Package ‘graposas’

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Type Package

Title Graphical Approach Optimal Sample Size

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Description Graphical approach provides a useful framework for multiplicity adjustment in clinical trials with multiple endpoints. This package includes statistical methods to optimize sample size over initial weight and transition probability in a graphical approach under a common setting, which is to use marginal power for each endpoint in a trial design.


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Encoding UTF-8

Depends R (>= 4.2.0)

Imports GA (>= 3.0.0), graphics (>= 4.2.0), mvtnorm (>= 1.1.0), stats

(>= 4.0.0)

RoxygenNote 7.2.3

NeedsCompilation no

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szgaGA

Sample size optimization using graphical approach in clinical trial design with three hypotheses

Description

This function computes the optimal design using graphical approach along with the minimum sample size when three hypotheses are considered in a clinical trial.

Usage

szgaGA(
  alpha,
  betaVec,
  deltaVec,
  cVec,
  rhoMat,
  lower = c(1, rep(1e-06, 2), rep(1e-06, 3)),
  upper = c(10000, rep(1 - 1e-06, 2), rep(1 - 1e-06, 3)),
  gaIter = c(20, 20),
  penPara = 0.1,
  seed = 2022
)

Arguments

alpha A value of overall type I error rate
betaVec A vector of one minus marginal powers for testing H1, H2 and H3, respectively
deltaVec A vector of effect sizes for testing H1, H2 and H3, respectively
cVec A vector of coefficients. When testing continuous endpoints, these coefficients are exactly one. When testing binary endpoints, the values are roughly one but not exactly one
rhoMat A matrix of the correlation coefficients among three hypotheses
lower A vector of lower limit of sample size n, initial weights w1 and w2, and transition probabilities g12, g23 and g31
upper A vector of upper limit of sample size n, initial weights w1 and w2, and transition probabilities g12, g23 and g31
gaIter A vector of two numbers. The first one is the parameter maxiter of the ga function, and the second one is the parameter run of the ga function
penPara A number of penalization parameter for optimization to balance the sample size requirement and the power requirement
seed A number of the seed of the random number generator
Details

R package GA is used for Genetic Algorithms.

Value

a vector of six numbers: the optimal sample size $n$, initial weights $w_1$ and $w_2$, and transition probabilities $g_{12}$, $g_{23}$ and $g_{31}$

Author(s)

Jiangtao Gou

References


Examples

```r
start <- Sys.time()
szgaGA(alpha = 0.025, betaVec = c(0.15, 0.20, 0.10),
       deltaVec = c(0.1111952, 0.1037179, 0.1182625),
       cVec = c(1.003086, 1.002686, 1.00349),
       rhoMat = matrix(c(1,0.5,0.8, 0.5,1,0.6, 0.8,0.6,1), nrow = 3, byrow = TRUE),
       lower = c(750, rep(0.01, 2), rep(0.01, 3)),
       upper = c(850, rep(0.99, 2), rep(0.99, 3)),
       gaIter = c(10, 5),
       penPara = 0.015,
       seed = 234)
end <- Sys.time()
data.frame(time = end - start)
```

Description

This function computes the optimal design using graphical approach along with the minimum sample size when three hypotheses are considered in a clinical trial. The transition matrix is pre-specified and fixed.
Usage

szgaGAw(
  alpha,
  betaVec,
  deltaVec,
  cVec,
  rhoMat,
  transMat,
  lower = c(1, rep(1e-06, 2)),
  upper = c(10000, rep(1 - 1e-06, 2)),
  gaIter = c(20, 20),
  penPara = 0.1,
  seed = 2022
)

Arguments

alpha        a value of overall type I error rate
betaVec      a vector of one minus marginal powers for testing H1, H2 and H3, respectively
deltaVec     a vector of effect sizes for testing H1, H2 and H3, respectively
cVec         a vector of coefficients. When testing continuous endpoints, these coefficients
              are exactly one. When testing binary endpoints, the values are roughly one but
              not exactly one
rhoMat       a matrix of the correlation coefficients among three hypotheses
transMat     a matrix of the fixed transition probabilities among three hypotheses
lower        a vector of lower limit of sample size n, and initial weights w1 and w2, where
              w3 is computed by 1 - w1 - w2
upper        a vector of upper limit of sample size n, and initial weights w1 and w2, where
              w3 is computed by 1 - w1 - w2
gaIter       a vector of two numbers. The first one is the parameter maxiter of the ga
              function, and the second one is the parameter run of the ga function
penPara      a number of penalization parameter for optimization to balance the sample size
              requirement and the power requirement
seed         a number of the seed of the random number generator

Details

R package GA is used for Genetic Algorithms.

Value

a vector of three numbers: the optimal sample size n, and initial weights w1 and w2

Author(s)

Jiangtao Gou
szgaViz

References


Examples

```r
start <- Sys.time()
szgaGAw(alpha = 0.025, betaVec = c(0.15, 0.20, 0.10),
       deltaVec = c(0.1111952, 0.1037179, 0.1335865),
       cVec = c(1.003086, 1.002686, 1.004451),
       rhoMat = matrix(c(1,0.5,0.8,0.5,1,0.6,0.8,0.6,1), nrow = 3, byrow = TRUE),
       transMat = matrix(c(0,0.50,0.50,0.5,0,0.5,0.5,0.5,0), nrow = 3, byrow = TRUE),
       lower = c(700, rep(0.05, 2)),
       upper = c(900, rep(0.95, 2)),
       gaIter = c(10, 5),
       penPara = 0.0135,
       seed = 234)
end <- Sys.time()
data.frame(time = end - start)
```

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szgaViz

Sample size optimization using graphical approach in clinical trial design with two hypotheses

Description

This function computes the optimal design using graphical approach along with the minimum sample size when two hypotheses are considered in a clinical trial.

Usage

```r
szgaViz(
    alpha,
    beta1,
    beta2,
    deltaVec,
    cVec,
    rho,
    wunit,
    initIntvl,
    visualization = TRUE
)
```
Arguments

- **alpha**: a value of overall type I error rate
- **beta1**: a value of one minus marginal powers for testing H1
- **beta2**: a value of one minus marginal powers for testing H2
- **deltaVec**: a vector of effect sizes for testing H1 and H2, respectively
- **cVec**: a vector of coefficients. When testing continuous endpoints, these coefficients are exactly one. When testing binary endpoints, the values are roughly one but not exactly one
- **rho**: a value of correlation coefficients between two hypotheses
- **wunit**: a value of initial weight on H1 for grid search and visualization
- **initIntvl**: a vector of lower and upper limits for searching optimal sample size
- **visualization**: a logical value, indicating whether a visualization is needed

Value

A vector of three numbers: the optimal weight on H1 $w_1$, and optimal sample size $n_1$ (based on H1) and $n_2$ (based on H2), where $n_1$ and $n_2$ should be roughly the same

Author(s)

Jiangtao Gou
Fengqing (Zoe) Zhang

References


Examples

```r
szgaViz(alpha = 0.05, beta1 = 0.20, beta2 = 0.20,
        deltaVec = c(0.3, 0.3), cVec = c(1,1), rho = 0.0,
        wunit = 0.01, initIntvl = c(1,1000),
        visualization = FALSE)
```
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