

Package: gen2stage (via r-universe)

November 1, 2024

Type Package

Title Generalized Two-Stage Designs for Phase II Single-Arm Studies

Version 1.0

Depends R (>= 2.0.0), graphics, stats, clinfun

Author Seongho Kim

Maintainer Seongho Kim <biostatistician.kim@gmail.com>

Description One can find single-stage and two-stage designs for a phase II single-arm study with either efficacy or safety/toxicity endpoints as described in Kim and Wong (2019) <[doi:10.29220/CSAM.2019.26.2.163](https://doi.org/10.29220/CSAM.2019.26.2.163)>.

License GPL (>= 2)

Encoding UTF-8

LazyData true

NeedsCompilation no

Repository CRAN

Date/Publication 2019-06-03 12:50:22 UTC

Contents

gen2stage-package	2
gen2simon	3
gen2single	4
oc.gentwostage.bdry	5

Index	7
--------------	----------

gen2stage-package

Generalized Two-Stage Designs for Phase II Single-Arm Studies

Description

The R package `gen2stage` can generate single-stage and two-stage designs for phase II single-arm efficacy or safety studies.

Details

Package: `gen2stage`
Type: Package
Version: 1.0
Date: 2017-10-05
License: GPL-2

Author(s)

Seongho Kim <biostatistician.kim@gmail.com>

References

Kim S and Wong WK. Phase II Two-Stage Single-Arm Clinical Trials for Testing Toxicity Levels. *Commun Stat Appl Methods*. 2019 Mar;26(2):163-173. <https://www.ncbi.nlm.nih.gov/pubmed/31106162>.

Examples

```
# Single-stage safety design with pu (p0) = 0.33 vs. pa (p1) = 0.20
gen2single(0.33, 0.20, 0.05, 0.20)

# Single-stage efficacy design with pu (p0) = 0.67 vs. pa (p1) = 0.80
gen2single(0.67, 0.80, 0.05, 0.20)

# save and print
safety1 = gen2single(0.33, 0.20, 0.05, 0.20)
print(safety1)

# Two-stage safety design with pu (p0) = 0.33 vs. pa (p1) = 0.20
gen2simon(0.33, 0.20, 0.05, 0.20)
gen2simon(0.33, 0.20, 0.05, 0.10, nmax=150)

# Two-stage efficacy design with pu (p0) = 0.67 vs. pa (p1) = 0.80
gen2simon(0.67, 0.80, 0.05, 0.20)
gen2simon(0.67, 0.80, 0.05, 0.10, nmax=150)
```

```
# save, print and plot
safety2 = gen2simon(0.33, 0.20, 0.05, 0.20)
print(safety2)
plot(safety2)
```

gen2simon

Generalized Simon's 2-stage phase II design

Description

Calculates generalized optimal and minimax 2-stage phase II designs based on the R function `ph2simon`.

Usage

```
gen2simon(pu, pa, ep1, ep2, nmax=100)
## S3 method for class 'gen2simon'
print(x, ...)
## S3 method for class 'gen2simon'
plot(x, ...)
```

Arguments

<code>pu</code>	unacceptable response/toxicity rate
<code>pa</code>	response/toxicity rate that is desirable
<code>ep1</code>	threshold for the probability of declaring drug/treatment desirable under p_0
<code>ep2</code>	threshold for the probability of rejecting the drug/treatment under p_1
<code>nmax</code>	maximum total sample size (default 100; can be at most 500)
<code>x</code>	object returned by <code>gen2simon</code>
<code>...</code>	arguments to be passed onto <code>plot</code> and <code>print</code> commands called within

Value

`gen2simon` returns a list with `pu`, `pa`, `alpha`, `beta` and `nmax` as above and:

<code>out</code>	matrix of best 2 stage designs for each value of total sample size n . The 6 columns are: r_1 , n_1 , r , n , $EN(p_0)$, $PET(p_0)$, <code>alpha</code> , <code>beta</code>
------------------	---

The "print" method formats and returns the minimax and optimal designs. The "plot" plots the expected sample size against the maximum sample size as in Jung et al., 2001

References

Kim S and Wong WK. Phase II Two-Stage Single-Arm Clinical Trials for Testing Toxicity Levels. *Commun Stat Appl Methods*. 2019 Mar;26(2):163-173. <https://www.ncbi.nlm.nih.gov/pubmed/31106162>.

Jung SH, Carey M and Kim KM. (2001). Graphical Search for Two-Stage Designs for Phase II Clinical Trials. *Controlled Clinical Trials* 22, 367-372.

Simon R. (1989). Optimal Two-Stage Designs for Phase II Clinical Trials. *Controlled Clinical Trials* 10, 1-10.

See Also

[oc.gentwostage.bdry](#)

Examples

```
# Two-stage safety design with pu (p0) = 0.33 vs. pa (p1) = 0.20
gen2simon(0.33, 0.20, 0.05, 0.20)
gen2simon(0.33, 0.20, 0.05, 0.10, nmax=150)

# Two-stage efficacy design with pu (p0) = 0.67 vs. pa (p1) = 0.80
gen2simon(0.67, 0.80, 0.05, 0.20)
gen2simon(0.67, 0.80, 0.05, 0.10, nmax=150)

# save, print and plot
safety2 = gen2simon(0.33, 0.20, 0.05, 0.20)
print(safety2)
plot(safety2)
```

gen2single

Generalized exact single stage phase II design

Description

Calculates the generalized exact one stage phase II design based on the R function ph2single.

Usage

```
gen2single(pu,pa,ep1,ep2,nsoln=5)
## S3 method for class 'gen2single'
print(x, ...)
```

Arguments

pu	unacceptable response/toxicity rate
pa	response/toxicity rate that is desirable
ep1	threshold for the probability of declaring drug/treatment desirable under p0

ep2 threshold for the probability of rejecting the drug/treatment under p_1
 nsoln number of designs with given alpha and beta
 x object returned by gen2single
 ... arguments to be passed onto print command called within

Value

gen2single returns the optimal design with p_u , p_a , alpha, and beta as above and:

out matrix of the single-stage designs up to nsoln. The 4 columns are: r, n, alpha (type I error), beta (type II error)

The "print" method formats and returns the optimal design.

References

Kim S and Wong WK. Phase II Two-Stage Single-Arm Clinical Trials for Testing Toxicity Levels. *Commun Stat Appl Methods*. 2019 Mar;26(2):163-173. <https://www.ncbi.nlm.nih.gov/pubmed/31106162>.

See Also

[gen2simon](#)

Examples

```
# Single-stage safety design with  $p_u (p_0) = 0.33$  vs.  $p_a (p_1) = 0.20$ 
gen2single(0.33, 0.20, 0.05, 0.20)

# Single-stage efficacy design with  $p_u (p_0) = 0.67$  vs.  $p_a (p_1) = 0.80$ 
gen2single(0.67, 0.80, 0.05, 0.20)

# save and print
safety1 = gen2single(0.33, 0.20, 0.05, 0.20)
print(safety1)
```

oc.gentwostage.bdry *Two-stage boundary operating characteristics*

Description

Calculates the operating characteristics of a two-stage boundary based on the R function oc.twostage.bdry.

Usage

```
oc.gentwostage.bdry(pu, pa, r1, n1, r, n)
```

Arguments

pu	unacceptable response rate
pa	response rate that is desirable
r1	first stage threshold to declare treatment undesirable
n1	first stage sample size
r	overall threshold to declare treatment undesirable
n	total sample size

Value

oc.gentwostage.bdry returns the type I and II error rates as well as the probability of early termination and expected sample size under pu for a specific boundary.

References

Kim S and Wong WK. Phase II Two-Stage Single-Arm Clinical Trials for Testing Toxicity Levels. *Commun Stat Appl Methods*. 2019 Mar;26(2):163-173. <https://www.ncbi.nlm.nih.gov/pubmed/31106162>.

See Also

[gen2simon](#)

Examples

```
# Optimal two-stage safety design with pu (p0) = 0.33 vs. pa (p1) = 0.20
oc.gentwostage.bdry(0.33, 0.20, 8, 26, 22, 85)

# Optimal two-stage efficacy design with pu (p0) = 0.67 vs. pa (p1) = 0.80
oc.gentwostage.bdry(0.67, 0.80, 18, 26, 63, 85)
```

Index

* design

- gen2simon, [3](#)
- gen2single, [4](#)
- gen2stage-package, [2](#)
- oc.gentwostage.bdry, [5](#)

- gen2simon, [3](#), [5](#), [6](#)
- gen2single, [4](#)
- gen2stage (gen2stage-package), [2](#)
- gen2stage-package, [2](#)

- oc.gentwostage.bdry, [4](#), [5](#)

- plot.gen2simon (gen2simon), [3](#)
- print.gen2simon (gen2simon), [3](#)
- print.gen2single (gen2single), [4](#)