Package 'mtdesign'

Type Package

Title Mander and Thompson Designs

Version 0.1.2

Date 2024-11-01

Description Implements Mander & Thompson's (2010)
<doi:10.1016/j.cct.2010.07.008> methods for two-stage designs
optimal under the alternative hypothesis for phase II [cancer] trials. Also
provides an implementation of Simon's (1989)
<doi:10.1016/0197-2456(89)90015-9> original methodology and
allows exploration of the operating characteristics of sub-optimal designs.

Language en-GB

License GPL (>= 3)

Encoding UTF-8

URL https://github.com/openpharma/mtdesign

BugReports https://github.com/openpharma/mtdesign/issues

RoxygenNote 7.3.2

Imports dplyr, futile.logger, ggplot2, magrittr, methods, Rcpp, rlang,
tibble, tidyr

LinkingTo Rcpp, BH

Suggests parallel, testthat (>= 3.0.0), withr

Config/testthat/edition 3

NeedsCompilation yes

Author John Kirkpatrick [aut, cre] (<https://orcid.org/0000-0001-7790-3708>)

Maintainer John Kirkpatrick <mtdesign@puzzledface.net>

Repository CRAN

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augmentGrid   *Augment a grid of candidate designs with type 1 and type 2 error prob-*
                            abilities, expected sample sizes and probabilities of early termination

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Description

Augment a grid of candidate designs with type 1 and type 2 error probabilities, expected sample
sizes and probabilities of early termination

Usage

```
augmentGrid(d, parallel = TRUE, cores = NA, minChunkSize = 1e+05)
```

Arguments

d	a tibble created by 'createGrid'
parallel	use parallelisation if available
cores	the number of cores to use when parallelising. If <code>NA</code>, all available cores are requested
minChunkSize	The minimum size of the grid before paralellisation is attempted

Value

an augmented grid tibble

Usage Notes

Regardless of the value of 'parallel', parallelisation is only used if the size of the grid is greater than
<code>chunkSize</code>. If paralellisation is requested and needed, an exception is thrown if the
parallel package is not available.

Examples

```
x <- createGrid(p0 = 0.1, p1 = 0.30, alpha = 0.1, beta = 0.1, nMin = 24, nMax = 32) %>%
  augmentGrid(parallel = FALSE)
```

---

createGrid   *Create a grid of candidate designs*

Description

Create a grid of candidate designs

Usage

```
createGrid(
  p0,
  p1,
  alpha = 0.1,
  beta = NA,
  power = ifelse(is.na(beta), 0.9, 1 - beta),
  nMin = NA,
  nMax = NA,
  mander = TRUE
)
```

Arguments

p0	the response rate under the null hypothesis
p1	the response rate under the alternate hypothesis
alpha	the desired (one-sided) type 1 error rate
beta	the desired type 2 error rate
power	an alternative to beta
nMin	the lower bound for the search grid. If NA, searchBounds is called to provide an appropriate value
nMax	the lower bound for the search grid. If NA, searchBounds is called to provide an appropriate value
mander	is a Mander & Thompson or a Simon's design required?

Value

a tibble. See Usage notes for a list and description of columns.

Examples

```
# Standard use for a Simon's 2-stage design
x <- createGrid(p0 = 0.1, p1 = 0.5, alpha = 0.1, beta = 0.1, mander = FALSE)
# Custom search bounds for a Mander & Thompson design
y <- createGrid(p0 = 0.1, p1 = 0.4, alpha = 0.1, beta = 0.1, nMin = 20, nMax = 30)
```

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obtainDesign   *Finds optimal and minimax designs for either Simon's 2-stage or Man-*
                                der & Thompson studies

Description

obtainDesign is essentially a wrapper for calls to [createGrid](#) and [augmentGrid](#) followed by some
simple filtering of the candidate designs to identify the optimal and minimax designs.

Usage

```
obtainDesign(
  grid = NULL,
  p0 = NA,
  p1 = NA,
  alpha = ifelse(is.null(grid), 0.05, NA),
  beta = ifelse(is.null(grid), 0.1, NA),
  fullGrid = FALSE,
  ...
)
```

Arguments

grid	Optional. A tibble created by createGrid. If NULL, then p0, p1, alpha and beta must be specified and createGrid is called to generate the required grid. If not NULL then p0, p1, alpha and beta are ignored
p0	the response rate under the null hypothesis
p1	the response rate under the alternate hypothesis
alpha	the desired (one-sided) type 1 error rate
beta	the desired type 2 error rate
fullGrid	should the full grid of all possible designs be returned, or simply the optimal and minimax solutions? For a Mander and Thompson design, optimal and minimax designs are returned for both the null and alternate hypotheses. See Usage Notes below.
...	passed to 'createGrid' or 'augmentGrid'. In particular mander=TRUE for a Mander & Thompson design or mander=FALSE for a Simon's 2-stage design.

Value

a tibble created by [createGrid](#). If fullGrid == FALSE the table contains an additional column,
Criterion indicating the type of design. Possible values for Criterion are "optimal" and "mini-
max" for Simon's designs and "optimalNull", "optimalAlt", "minimaxNull" and "minimaxAlt" for
Mander & Thompson designs.

Usage notes

If grid is not NULL it is possible that none of the candidate designs are acceptable (that is, satisfy both the significance level and power requirements). If this is the case and fullGrid == FALSE, then an empty tibble is returned. If versbose == TRUE a warning message is also printed. If fullGrid == TRUE the full grid of all designs considered is returned. This can then be further interrogated to find optimal designs under constraints - for example with fixed stage sizes.

Examples

```
# Standard use (Simon's 2-stage design)
createGrid(p0 = 0.05, p1 = 0.25, alpha = 0.05, beta = 0.2, mander = FALSE) %>%
  augmentGrid(parallel = FALSE) %>%
  obtainDesign()
# Constrained stage sizes
createGrid(p0 = 0.25, p1 = 0.45, alpha = 0.05, beta = 0.2) %>%
  dplyr::filter(nStage1 == 8) %>%
  augmentGrid(parallel = FALSE) %>%
  obtainDesign()
```

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powerPlot   *Plot the power curve(s) for the given design(s)*

Description

Plot the power curve(s) for the given design(s)

Usage

```
powerPlot(grid, probs = seq(0, 1, 0.01))
```

Arguments

grid   the tibble containing the designs to be plotted

probs   the response rates for which the rejection probabilities are to be plotted

Value

the ggplot object containing the power curve(s)

Examples

```
createGrid(p0 = 0.05, p1 = 0.25, alpha = 0.05, beta = 0.2, mander = FALSE) %>%
  augmentGrid(cores = 2) %>%
  obtainDesign() %>%
  powerPlot(probs = seq(0, 0.5, 0.025))
```

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searchBounds   *Obtain default bounds for the construction of the search grid.*

Description

The formula used is the continuity corrected Normal approximation from Fleiss et al (2003).

Usage

```
searchBounds(p0, p1, alpha = 0.05, beta = 0.2, twoSided = TRUE)
```

Arguments

p0	the response rate under the null hypothesis
p1	the response rate under the alternate hypothesis
alpha	the desired (one-sided) type 1 error rate
beta	the desired type 2 error rate
twoSided	two- or one-sided significance level?

Value

a list with three elements: "n" - the single stage sample size from Fleiss et al; "min" - the lower bound, 0.8*n; "max" - the upper bound, 2*n. floor() and ceiling() are applied as appropriate.

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