp$y, sbp$sigmak, method = "APX")

Description

A function for plotting of 'cima' objects.

Usage

## S3 method for class 'cima'
plot(x, y = NULL, title = "Forest plot",
     base_size = 16, base_family = "", digits = 3, studylabel = NULL,
     ntick = NULL, trans = c("identity", "exp"), ...)

Arguments

x 'cima' object to plot
y is not used
title graph title
base_size base font size
base_family base font family
digits a value for digits specifies the minimum number of significant digits to be
       printed in values.
studylabel labels for each study
ntick the number of x-axis ticks
trans transformation for logarithmic scale outcomes ("identity" [default] or "exp").
... further arguments passed to or from other methods.
Examples

```r
data(sbp, package = "pimeta")
ciex <- pimeta::cima(sbp$y, sbp$sigmak, method = "DL")
cairo_pdf("forestplot.pdf", width = 6, height = 3, family = "Arial")
plot(ciex, digits = 2, base_size = 10, studylabel = sbp$label)
dev.off()
```

---

plot.pima  
*Plot Results*

Description

A function for plotting of ‘pima’ objects.

Usage

```r
## S3 method for class 'pima'
plot(x, y = NULL, title = "Forest plot", 
     base_size = 16, base_family = ",", digits = 3, studylabel = NULL, 
     ntick = NULL, trans = c("identity", "exp"), ...)
```

Arguments

- `x`: ‘pima’ object to plot
- `y`: is not used
- `title`: graph title
- `base_size`: base font size
- `base_family`: base font family
- `digits`: a value for digits specifies the minimum number of significant digits to be printed in values.
- `studylabel`: labels for each study
- `ntick`: the number of x-axis ticks
- `trans`: transformation for logarithmic scale outcomes ("identity" [default] or "exp").
- `...`: further arguments passed to or from other methods.

Examples

```r
data(sbp, package = "pimeta")
piaux <- pimeta::pima(sbp$y, sbp$sigmak, method = "HTS")
cairo_pdf("forestplot.pdf", width = 6, height = 3, family = "Arial")
plot(piaux, digits = 2, base_size = 10, studylabel = sbp$label)
dev.off()
```
Description

print prints its argument and returns it invisibly (via invisible(x)).

Usage

## S3 method for class 'cima'
print(x, digits = 4, trans = c("identity", "exp"), ...)

Arguments

- **x**
  - print to display
- **digits**
  - a value for digits specifies the minimum number of significant digits to be printed in values.
- **trans**
  - transformation for logarithmic scale outcomes ("identity" [default] or "exp").
- **...**
  - further arguments passed to or from other methods.

---

Description

print prints its argument and returns it invisibly (via invisible(x)).

Usage

## S3 method for class 'pima'
print(x, digits = 4, trans = c("identity", "exp"), ...)

Arguments

- **x**
  - print to display
- **digits**
  - a value for digits specifies the minimum number of significant digits to be printed in values.
- **trans**
  - transformation for logarithmic scale outcomes ("identity" [default] or "exp").
- **...**
  - further arguments passed to or from other methods.
Description

`print` prints its argument and returns it invisibly (via `invisible(x)`).

Usage

```r
## S3 method for class 'pima_tau2h'
print(x, digits = 3, ...)
```

Arguments

- `x`  print to display
- `digits` a value for `digits` specifies the minimum number of significant digits to be printed in values.
- `...` further arguments passed to or from other methods.

---

**pwchisq**

The Distribution of a Positive Linear Combination of Chi-square Random Variables

Description

The cumulative distribution function for the distribution of a positive linear combination of \( \chi^2 \) random variables with the weights \((\lambda_1, \ldots, \lambda_K)\), degrees of freedom \((\nu_1, \ldots, \nu_K)\), and non-centrality parameters \((\delta_1, \ldots, \delta_K)\).

Usage

```r
pwchisq(x, lambda = 1, nu = 1, delta = 0, mode = 1, 
        maxit1 = 1e+05, eps = 10^(-10))
```

Arguments

- `x` numeric; value of \( x > 0 \) (\( P[X \leq x] \)).
- `lambda` numeric vector; weights \((\lambda_1, \ldots, \lambda_K)\).
- `nu` integer vector; degrees of freedom \((\nu_1, \ldots, \nu_K)\).
- `delta` numeric vector; non-centrality parameters \((\delta_1, \ldots, \delta_K)\).
- `mode` numeric; the mode of calculation (see Farabrother, 1984)
- `maxit1` integer; the maximum number of iteration.
- `eps` numeric; the desired level of accuracy.
sbp

Value

• prob: the distribution function.

References


Examples

# Table 1 of Farebrother (1984)
# Q6 (The target values are 0.0061, 0.5913, and 0.9779)

```
pimeta::pwchisq(20, lambda = c(7,3), nu = c(6,2), delta = c(6,2))
pimeta::pwchisq(100, lambda = c(7,3), nu = c(6,2), delta = c(6,2))
pimeta::pwchisq(200, lambda = c(7,3), nu = c(6,2), delta = c(6,2))
```

# [1] 0.006117973
# [1] 0.5913421
# [1] 0.9779184

sbp

* Systolic blood pressure (SBP) data *

Description

Riley et al. (2011) analyzed a hypothetical meta-analysis. They generated a data set of 10 studies examining the same antihypertensive drug. Negative estimates suggested reduced blood pressure in the treatment group.

Usage

data(sbp)

Format

A data frame with 10 rows and 2 variables

Details

• y: Standardized mean difference
• sigmak: Standard error
• label: Labels for each generated study

References

setshift  

**Set-shifting data**

**Description**

Higgins et al. (2009) re-analyzed data (Roberts et al., 2007) that included 14 studies evaluating the set-shifting ability in people with eating disorders by using a prediction interval. Standardized mean differences in the time taken to complete Trail Making Test between subjects with eating disorders and healthy controls were collected. Positive estimates indicate impairment in set shifting ability in people with eating disorders.

**Usage**

data(setshift)

**Format**

A data frame with 14 rows and 2 variables

**Details**

- **y**: Standardized mean difference
- **sigmak**: Standard error

**References**


---

**tau2h**  

**Calculating Heterogeneity Variance**

**Description**

Returns a heterogeneity variance estimate and its confidence interval.

**Usage**

tau2h(y, se, maxiter = 100, method = c("DL", "VC", "PM", "HM", "HS", "ML", "REML", "AREML", "SJ", "SJ2", "EB", "BM"), methodci = c(NA, "ML", "REML"), alpha = 0.05)
**Arguments**

- `y`: the effect size estimates vector
- `se`: the within studies standard errors vector
- `maxiter`: the maximum number of iterations
- `method`: the calculation method for heterogeneity variance (default = "DL").
  - `VC`: Variance component type estimator (Hedges, 1983).
  - `PM`: Paule–Mandel estimator (Paule & Mandel, 1982).
  - `HS`: Hunter–Schmidt estimator (Hunter & Schmidt, 2004). This estimator has negative bias (Viechtbauer, 2005).
  - `ML`: Maximum likelihood (ML) estimator (e.g., DerSimonian & Laird, 1986).
  - `REML`: Restricted maximum likelihood (REML) estimator (e.g., DerSimonian & Laird, 1986).
  - `AREML`: Approximate restricted maximum likelihood estimator (Thompson & Sharp, 1999).
  - `BM`: Bayes modal estimator (Chung, et al., 2013).
- `methodci`: the calculation method for a confidence interval of heterogeneity variance (default = NA).
  - `NA`: a confidence interval will not be calculated.
  - `ML`: Wald confidence interval with a ML estimator (Biggerstaff & Tweedie, 1997).
  - `REML`: Wald confidence interval with a REML estimator (Biggerstaff & Tweedie, 1997).
- `alpha`: the alpha level of the confidence interval

**Details**

Excellent reviews of heterogeneity variance estimation have been published (Sidik & Jonkman, 2007; Veroniki, et al., 2016; Langan, et al., 2018).

**Value**

- `tau2h`: the estimate for $\tau^2$.
- `lci, uci`: the lower and upper confidence limits $\hat{\tau}_l^2$ and $\hat{\tau}_u^2$.

**References**


Examples

data(sbp, package = "pimeta")
pimeta::tau2h(sbp$sy, sbp$sigmak)
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