Package: twotrials (via r-universe)

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Title Compatible Point Estimates, Confidence Intervals, and P-Values for Two Trials

Description Implements combined p-value functions for two trials along with compatible combined point and interval estimates as described in Pawel, Roos, and Held (2025) <doi:10.48550/arXiv.2503.10246>.

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Encoding UTF-8

Suggests roxygen2, tinytest

NeedsCompilation no

RoxygenNote 7.3.1

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BugReports https://github.com/SamCH93/twotrials/issues

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`mu2TR` *Combined estimation function from the two-trials rule*

Description

This function computes parameter estimates from the combined estimation function based on the two-trials rule

Usage

```
mu2TR(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments (for consistency with other estimation functions)

Value

The parameter estimate based on the two-trials rule

Author(s)

Samuel Pawel

See Also

`p2TR`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
mu2TR(a = c(0.975, 0.5, 0.025), t1 = -0.4942, t2 = -0.1847, se1 = 0.1833,
      se2 = 0.1738, alternative = "less")
```

`muEdgington` *Combined estimation function from Edgington's method*

Description

This function computes parameter estimates from the combined estimation function based on Edgington's method

Usage

```
muEdgington(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments for `stats::uniroot`

Value

The parameter estimate based on Edgington's method

Author(s)

Samuel Pawel

See Also

`pEdgington`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
muEdgington(a = c(0.975, 0.5, 0.025), t1 = -0.4942, t2 = -0.1847, se1 = 0.1833,
            se2 = 0.1738, alternative = "less")
```

`muFisher` *Combined estimation function from Fisher's method*

Description

This function computes parameter estimates from the combined estimation function based on Fisher's method

Usage

```
muFisher(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments for `stats::uniroot`

Value

The parameter estimate based on Fisher's method

Author(s)

Samuel Pawel

See Also

`pFisher`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
muFisher(a = c(0.975, 0.5, 0.025), t1 = -0.4942, t2 = -0.1847, se1 = 0.1833,
         se2 = 0.1738, alternative = "less")
```

`muMA` *Combined estimation function from fixed-effect meta-analysis*

Description

This function computes parameter estimates from the combined estimation function based on fixed-effect meta-analysis

Usage

```
muMA(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments (for consistency with other estimation functions)

Value

The parameter estimate based on fixed-effect meta-analysis

Author(s)

Samuel Pawel

See Also

`muMA`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
muMA(a = c(0.975, 0.5, 0.025), t1 = -0.4942, t2 = -0.1847, se1 = 0.1833,
     se2 = 0.1738, alternative = "less")
```

`muPearson` *Combined estimation function from Pearson's method*

Description

This function computes parameter estimates from the combined estimation function based on Pearson's method

Usage

```
muPearson(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments for `stats::uniroot`

Value

The parameter estimate based on Pearson's method

Author(s)

Samuel Pawel

See Also

`pPearson`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
muPearson(a = c(0.975, 0.5, 0.025), t1 = -0.4942, t2 = -0.1847, se1 = 0.1833,
          se2 = 0.1738, alternative = "less")
```

`muTippett` *Combined estimation function from Tippett's method*

Description

This function computes parameter estimates from the combined estimation function based on Tippett's method

Usage

```
muTippett(a = 0.5, t1, t2, se1, se2, alternative = "greater", ...)
```

Arguments

`a`	P-value function quantile corresponding to the parameter estimate. Defaults to `0.5`, which corresponds to the median estimate. Set to `a = c(0.025, 0.975)` to obtain limits of a 95% confidence interval
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`...`	Additional arguments (for consistency with other estimation functions)

Value

The parameter estimate based on Tippett's method

Author(s)

Samuel Pawel

See Also

`pTippett`

Examples

```
## 95% CI and median estimate for logRR in RESPIRE trials
muTippett(a = c(0.975, 0.5, 0.025), t1 = -0.491, t2 = -0.185, se1 = 0.179,
          se2 = 0.174, alternative = "less")
```

`p2TR` *Combined p-value from the two-trials rule*

Description

This function computes the combined p-value based on two parameter estimates using the two-trials rule (also known as the maximum method)

Usage

```
p2TR(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on the two-trials rule

Author(s)

Samuel Pawel

See Also

`mu2TR`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
p2TR(mu = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
     alternative = "less")
```

`pEdgington` *Combined p-value from Edgington's method*

Description

This function computes the combined p-value based on two parameter estimates using Edgington's method (also known as the sum method)

Usage

```
pEdgington(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on Edgington's method

Author(s)

Samuel Pawel

See Also

`muEdgington`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
pEdgington(mu = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
           alternative = "less")
```

`pFisher` *Combined p-value from Fisher's method*

Description

This function computes the combined p-value based on two parameter estimates using the Fisher's method (also known as the product method)

Usage

```
pFisher(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on Fisher's method

Author(s)

Samuel Pawel

See Also

`muFisher`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
pFisher(mu = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
        alternative = "less")
```

`plot.twotrials` *Plot method for class* `"twotrials"`

Description

Plot method for class `"twotrials"`

Usage

```
## S3 method for class 'twotrials'
plot(
  x,
  xlim = c(min(x$isummaries$lower), max(x$isummaries$upper)),
  two.sided = FALSE,
  plot = TRUE,
  ...
)
```

Arguments

`x`	Object of class `"twotrials"`
`xlim`	x-axis limits. Defaults to the confidence interval range of trial 1 and trial 2
`two.sided`	Logical indicating whether the p-value functions should be converted to a two-sided p-value function via the centrality function 2min(p, 1 - p). Defaults to `FALSE`
`plot`	Logical indicating whether p-value functions should be plotted. Defaults to `TRUE`
`...`	Other arguments (for consistency with the generic)

Value

Plots combined p-value functions and invisibly returns a data frame containing the data underlying the plot

Author(s)

Samuel Pawel

See Also

`twotrials`

Examples

```
## logRR estimates from RESPIRE trials
res <- twotrials(null = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
                 alternative = "less", level = 0.95)
plot(res) # one-sided p-value functions
plot(res, two.sided = TRUE) # two-sided p-value functions
```

`pMA` *Combined p-value from fixed-effect meta-analysis*

Description

This function computes the combined p-value based on two parameter estimates using fixed-effect meta-analysis (equivalent to Stouffer's p-value combination method with suitable weights)

Usage

```
pMA(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on fixed-effect meta-analysis

Author(s)

Samuel Pawel

See Also

`pMA`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
pMA(mu = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
    alternative = "less")
```

`pPearson` *Combined p-value from Pearson's method*

Description

This function computes the combined p-value based on two parameter estimates using Pearson's method

Usage

```
pPearson(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on Pearson's method

Author(s)

Samuel Pawel

See Also

`muPearson`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
pPearson(mu = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
         alternative = "less")
```

`print.twotrials` *Print method for class* `"twotrials"`

Description

Print method for class `"twotrials"`

Usage

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

Arguments

`x`	Object of class `"twotrials"`
`digits`	Number of digits for formatting of numbers
`...`	Other arguments (for consistency with the generic)

Value

Prints text summary in the console and invisibly returns the `"twotrials"` object

Author(s)

Samuel Pawel

See Also

`twotrials`

Examples

```
## logRR estimates from RESPIRE trials
twotrials(null = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
          alternative = "less", level = 0.95)
```

`pTippett` *Combined p-value from Tippett's method*

Description

This function computes the combined p-value based on two parameter estimates using Tippett's method (also known as the minimum method)

Usage

```
pTippett(mu = 0, t1, t2, se1, se2, alternative = "greater")
```

Arguments

`mu`	Null value. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`

Value

The combined p-value based on Tippett's method

Author(s)

Samuel Pawel

See Also

`muTippett`

Examples

```
## p-value for H0: logRR = 0 in RESPIRE trials
pTippett(mu = 0, t1 = -0.491, t2 = -0.185, se1 = 0.179, se2 = 0.174,
         alternative = "less")
```

`twotrials` *Combined p-value function inference for two trials*

Description

This function computes combined p-values, point estimates, and confidence intervals based on two parameter estimates using fixed-effect meta-analysis, the two-trials rule, Edgington's, Fisher's, Pearson's, and Tippett's combination methods

Usage

```
twotrials(null = 0, t1, t2, se1, se2, alternative = "greater", level = 0.95)
```

Arguments

`null`	Null value for which p-values should be computed. Defaults to `0`
`t1`	Parameter estimate from trial 1
`t2`	Parameter estimate from trial 2
`se1`	Standard error of the parameter estimate from trial 1
`se2`	Standard error of the parameter estimate from trial 2
`alternative`	One-sided alternative hypothesis. Can be either `"greater"` or `"less"`. Defaults to `"greater"`
`level`	Confidence interval level. Defaults to `0.95`

Value

Object of class `"twotrials"`, which is a list of the supplied arguments augmented with `pfuns` and `ipfuns` (combined and individual p-value functions), `mufuns` and `imufuns` (combined and individual estimation functions), and `summaries` and `isummaries` (combined and individual confidence intervals, point estimates, p-values, implicit weights) elements

Author(s)

Samuel Pawel

See Also

`pEdgington`, `muEdgington`, `pMA`, `muMA`, `pTippett`, `muTippett`, `p2TR`, `mu2TR`, `pFisher`, `muFisher`, `pPearson`, `muPearson`, `plot.twotrials`, `print.twotrials`

Examples

```
## logRR estimates from RESPIRE trials
twotrials(null = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
          alternative = "less", level = 0.95)

## compute 99.875% CIs instead
twotrials(null = 0, t1 = -0.4942, t2 = -0.1847, se1 = 0.1833, se2 = 0.1738,
          alternative = "less", level = 0.99875)
```

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