

Package ‘gset’

February 20, 2015

Type Package

Title Group Sequential Design in Equivalence Studies

Version 1.1.0

Date 2014-11-16

Author Fang Liu [aut, cre]

Maintainer Fang Liu <fang.liu.131@nd.edu>

Depends R (>= 3.0.2), Hmisc, mvtnorm, MCMCpack, graphics

Description calculate equivalence and futility boundaries based on the exact bivariate T test statistics for group sequential designs in studies with equivalence hypotheses.

URL <http://www.r-project.org>, <http://www3.nd.edu/~fliu2/>

BugReports <http://www3.nd.edu/~fliu2/>

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2014-11-20 00:47:24

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gset-package	<i>group sequential design of equivalence studies based on exact bivariate t statistics</i>
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Description

gset computes the critical values in the sequential testing of an equivalence hypothesis. The package calculates the exact equivalence boundaries and futility boundaries (binding or nonbinding) using the exact sequential test based on the bivariate non-central t statistics. It also produces the boundaries plots; and examines the operating characteristics of a given sequential design via the calculation of empirical Type I error rate, empirical power, expected sample size, and the probability of stopping at interim look due to equivalence or futility.

Details

Package: gset
Type: Package
Version: 1.1.0
Date: 2014-11-16
License: GLP (>=2)

The package contains 8 functions: 4 functions can be used to compute the equivalence and futilities boundaries (equivonly, nonbinding, binding, nminmax); 1 function to compute the sample size of an equivalence study in the traditional nonsequential setting (nfix); 1 function to compute the sample size of an equivalence study in the sequential setting (nminmax); 2 functions for generating the boundary plots (figureE, figureEF); and 1 function to examine the the operating characteristics of a given sequential design.

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, Computational Statistics and Data Analysis, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, the R Journal (to appear)

Examples

```
## Not run:  
L <- -0.2  
U <- 0.2  
theta <- 0  
sigma <- 0.4
```

```

alpha <- 0.05
beta <- 0.2
K <- 4
r <- 1

# non-sequential
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

# sequential without futility
bound1<- equivonly(L, U, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)
# figureE (bound1, K)

# sequential with nonbinding futility
bound2 <- nonbinding(L,U,theta,sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha,beta)

# sequential with binding futility
bound3 <- binding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)

# finding nminmax with nonbinding futility
bound4 <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)
figureEF(bound4, K)

# finding nminmax with binding futility
bound5 <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)
figureEF(bound5, K)

# operating characteristics under H0
theta <- L
oc1 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound1, futility=FALSE)
oc2 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound2, futility=TRUE)
oc3 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound3, futility=TRUE, binding=TRUE)
oc4 <- oc(L, U, theta, sigma, K, bound4$n1minmax, bound4$n2minmax, bound4, futility=TRUE)
oc5 <- oc(L, U, theta, sigma, K, bound5$n1minmax, bound5$n2minmax, bound5,
futility=TRUE, binding=TRUE)

# operating characteristics under H1
theta <- 0
oc6 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound1, futility=FALSE)
oc7 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound2, futility=TRUE)
oc8 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound3, futility=TRUE, binding=TRUE)
oc9 <- oc(L, U, theta, sigma, K, bound4$n1minmax, bound4$n2minmax, bound4, futility=TRUE)
oc10<- oc(L, U, theta, sigma, K, bound5$n1minmax, bound5$n2minmax, bound5,
futility=TRUE, binding=TRUE)

## End(Not run)

```

Description

Computation of equivalence and binding futility boundaries for group sequential designs in studies with equivalence hypothesis via Monte Carlo simulations

Usage

```
binding(l, u, theta, sigma, n1, n2, t.vec, type1, type2, gamma = rep(-4, 2),
       crange = c(-10, 10), drange = c(-10, 10), force = TRUE, plot = TRUE,
       ll = 3, ul = 6, n.sim = 10000, seed = NULL)
```

Arguments

l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
theta	true mean difference between 2 groups
sigma	between-subject standard deviation of the response variable for two independent groups; within subject standard deviation of the response variable for paired groups
n1	size (number of subjects) in group 1
n2	size (number of subjects) in group 2
t.vec	cumulative time points for the interim looks assuming a constant accrual rate. For example, if a study has equally spaced 4 looks including the final look, then t.vec=1:4/4. It can any vector as long as it is increasing and the last element is 1.
type1	overall Type I error rate
type2	overall Type II error rate
gamma	The gamma parameter in the gamma cumulative error spending function (Hwang, Shih, and DeCani 1990). Error spending given a t.vec is = total error rate*(1-exp(-gamma*t.vec))/(1-exp(-gamma)). gamma= 1 produces Pocock-type error spending function; gamma = -4 produces O'Brien-Fleming type error spending function. Default gamma = -4
crange	a 2-dimensional vector containing the end-points of the interval from which the critical values for claiming equivalence will be solved. Default crange = c(-10,10)
drange	a 2-dimensional vector containing the end-points of the interval from which the critical values for claiming futility will be solved. Default drange = c(-10,10)
force	Whether to force the futility boundaries to equal to the equivalence boundaries in the last look. Default force = TRUE
plot	Whether to generate the boundaries plot. Default plot = TRUE
ll	a parameter in the boundary plot; the short arm of the t(L) and t(U) axes
ul	a parameter in the boundary plot; the long arm of the t(L) and t(U) axes
n.sim	number of randomly simulated samples in computation of the boundaries via the Monte Carlo simulation approach. Default n.sim=1e4
seed	seed used in the Monte Carlo computation. If non-specified, the seed is set randomly.

Value

typeI	vector of cumulative stage Type I error rate
typeII	vector of cumulative stage Type II error rate
equivL	vector of the equivalence boundary $c(L)$ at each stage
equivU	vector of the equivalence boundary $c(U)$ at each stage
futilL	vector of the futility boundary $d(L)$ at each stage
futilU	vector of the futility boundary $d(U)$ at each stage
boundary plots	if <code>plot=TRUE</code> , a series of boundary plots will be produced, one for look

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

- Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral F -statistics, *Computational Statistics and Data Analysis*, 77:14-24
- Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central F -statistics, *the R Journal* (to appear)

See Also

[nonbinding](#), [equivonly](#), [nminmax](#), [nfix](#), [oc](#), [figureE](#), [figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
r <- 1
# the sample size per group with a traditional nonsequential design
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

# default
# there are two ways to generate the boundary plots
# 1. specify plot=TRUE (default) in "binding()"
binding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)

# 2. specify plot=FALSE in "binding()" and apply the "figureEF()" command
bound <- binding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, plot=FALSE)
figureEF(bound, K)

# obtain nminmax
```

```

bound <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, binding=TRUE)
bound
figureEF(bound, K)

## End(Not run)

```

equivonly	<i>equivalence boundaries in group sequential equivalence studies that only stop for equivalence</i>
-----------	--

Description

Computation of equivalence boundaries for group sequential designs in studies with equivalence hypothesis that only stop for equivalence via Monte Carlo simulations

Usage

```

equivonly(l, u, sigma, n1, n2, t.vec, type1, gamma = -4, crange = c(-10, 10),
plot = TRUE, ll = 3, ul = 6, n.sim = 10000, seed = NULL)

```

Arguments

l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
sigma	between-subject standard deviation of the response variable for two independent groups; within subject standard deviation of the response variable for paired groups
n1	size (number of subjects) in group 1
n2	size (number of subjects) in group 2
t.vec	cumulative time points for the interim looks assuming a constant accrual rate. For example, if a study has equally spaced 4 looks including the final look, then t.vec=1:4/4. It can any vector as long as it is increasing and the last element is 1.
type1	overall Type I error rate
gamma	The gamma parameter in the gamma cumulative error spending function (Hwang, Shih, and DeCani 1990). Error spending given a t.vec is = total error rate*(1-exp(-gamma*t.vec))/(1-exp(-gamma)). gamma= 1 produces Pocock-type error spending function; gamma = -4 produces O'Brien-Fleming type error spending function. Default gamma = -4
crange	a 2-dimensional vector containing the end-points of the interval from which the critical values for claiming equivalence will be solved. Default crange = c(-10,10)
plot	Whether to generate the boundaries plot. Default plot = TRUE
ll	a parameter in the boundary plot. the short arm of the t(L) and t(U) axes

<code>u1</code>	a parameter in the boundary plot. the long arm of the t(L) and t(U) axes
<code>n.sim</code>	the number of randomly simulated samples in the computation of the boundaries via the Monte Carlo simulation approach. Default <code>n.sim=1e4</code>
<code>seed</code>	seed used in the Monte Carlo computation. If non-specified, the seed is set randomly.

Details

The exactly same equivalence boundaries can also be obtained using the command [nonbinding](#)

Value

<code>typeI</code>	vector of cumulative stage Type I error rate
<code>equivL</code>	vector of the equivalence boundary $c(L)$ at each stage
<code>equivU</code>	vector of the equivalence boundary $c(U)$ at each stage
<code>boundary plots</code>	if <code>plot=TRUE</code> , a series of boundary plots will be produced, one for look

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

- Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, Computational Statistics and Data Analysis, 77:14-24
- Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, the R Journal (to appear)

See Also

[nonbinding](#),[binding](#),[nminmax](#),[nfix](#),[oc](#),[figureE](#),[figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4

# the sample size per group with a traditional nonsequential design
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

# default
# there are two ways to generate the boundary plots
# 1. specify plot=TRUE (default) in "binding()"
```

```

equivonly(L, U, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha)

# 2. specify plot=FALSE in "binding()" and apply the "figureE()" command
bound <- equivonly(L, U, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, plot=FALSE)
figureE(bound, K)

## End(Not run)

```

figureE	<i>equivalence boundary plots in group sequential designs of equivalence studies</i>
---------	--

Description

produces the 2-dimensional equivalence boundary plot for each stage in group sequential designs of equivalence studies

Usage

```
figureE(boundary, K, sm=3, lg=6)
```

Arguments

boundary	the equivalence boundaries $c(L)$ and $c(U)$ at each stage
K	number of stages/looks
sm	the short arm of the $t(L)$ and $t(U)$ axes; default is 3
lg	the short arm of the $t(L)$ and $t(U)$ axes; default is 6

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, *Computational Statistics and Data Analysis*, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, *the R Journal* (to appear)

See Also

[nonbinding](#), [binding](#), [equivonly](#), [nminmax](#), [nfix](#), [oc](#), [figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
bound <- equivonly(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, plot=FALSE)
figureE(bound, K, 3,6)

## End(Not run)
```

figureEF	<i>equivalence and futility boundary plots in group sequential designs of equivalence studies</i>
----------	---

Description

produces the 2-dimensional equivalence and futility boundary plot for each stage in group sequential designs of equivalence studies

Usage

```
figureEF(boundary, K, sm=3, lg=6)
```

Arguments

boundary	the equivalence boundaries $c(L)$ and $c(U)$ at each stage
K	number of stages/looks
sm	the short arm of the $t(L)$ and $t(U)$ axes; default is 3
lg	the short arm of the $t(L)$ and $t(U)$ axes; default is 6

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, Computational Statistics and Data Analysis, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, the R Journal (to appear)

See Also

[nonbinding](#), [binding](#), [equivonly](#), [nminmax](#), [nfix](#), [oc](#), [figureE](#)

Examples

```

## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
bound <- binding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, plot=FALSE)
figureEF(bound, K, 3,6)

## End(Not run)

```

nfix

sample size calculation for equivalence studies

Description

calculates sample size for equivalence studies in the traditional non-sequential setting

Usage

```
nfix(r, l, u, theta, sigma, type1, type2, nrange = c(0, 1000))
```

Arguments

r	sampling ratio of the two groups. For paired samples (such as in crossover studies), r=1
l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
theta	true mean difference between 2 groups
sigma	between-subject standard deviation of the response variable for two independent groups; within subject standard deviation of the response variable for paired groups
type1	overall Type I error rate
type2	overall Type II error rate
nrange	a 2-dimensional vector containing the end-points of the interval from which the sample size will be solved. Default crange = c(0,1000)

Value

n1	sample size in group 1
n2	sample size in group 1

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, Computational Statistics and Data Analysis, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, the R Journal (to appear)

See Also

[nonbinding](#),[binding](#),[equivonly](#),[nminmax](#), [oc](#),[figureE](#),[figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
r <- 1
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

## End(Not run)
```

nminmax

sample size calculation for group sequential equivalence studies

Description

calculates sample size for group sequential designs in equivalence studies that can stop for equivalence, or for either equivalence or futility (binding or non-binding). The calculated samples size is referred to as n.minmax, "min" in the sense that the calculated n is the minimum required sample size to reach a given power level, "max" in the sense that it would be the max spent sample size which only happens if the study stops in the last stage

Usage

```
nminmax(l, u, theta, sigma, n1.lower, n2.lower, t.vec, type1, type2,
gamma = rep(-4, 2), binding = FALSE, n1.upper = ceiling(2 * n1.lower),
n2.upper = ceiling(2 * n2.lower), n.sim = 10000, seed = NULL)
```

Arguments

l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
theta	true mean difference between 2 groups
sigma	between-subject standard deviation of the response variable for two independent groups; within subject standard deviation of the response variable for paired groups
n1.lower	the lower bound of the interval from which n.minmax in group 1 will be solved using a bisection method
n2.lower	the lower bound of the interval from which n.minmax in group 2 will be solved using a bisection method
t.vec	cumulative time points for the interim looks assuming a constant accrual rate. For example, if a study has equally spaced 4 looks including the final look, then t.vec=1:4/4. It can any vector as long as it is increasing and the last element is 1.
type1	overall Type I error rate
type2	overall Type II error rate
gamma	The gamma parameter in the gamma cumulative error spending function (Hwang, Shih, and DeCani 1990). Error spending given a t.vec is = total error rate*(1-exp(-gamma*t.vec))/(1-exp(-gamma)). gamma= 1 produces Pocock-type error spending function; gamma = -4 produces O'Brien-Fleming type error spending function. Default gamma = -4
binding	whether the futility boundaries are binding; default = FALSE
n1.upper	the upper bound of the interval from which n.minmax in group 1 will be solved using a bisection method; default = 2*n1.lower
n2.upper	the upper bound of the interval from which n.minmax in group 2 will be solved using a bisection method; default = 2*n2.lower
n.sim	number of randomly simulated samples in computation of n.minmax via the Monte Carlo simulation approach. Default n.sim=1e4
seed	seed used in the Monte Carlo computation. If non-specified, the seed is set randomly.

Value

n1minmax	n.minmax in group 1
n2minmax	n.minmax in group 2
typeI	vector of cumulative stage Type I error rate
typeII	vector of cumulative stage Type II error rate
equivL	vector of the equivalence boundary c(L) at each stage
equivU	vector of the equivalence boundary c(U) at each stage
futilL	vector of the futility boundary d(L) at each stage
futilU	vector of the futility boundary d(U) at each stage

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

- Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral F -statistics, Computational Statistics and Data Analysis, 77:14-24
- Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central F -statistics, the R Journal (to appear)

See Also

[nonbinding](#), [binding](#), [equivonly](#), [nfix](#), [oc](#), [figureE](#), [figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
r <- 1

# the sample size per group with a traditional nonsequential design
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

# nminmax with nonbinding futility
bound1 <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)
figureEF(bound1, K)

# nminmax with binding futility
bound2 <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, binding=TRUE)
figureEF(bound2, K)

## End(Not run)
```

nonbinding

equivalence and non-binding futility boundaries in group sequential equivalence studies

Description

Computation of equivalence and non-binding futility boundaries for group sequential designs in studies with equivalence hypothesis via Monte Carlo simulations

Usage

```
nonbinding(l, u, theta, sigma, n1, n2, t.vec, type1, type2,
gamma = rep(-4, 2), crange = c(-10, 10), drange = c(-10, 10),
force = TRUE, plot = TRUE, ll = 3, ul = 6, n.sim = 10000, seed = NULL)
```

Arguments

l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
theta	true mean difference between 2 groups
sigma	between-subject standard deviation of the response variable for two independent groups; within subject standard deviation of the response variable for paired groups
n1	size (number of subjects) in group 1
n2	size (number of subjects) in group 2
t.vec	umulative time points for the interim looks assuming a constant accrual rate. For example, if a study has equally spaced 4 looks including the final look, then t.vec=1:4/4. It can any vector as long as it is increasing and the last element is 1.
type1	overall Type I error rate
type2	overall Type II error rate
gamma	The gamma parameter in the gamma cumulative error spending function (Hwang, Shih, and DeCani 1990). Error spending given a t.vec is = total error rate*(1-exp(-gamma*t.vec))/(1-exp(-gamma)). gamma= 1 produces Pocock-type error spending function; gamma = -4 produces O'Brien-Fleming type error spending function. Default gamma = -4
crange	a 2-dimensional vector containing the end-points of the interval from which the critical values for claiming equivalence will be solved. Default crange = c(-10,10)
drange	a 2-dimensional vector containing the end-points of the interval from which the critical values for claiming fulltality will be solved. Default drange = c(-10,10)
force	Whether to force the futlility boundaries to equal to the equilvence boundaries in the last look. Default force = TRUE
plot	Whether to generate the boundaries plot. Default plot = TRUE
ll	a parameter in the boundary plot. the short arm of the t(L) and t(U) axes
ul	a parameter in the boundary plot. the long arm of the t(L) and t(U) axes
n.sim	the number of randomly simulated samples in the computation of the boundaries via the Monte Carlo simulation approach. Default n.sim=1e4
seed	seed used in the Monte Carlo computation. If non-specified, the seed is set randomly.

Value

typeI	vector of cumulative stage Type I error rate
typeII	vector of cumulative stage Type II error rate
equivL	vector of the equivalence boundary $c(L)$ at each stage
equivU	vector of the equivalence boundary $c(U)$ at each stage
futilL	vector of the futility boundary $d(L)$ at each stage
futilU	vector of the futility boundary $d(U)$ at each stage
boundary plots	if <code>plot=TRUE</code> , a series of boundary plots will be produced, one for look

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, *Computational Statistics and Data Analysis*, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, *the R Journal* (to appear)

See Also

[binding](#), [equivonly](#), [nminmax](#), [nfix](#), [oc](#), [figureE](#), [figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
r <- 1
# the sample size per group with a traditional nonsequential design
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

# there are two ways to generate the boundary plots

# 1. specify plot=TRUE (default) in "binding()"
nonbinding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)

# 2. specify plot=FALSE in "binding()" and apply the "figureEF()" command
bound <- nonbinding(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, plot=FALSE)
figureEF(bound, K)

# obtain nminmax
bound <- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta, binding=FALSE)
```

```

bound
figureEF(bound, K)

## End(Not run)

```

oc *examination of the operating characteristics of a group sequential design for equivalence studies*

Description

empirical examination of the operating characteristics of a group sequential design via the Monte Carlo simulation approach. users need to supply the design, including the lower and upper bounds of the equivalence hypothesis, the true difference between 2 groups, and the corresponding variance parameter, and the number of looks (including the final look), the group sizes, and the equivalence and futility boundaries. It outputs empirical type I or type II error rates, expected sample sizes in the 2 groups, and the probability of stopping at each stage due to either equivalence or futility

Usage

```

oc(l, u, theta, sigma, K, n1, n2, boundaries,
futility = TRUE, binding = FALSE, n.sim = 10000)

```

Arguments

l	lower equivalence bound as given in the equivalence hypothesis
u	upper equivalence bound as given in the equivalence hypothesis
theta	true mean difference between 2 groups
sigma	between-subject standard deviaton of the response variables for two inpedent groups; within subject standard deviaton of the response variables for paired groups
K	number of looks/stages
n1	size (number of subjects) in group 1 in the actual study
n2	size (number of subjects) in group 2 in the actual study
boundaries	a list that contains four vectors that correspond to the stagewise lower equivalence boundaries $c(L)$, upper equivalence boundaries $c(U)$, lower futility boundaries $d(L)$, and upper futility boundaries $d(U)$, respectively. the boundaries can be obtained using functions <code>binding()</code> , <code>nonbinding()</code> , and <code>nminmax()</code> .
futility	whether the stop will stop for futility; default = TRUE
binding	whether hte futility boundaries are binding; default = FALSE
n.sim	number of randomly simulated studies for the empirical examination of the operating characteristics of a group sequential design via the Monte Carlo simulation approach. Default <code>n.sim=1e4</code>

Value

reject.rate	rate of rejection of H_0 (non-equivalence). If H_0 is true, then reject.rate is the empirical type I error rate; if H_1 is true, then reject.rate is the empirical power
En1	sample size that is expected to spend in group 1; smaller than n1.minmax due to early stopping
En2	sample size that is expected to spend in group 2; smaller than n2.minmax due to early stopping
prob.stop	probability of stopping at each stage due to either equivalence or futility
prob.stopE	probability of stopping at each stage due to equivalence
prob.stopF	probability of stopping at each stage due to futility

Author(s)

Fang Liu (fang.liu.131@nd.edu)

References

Liu, F. and Li, Q. (2014), Sequential Equivalence Testing based on the Exact Distribution of Bivariate Noncentral t -statistics, Computational Statistics and Data Analysis, 77:14-24

Liu, F. (2014), gset: an R package for exact sequential test of equivalence hypothesis based on bivariate non-central t -statistics, the R Journal (to appear)

See Also

[nonbinding](#), [binding](#), [equivonly](#), [nminmax](#), [nfix](#), [figureE](#), [figureEF](#)

Examples

```
## Not run:
L <- -0.2
U <- 0.2
theta <- 0
sigma <- 0.4
alpha <- 0.05
beta <- 0.2
K <- 4
r <- 1
n.fix <- nfix(r, L,U,theta,sigma,alpha,beta)

bound1 <- nonbinding(L,U,theta,sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha,beta, plot=FALSE)
bound2<- nminmax(L, U, theta, sigma, n.fix$n1, n.fix$n2, 1:K/K, alpha, beta)

theta <- L
oc1 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound1, futility=TRUE)
oc2 <- oc(L, U, theta, sigma, K, bound2$n1minmax, bound2$n2minmax, bound2, futility=TRUE)

theta <- 0
oc3 <- oc(L, U, theta, sigma, K, n.fix$n1, n.fix$n2, bound1, futility=TRUE)
oc4 <- oc(L, U, theta, sigma, K, bound2$n1minmax, bound2$n2minmax, bound2, futility=TRUE)
```

End(Not run)

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