

Package ‘VisualizeSimon2Stage’

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Type Package

Title Visualize Simon's Two-Stage Design

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Description To visualize the probabilities of early termination, fail and success of Simon's two-stage design. To evaluate and visualize the operating characteristics of Simon's two-stage design.

License GPL-2

Imports methods

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Depends R (>= 4.3.0), ggplot2

Suggests clinfun

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Collate '0info.R' 'Simon_pr.R' 'Simon_oc.R' 'ph2simon_etc.R'

NeedsCompilation no

Author Tingting Zhan [aut, cre, cph]

Maintainer Tingting Zhan <tingtingzhan@gmail.com>

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autoplot.ph2simon	<i>Plot Simon's Two-Stage Design</i>
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Description

Plot `ph2simon` object using **ggplot2**.

Usage

```
## S3 method for class 'ph2simon'
autoplot(object, ...)
```

Arguments

object	<code>ph2simon</code> object
...	potential parameters, currently not in use

Value

Function `autoplot.ph2simon()` returns a `ggplot` object.

Examples

```
library(cclinfun)
(x = ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
class(x)
autoplot(x, type = 'minimax')
autoplot(x, type = 'optimal')
autoplot(x, type = 'n1')
autoplot(x, type = 'maximax')

# example with r1 = 0
(des = ph2simon(pu = .05, pa = .3, ep1 = .05, ep2 = .2))
autoplot(des, type = 'optimal')
autoplot(des, type = 'minimax')
```

print_ph2simon	<i>Alternate Print Method for a Simon's Two-Stage Design</i>
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Description

An alternate [print](#) method for [ph2simon](#) object.

Usage

```
print_ph2simon(x, ...)
```

Arguments

x	a ph2simon object
...	additional parameters, currently not in use

Value

Function [print_ph2simon\(\)](#) does not have a returned value.

Note

We do not overwrite `clinfun:::print.ph2simon`.

Examples

```
library(clinfun)
(x = ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
print_ph2simon(x)
```

r_simon	<i>Random Generator based on Simon's Two-Stage Design</i>
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Description

Random generator based on Simon's two-stage design.

Usage

```
r_simon(R, n1, n, r1, prob)
```

Arguments

R	positive integer scalar, number of trials R
n1, n	positive integer scalars, Stage-1 sample size n_1 and total sample size n
r1	non-negative integer scalar, number of response in Stage-1 r_1 required <i>exclusively</i> . In other words, passing Stage-1 indicates observing $> r_1$ responses
prob	numeric scalar, true response rate p

Details

Function `r_simon()` generates R copies of the number of responses y in the Simon's two-stage design. The conclusion of the trials are,

$y \leq r_1$ indicates early termination

$r_1 < y \leq r$ indicates failure to reject H_0

$y > r$ indicates success to reject H_0

Here r is not needed to *generate* the random number of responses y . Instead, r is needed to *determine* if the trial is a failure or a success. Therefore, r is not a parameter in `r_simon`.

Value

Function `r_simon()` returns an [integer vector](#) of length R , which are the R copies of the number of responses in the Simon's two-stage design.

Examples

```
library(clinfun)
ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1) # using 'Optimal'
# set.seed if needed
(ys = r_simon(R = 10L, n1 = 19L, n = 54L, r1 = 4L, prob = .3))
cut.default(ys, breaks = c(0, 4L, 15L, 54L), right = TRUE,
  labels = c('early-termination', 'fail', 'success'))
```

show,Simon_oc-method *Show [Simon_oc](#) Object*

Description

Show [Simon_oc](#) object

Usage

```
## S4 method for signature 'Simon_oc'
show(object)
```

Arguments

object [Simon_oc](#) object

Value

The [show](#) method for [Simon_oc](#) object does not have a returned value.

show,Simon_pr-method *Show [Simon_pr](#) Object*

Description

Show [Simon_pr](#) object

Usage

```
## S4 method for signature 'Simon_pr'
show(object)
```

Arguments

object [Simon_pr](#) object

Value

The [show](#) method for [Simon_pr](#) object does not have a returned value.

[Simon_oc](#) *[Simon_oc](#): Operating Characteristics of Simon's Two-Stage Design*

Description

Operating characteristics of Simon's two-stage design.

Usage

```
Simon_oc(
  prob,
  simon,
  type = c("minimax", "optimal", "n1", "maximax"),
  R = 10000L,
  n1 = stop("must provide `n1`"),
  n = stop("must provide `n`"),
  r1 = stop("must provide `r1`"),
  r = stop("must provide `r`"),
  ...
)
```

Arguments

prob	<i>named numeric vector</i> , true response rate(s) of (multiple) drug(s). The names(prob) should be the respective keyword(s) for the drug(s).
simon	<i>ph2simon</i> object
type	<i>character</i> scalar, type of Simon's two-stage design. Currently supports 'minimax' (default) for minimum total sample size, 'optimal' for minimum expected total sample size <i>under</i> p_0 , 'n1' for minimum Stage-1 sample size n_1 , 'maximax' to use up the user-provided maximum total sample size (parameter nmax of <i>ph2simon</i>)
R	<i>integer</i> scalar, number of simulations. Default 1e4L.
n1, n	(optional) <i>integer</i> scalars, Stage-1 sample size n_1 and total sample size n . Will be overridden if simon is given
r1, r	(optional) <i>integer</i> scalars, number of response in Stage-1 r_1 and overall r required <i>exclusively</i> . In other words, passing Stage-1 means observing $> r_1$ response. Will be overridden if simon is given
...	potential parameters, currently not in use

Details

..

Value

Function *Simon_oc()* returns *Simon_oc* object

Slots

.Data *Simon_pr* object

maxResp *integer vector* of length p , the frequencies of each regime having maximum response. The summation of maxResp is the number of simulation copies.

Simon_maxResp *integer vector* of length p , the frequencies of each regime having maximum response and success in Simon's two-stage trial.

References

[doi:10.1016/01972456\(89\)900159](https://doi.org/10.1016/01972456(89)900159)

Examples

```
library(clinfun)
(x = ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
Simon_oc(prob = c(A = .3, B = .2, C = .15), simon = x, type = 'minimax', R = 1e3L)
Simon_oc(prob = c(A = .3, B = .2, C = .15), simon = x, type = 'optimal', R = 1e3L)
```

Simon_pr

*Simon_pr: Probabilities of a Simon's Two-Stage Design***Description**

Probability of frail (i.e., early termination), fail (to reject the null) and success (to reject the null) of a Simon's two-stage design, at given true response rate(s).

Usage

```
Simon_pr(prob, n1, n, r1, r)
```

Arguments

prob **numeric vector**, true response rate(s) p
 n1, n positive **integer** scalars, Stage-1 sample size n_1 and total sample size n
 r1, r non-negative **integer** scalars, number of response in Stage-1 r_1 and overall r required *exclusively*. In other words, passing Stage-1 indicates observing $> r_1$ responses, and rejecting H_0 indicates observing $> r$ responses.

Details

Given the Simon's two-stage design (n_1, r_1, n, r) , for a response rate p , we have the number of Stage-1 positive responses $X_1 \sim \text{Binom}(n_1, p)$ and the number of Stage-2 positive responses $X_2 \sim \text{Binom}(n - n_1, p)$. Obviously X_1 and X_2 are independent.

The probability of early termination is $\Pr(X_1 \leq r_1)$.

The probability of failure to reject H_0 is

$$\sum_{s_1=r_1+1}^{n_1} \Pr(X_1 = s_1) \cdot \Pr(X_2 \leq (r - s_1))$$

The probability of rejecting H_0 is

$$\sum_{s_1=r_1+1}^{n_1} \Pr(X_1 = s_1) \cdot \Pr(X_2 > (r - s_1))$$

Parameters nomenclature of n1, n, r1 and r follows that of PASS and [ph2simon](#).

Value

`Simon_pr` returns `Simon_pr` object.

Slots

.Data $l \times 3$ **numeric matrix**, probability of frail (i.e., early termination), fail (to reject the null) and success (to reject the null), at each response rate p given in @prob

eN **numeric vector** of length l , expected sample size(s) $E(N)$

prob **numeric vector** of length l , response rate(s) p

References

[doi:10.1016/01972456\(89\)900159](https://doi.org/10.1016/01972456(89)900159)

<https://www.ncss.com/software/pass/>

Examples

```
Simon_pr(prob = c(.2, .4), n1 = 15L, r1 = 3L, n = 24L, r = 7L)
```

Sprintf.ph2simon *Short Paragraph to Describe a [ph2simon](#) Object*

Description

To create a short paragraph to describe a [ph2simon](#) object.

Usage

```
Sprintf.ph2simon(model, type = c("minimax", "optimal", "n1", "maximax"), ...)
```

Arguments

model	ph2simon object
type	character scalar, type of Simon's two-stage design, 'minimax' (default) minimum total sample size 'optimal' minimum expected total sample size <i>under</i> p_0 'n1' minimum Stage-1 sample size 'maximax' maximum total sample size (as provided by end-user)
...	additional parameters, currently not in use

Value

Function [Sprintf.ph2simon\(\)](#) returns a [noquote character](#) scalar.

Examples

```
library(clinfun)
(x = ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
Sprintf.ph2simon(x, type = 'minimax')
Sprintf.ph2simon(x, type = 'optimal')
Sprintf.ph2simon(x, type = 'n1')
Sprintf.ph2simon(x, type = 'maximax')
```

Sprintf.Simon_oc *Short Paragraph to Describe a [Simon_oc](#) Object*

Description

To create a short paragraph to describe a [Simon_oc](#) object.

Usage

```
Sprintf.Simon_oc(model, ...)
```

Arguments

model	Simon_oc object
...	additional parameters, currently not in use

Value

[Sprintf.Simon_oc](#) returns a [noquote character](#) scalar.

summary.ph2simon *Summarize a Simon's Two-Stage Design*

Description

Summarize a Simon's two-stage design

Usage

```
## S3 method for class 'ph2simon'
summary(object, ...)
```

Arguments

object	ph2simon object
...	potential parameters, currently not in use

Value

Function [summary.ph2simon](#) returns a [list](#) with three (3) elements

```
'design' integer matrix
'EN' double matrix
'p' double matrix
```

Examples

```
library(clinfun)
(x = ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
summary(x)
```

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