

# Package ‘twotrials’

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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](https://doi.org/10.48550/arXiv.2503.10246)>.

**License** GPL-3

**Encoding** UTF-8

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**URL** <https://github.com/SamCH93/twotrials>

**BugReports** <https://github.com/SamCH93/twotrials/issues>

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|       |                                                              |
|-------|--------------------------------------------------------------|
| mu2TR | <i>Combined estimation function from the two-trials rule</i> |
|-------|--------------------------------------------------------------|

---

**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 | <i>Plot method for class "twotrials"</i> |
|----------------|------------------------------------------|

---

## 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 $2\min(p, 1 - p)$ . 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 | <i>Print method for class "twotrials"</i> |
|-----------------|-------------------------------------------|

---

## 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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