Package: OssaNMA (via r-universe)

October 23, 2024

Type Package

Title Optimal Sample Size and Allocation with a Network Meta-Analysis

Version 0.1.2

Description A system for calculating the minimum total sample size needed to achieve a prespecified power or the optimal allocation for each treatment group with a fixed total sample size to maximize the power.

License GPL-3

Imports NlcOptim (>= 0.6), DEoptimR (>= 1.0.11)

Depends R(>= 3.5.0)

URL `https://github.com/fangshuye/OssaNMA`

BugReports `https://github.com/fangshuye/OssaNMA/issues`

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.2

Suggests knitr, rmarkdown, netmeta

VignetteBuilder knitr

Repository https://fangshuye.r-universe.dev

RemoteUrl https://github.com/fangshuye/ossanma

RemoteRef HEAD

RemoteSha 455d660783231a5ee7caf227cd93d177dcf08db3

Contents

`BRDdat` *Example dataset for network meta-analysis*

Description

This example dataset represents a previously published network of interventions for the treatment of Bovine Respiratory Disease (BRD) in feedlot cattle (O'Connor, Yuan, Cullen, Coetzee, Da Silva, and Wang, 2016). The dataset is comprised of 98 trials, 13 treatments and 204 arms. Each row represents the summary statistics for a pairwise comparison between two treatment in a trial.

Usage

```
data(BRDdat)
```

Format

An object of class `"data.frame"`

studlab study id (integer)

treat1 name of treatment 1 (character)

treat2 name of treatment 2 (character)

TE estimated treatment effect size (log odds ratio) between treat1 and treat2

seTE standard error of TE

References

O'Connor, A. M., Yuan, C., Cullen, J. N., Coetzee, J. F., Da Silva, N., & Wang, C. (2016). A mixed treatment meta-analysis of antibiotic treatment options for bovine respiratory disease–an update. Preventive veterinary medicine, 132, 130-139..

Examples

```
data(BRDdat)
head(BRDdat)
```

`ssanma` *Calculate the optimal sample size allocation for a new two-arm trial when analyze it with the existing network*

Description

This function calculates the optimal sample size allocation for each treatment group with a fixed total sample size when planning a new two-arm trial with binary outcome.

Usage

```
ssanma(
  p1,
  p2,
  enma_sigma,
  N,
  sig.level = 0.05,
  method = "with",
  allocation = "uneven"
)
```

Arguments

`p1`	Risk of treatment 1
`p2`	Risk of treatment 2
`enma_sigma`	Standard error of the estimated effect size (log odds ratio) between treatment 1 and treatment 2 from the existing network
`N`	Number of total sample size
`sig.level`	Significance level, the default value is 0.05
`method`	a character string specifying the method of analyzing the new trial, must be one of 'with' (default) or 'without'
`allocation`	a character string specifying the type of sample size allocation between two groups, must be one of 'uneven' (default) or 'even'.

Value

A list with the following components:

`sample_alloc`	Sample size allocation to each treatment group.
`power`	Power of the test.

Examples

```
ssanma(p1 = 0.2, p2 = 0.3, enma_sigma = 0.4, N = 200)
```

`ssnma` *Calculate the optimal sample sizes for a new two-arm trial when analyze it with the existing network*

Description

This function calculates the optimal sample size for each treatment group to achieve a pre-specified power when planning a new two-arm trial with binary outcome.

Usage

```
ssnma(
  p1,
  p2,
  enma_sigma = NULL,
  power.level,
  sig.level = 0.05,
  method = "with",
  allocation = "uneven"
)
```

Arguments

`p1`	Risk of treatment 1
`p2`	Risk of treatment 2
`enma_sigma`	Standard error of the estimated effect size (log odds ratio) between treatment 1 and treatment 2 from the existing network
`power.level`	Power of test we want to obtain
`sig.level`	Significance level, the default value is 0.05
`method`	a character string specifying the method of analyzing the new trial, must be one of 'with' (default) or 'without'
`allocation`	a character string specifying the type of sample size allocation between two groups, must be one of 'uneven' (default) or 'even'.

Value

A list with the following components:

`sample_size`	Sample size for each treatment group.
`power`	Power of the test.

Examples

```
ssnma(p1 = 0.2, p2 = 0.3, enma_sigma = 0.4, power = 0.8)
```

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