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Contents

pimeta-package . . . 2
cima . . . 2
convert_bin . . . 5
hyp . . . 6
i2h . . . 7
pain . . . 8
pima . . . 8
plot.cima . . . 11
plot.pima . . . 12
print.cima . . . 13
print.pima . . . 13
print.pima_tau2h . . . 14
pwchisq . . . 14
sbp . . . 15
setshift . . . 16
tau2h . . . 16

Index **19**

`pimeta-package` *Prediction Intervals for Random-Effects Meta-Analysis*

Description

Prediction Intervals for Random-Effects Meta-Analysis

Author(s)

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`cima` *Calculating Confidence Intervals*

Description

This function calculates confidence intervals.

Usage

```
cima(y, se, v = NULL, alpha = 0.05, method = c("boot", "DL", "HK",
  "SJ", "KR", "APX", "PL", "BC"), 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 errors vector
v	the within studies variance estimates vector
alpha	the alpha level of the prediction interval
method	the calculation method for the pretiction interval (default = "boot").

- boot: A parametric bootstrap confidence interval (Nagashima et al., 2018).
- DL: A Wald-type t-distribution confidence interval (the DerSimonian & Laird estimator for τ^2 with an approximate variance estimator for the average effect, $(1/\sum \hat{w}_i)^{-1}$, $df = K - 1$).
- HK: A Wald-type t-distribution confidence interval (the REML estimator for τ^2 with the Hartung (1999)'s varance estimator [the Hartung and Knapp (2001)'s estimator] for the average effect, $df = K - 1$).
- SJ: A Wald-type t-distribution confidence interval (the REML estimator for τ^2 with the Sidik and Jonkman (2006)'s bias coreccted SE estimator for the average effect, $df = K - 1$).
- KR: Partlett–Riley (2017) confidence interval / (the REML estimator for τ^2 with the Kenward and Roger (1997)'s approach for the average effect, $df = \nu$).
- APX: A Wald-type t-distribution confidence interval / (the REML estimator for τ^2 with an approximate variance estimator for the average effect, $df = K - 1$).
- PL: Profile likelihood confidence interval (Hardy & Thompson, 1996).
- BC: Profile likelihood confidence interval with Bartlett-type correction (Noma, 2011).

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 τ^2
upper	the lower upper of random numbers of τ^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 τ^2
maxiter	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 τ^2.
- i2h: the estimate for I^2.
- nuc: degrees of freedom for the confidence interval.
- vmuhat: the variance estimate for $\hat{\mu}$.

References

Veroniki, A. A., Jackson, D., Bender, R., Kuss, O., Langan, D., Higgins, J. P. T., Knapp, G., and Salanti, J. (2016). Methods to calculate uncertainty in the estimated overall effect size from a random-effects meta-analysis *Res Syn Meth. In press*. https://doi.org/10.1002/jrsm.1319.

Nagashima, K., Noma, H., and Furukawa, T. A. (2018). Prediction intervals for random-effects meta-analysis: a confidence distribution approach. *Stat Methods Med Res. In press*. https://doi.org/10.1177/0962280218773520.

Higgins, J. P. T, Thompson, S. G., Spiegelhalter, D. J. (2009). A re-evaluation of random-effects meta-analysis. *J R Stat Soc Ser A Stat Soc.* **172**(1): 137-159. https://doi.org/10.1111/j.1467-985X.2008.00552.x

Partlett, C, and Riley, R. D. (2017). Random effects meta-analysis: Coverage performance of 95 confidence and prediction intervals following REML estimation. *Stat Med.* **36**(2): 301-317. https://doi.org/10.1002/sim.7140

Hartung, J., and Knapp, G. (2001). On tests of the overall treatment effect in meta-analysis with normally distributed responses. *Stat Med.* **20**(12): 1771-1782. https://doi.org/10.1002/sim.791

Sidik, K., and Jonkman, J. N. (2006). Robust variance estimation for random effects meta-analysis. *Comput Stat Data Anal.* **50**(12): 3681-3701. https://doi.org/10.1016/j.csda.2005.07.019

Noma H. (2011) Confidence intervals for a random-effects meta-analysis based on Bartlett-type corrections. *Stat Med.* **30**(28): 3304-3312. https://doi.org/10.1002/sim.4350

See Also

pima

Examples

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

# Nagashima-Noma-Furukawa confidence interval
pimeta::cima(sbp$y, sbp$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 $= \log \frac{(m1+0.5)(n2-m2+0.5)}{(n1-m1+0.5)(m2+0.5)}$. • `logRR`: logarithmic relative risk, which is defined by $= \log \frac{(m1+0.5)(n2+0.5)}{(n1+0.5)(m2+0.5)}$. • `RD`: risk difference, which is defined by $= \frac{m1}{n1} - \frac{m2}{n2}$.

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

Hartung, J., and Knapp, G. (2001). A refined method for the meta-analysis of controlled clinical trials with binary outcome. *Stat Med.* **20**(24): 3875-3889. https://doi.org/10.1002/sim.1009

Examples

```
m1 <- c(15,12,29,42,14,44,14,29,10,17,38,19,21)
n1 <- c(16,16,34,56,22,54,17,58,14,26,44,29,38)
m2 <- c( 9, 1,18,31, 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

```
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

Wang, J. G., Staessen, J. A., Franklin, S. S., Fagard, R., and Gueyffier, F. (2005). Systolic and diastolic blood pressure lowering as determinants of cardiovascular outcome. *Hypertension.* **45**(5): 907-913. https://doi.org/10.1161/01.HYP.0000165020.14745.79

`i2h` *I^2 heterogeneity measure*

Description

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

Usage

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

Arguments

`se`	the within studies standard errors vector
`tau2h`	the estimate of τ^2

Value

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

References

Higgins, J. P. T., and Thompson, S. G. (2002). Quantifying heterogeneity in a meta-analysis. *Stat Med.* **21**(11): 1539-1558. https://doi.org/10.1002/sim.1186

Examples

```
data(sbp, package = "pimeta")
tau2h <- pimeta::tau2h(sbp$y, sbp$sigmak)
pimeta::i2h(sbp$sigmak, tau2h$tau2h)
```

pain *Pain data*

Description

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

Hauser, W., Bernardy, K, Uceyler, N., and Sommer, C. (2009). Treatment of fibromyalgia syndrome with antidepressants: a meta-analysis. *JAMA*. **301**(2): 198-209. https://doi.org/10.1001/jama.2008.944

Riley, R. D., Higgins, J. P. T, and Deeks, J. J. (2011). Interpretation of random effects meta-analyses. *BMJ*. **342**: d549. https://doi.org/10.1136/bmj.d549

pima *Calculating Prediction Intervals*

Description

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 alpha level of the prediction interval
method	the calculation method for the pretiction 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 τ^2 with an approximate variance estimator for the average effect, $(1/\sum \hat{w}_i)^{-1}$, $df = K - 2$).
- HK: Partlett–Riley (2017) prediction interval (the REML estimator for τ^2 with the Hartung (1999)'s variance estimator [the Hartung and Knapp (2001)'s estimator] for the average effect, $df = K - 2$).
- SJ: Partlett–Riley (2017) prediction interval / (the REML estimator for τ^2 with the Sidik and Jonkman (2006)'s bias coreccted variance estimator for the average effect, $df = K - 2$).
- KR: Partlett–Riley (2017) prediction interval / (the REML estimator for τ^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 τ^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 τ^2
upper	the upper limit of random numbers of τ^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 τ^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 τ^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

Higgins, J. P. T, Thompson, S. G., Spiegelhalter, D. J. (2009). A re-evaluation of random-effects meta-analysis. *J R Stat Soc Ser A Stat Soc.* **172**(1): 137-159. https://doi.org/10.1111/j.1467-985X.2008.00552.x

Partlett, C, and Riley, R. D. (2017). Random effects meta-analysis: Coverage performance of 95 confidence and prediction intervals following REML estimation. *Stat Med.* **36**(2): 301-317. https://doi.org/10.1002/sim.7140

Nagashima, K., Noma, H., and Furukawa, T. A. (2018). Prediction intervals for random-effects meta-analysis: a confidence distribution approach. *Stat Methods Med Res. In press*. https://doi.org/10.1177/0962280218773520.

Hartung, J. (1999). An alternative method for meta-analysis. *Biom J.* **41**(8): 901-916. https://doi.org/10.1002/(SICI)1521-4036(199912)41:8<901::AID-BIMJ901>3.0.CO;2-W.

Hartung, J., and Knapp, G. (2001). On tests of the overall treatment effect in meta-analysis with normally distributed responses. *Stat Med.* **20**(12): 1771-1782. https://doi.org/10.1002/sim.791.

Sidik, K., and Jonkman, J. N. (2006). Robust variance estimation for random effects meta-analysis. *Comput Stat Data Anal.* **50**(12): 3681-3701. https://doi.org/10.1016/j.csda.2005.07.019.

Kenward, M. G., and Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics.* **53**(3): 983-997. https://www.ncbi.nlm.nih.gov/pubmed/9333350.

DerSimonian, R., and Laird, N. (1986). Meta-analysis in clinical trials. *Control Clin Trials.* **7**(3): 177-188.

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")
```

`plot.cima` *Plot Results*

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

```
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

```
## 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

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

print.cima *Print Results*

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.

print.pima *Print Results*

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.

print.pima_tau2h *Print Results*

Description

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

Usage

```
## 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 Chiqaure Random Variables*

Description

The cumulative distribution function for the distribution of a positive linear combination of χ^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

```
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.

Value

- prob: the distribution function.

References

Farebrother, R. W. (1984). Algorithm AS 204: the distribution of a positive linear combination of χ^2 random variables. *J R Stat Soc Ser C Appl Stat.* **33**(3): 332–339. https://rss.onlinelibrary.wiley.com/doi/10.2307/2347721.

Examples

```
# Table 1 of Farabrother (1984)
# Q6 (The taget 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

Riley, R. D., Higgins, J. P. T, and Deeks, J. J. (2011). Interpretation of random effects meta-analyses. *BMJ.* **342**: d549. https://doi.org/10.1136/bmj.d549

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

Roberts, M. E., Tchanturia, K., Stahl, D., Southgate, L., and Treasure, J. (2007). A systematic review and meta-analysis of set-shifting ability in eating disorders. *Psychol Med.* **37**(8): 1075-1084. https://doi.org/10.1017/S0033291707009877

Higgins, J. P. T, Thompson, S. G., Spiegelhalter, D. J. (2009). A re-evaluation of random-effects meta-analysis. *J R Stat Soc Ser A Stat Soc.* **172**(1): 137-159. https://doi.org/10.1111/j.1467-985X.2008.00552.x

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").

- DL: DerSimonian–Laird estimator (DerSimonian & Laird, 1986).
- VC: Variance component type estimator (Hedges, 1983).
- PM: Paule–Mandel estimator (Paule & Mandel, 1982).
- HM: Hartung–Makambi estimator (Hartung & Makambi, 2003).
- 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).
- SJ: Sidik–Jonkman estimator (Sidik & Jonkman, 2005).
- SJ2: Sidik–Jonkman improved estimator (Sidik & Jonkman, 2007).
- EB: Empirical Bayes estimator (Morris, 1983).
- 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 τ^2.
- lci, uci: the lower and upper confidence limits $\hat{\tau}_l^2$ and $\hat{\tau}_u^2$.

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Examples

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

Index

∗ **datasets**
hyp, 6
pain, 8
sbp, 15
setshift, 16
∗ **package**
pimeta-package, 2

bootPI *(*pima*)*, 8

cima, 2, *10*
convert_bin, 5

htsdl *(*pima*)*, 8
htsreml *(*pima*)*, 8
hyp, 6

i2h, 7

pain, 8
pima, *4*, 8
pima_boot *(*pima*)*, 8
pima_hts *(*pima*)*, 8
pima_htsreml *(*pima*)*, 8
pimeta-package, 2
plot.cima, 11
plot.pima, *10*, 12
print.cima, 13
print.pima, *10*, 13
print.pima_tau2h, 14
pwchisq, 14

sbp, 15
setshift, 16

tau2h, 16