

# 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

**Encoding** UTF-8

**Language** en-US

**Depends** R (>= 4.4.0), ggplot2

**Suggests** clinfun

**RoxygenNote** 7.3.2

**NeedsCompilation** no

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**VisualizeSimon2Stage-package**  
*Visualize Simon\’s Two-Stage Design*

## Description

Functions for visualizing the probabilities of early termination, fail and success of Simon’s two-stage design. Functions for evaluating and visualizing the operating characteristics of Simon’s two-stage design.

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## References

[doi:10.1016/01972456\(89\)900159](https://doi.org/10.1016/01972456(89)900159)  
<https://www.ncss.com/software/pass/>

## Examples

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

# an alternative print
print_ph2simon(x)

# language for a report
Sprintf.ph2simon(x, type = 'minimax')
Sprintf.ph2simon(x, type = 'optimal')
Sprintf.ph2simon(x, type = 'n1')
Sprintf.ph2simon(x, type = 'maximax')

autoplot(x, type = 'minimax')
autoplot(x, type = 'optimal')
autoplot(x, type = 'n1')
autoplot(x, type = 'maximax')

# operating characteristics
simon_oc(prob = c(A = .3, B = .2, C = .15), object = x, type = 'minimax')
simon_oc(prob = c(A = .3, B = .2, C = .15), object = x, type = 'optimal')

# example with r1 = 0
(x1 = clinfun::ph2simon(pu = .05, pa = .3, ep1 = .05, ep2 = .2))
# works with all of our functions
autoplot(x1, type = 'optimal') # etc.
```

---

r\_simonRandom Generator based on Simon's Two-Stage Design

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**Description**

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

**Usage**

```
r_simon(R, prob, object, ...)

## S3 method for class 'ph2simon'
r_simon(R, prob, object, ...)

## S3 method for class 'ph2simon4'
r_simon(
  R,
  prob,
  object,
  ...,
  r1 = object@r1,
  n1 = object@n1,
  r = object@r,
  n = object@n
)
```

**Arguments**

R	positive <code>integer</code> scalar, number of trials $R$
prob	<code>double</code> scalar, true response rate $p$
object	a <code>ph2simon</code> or <code>ph2simon4</code> object
...	parameters of function <code>ph2simon4()</code> , most importantly type
r1, n1, r, n	(optional) <code>integer</code> scalars, see <code>ph2simon4</code> .

**Details**

Function `r_simon()` generates  $R$  copies of the number of responses  $y$  in one 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 of function `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

```
(x = clinfun::ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
set.seed(1532); r = r_simon(R = 1e2L, prob = .2, object = x)
set.seed(1532); r1 = r_simon.ph2simon4(R = 1e2L, prob = .2, r1 = 5L, n1 = 24L, r = 13L, n = 45L)
stopifnot(identical(r, r1))
table(attr(r, 'dx')) # look at beta, <10%
set.seed(24315); r2 = r_simon(R = 1e2L, prob = .4, object = x)
table(attr(r2, 'dx')) # look at alpha, <5%
```

## Description

Operating characteristics of **one** Simon's two-stage design.

## Usage

```
simon_oc(prob, R, object, ...)

## S3 method for class 'ph2simon'
simon_oc(prob, R = 10000L, object, ...)

## S3 method for class 'ph2simon4'
simon_oc(
  prob,
  R = 10000L,
  object,
  ...,
  r1 = object@r1,
  n1 = object@n1,
  r = object@r,
  n = object@n
)
```

## Arguments

<code>prob</code>	<code>named double vector</code> , true response rate(s) $p$ of (multiple) drug(s). The <code>names(prob)</code> should be the name(s) of the drug(s).
<code>R</code>	<code>integer</code> scalar, number of simulations. Default <code>1e4L</code> .
<code>object</code>	<code>ph2simon</code> or <code>ph2simon4</code> object
<code>...</code>	parameters of function <code>ph2simon4()</code> , most importantly type (optional) <code>integer</code> scalars, see <code>ph2simon4</code> .
<code>r1, n1, r, n</code>	

**Value**

Function `simon_oc()` returns `simon_oc` object.

**Slots**

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

`simon_maxResp` `integer vector` of same length as  $p$ , the frequencies of each regime having maximum response and success in Simon's two-stage trial.

simon\_pr

*Probabilities of one Simon's Two-Stage Design***Description**

Probabilities of frail (i.e., early termination) and success (to reject  $H_0$ ) of **one** Simon's two-stage design, at given true response rate(s).

**Usage**

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

## S3 method for class 'ph2simon4'
simon_pr(
  prob,
  object,
  r1 = object@r1,
  n1 = object@n1,
  r = object@r,
  n = object@n,
  ...
)
```

**Arguments**

<code>prob</code>	<code>double</code> scalar or <code>vector</code> , true response rate(s) $p$
<code>object</code>	a <code>ph2simon</code> or <code>ph2simon4</code> object
<code>...</code>	parameters of function <code>ph2simon4()</code> , most importantly type
<code>r1, n1, r, n</code>	(optional) <code>integer</code> scalars, see <code>ph2simon4</code> .

## Details

Given one Simon's two-stage design  $(r_1, n_1, r, n)$  and a true 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

$$p_{\text{frail}} = \Pr(X_1 \leq r_1)$$

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 successfully rejecting  $H_0$  is

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

The expected sample size is

$$E(n) = p_{\text{frail}} \cdot n_1 + (1 - p_{\text{frail}}) \cdot n$$

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

## Value

Function [simon\\_pr\(\)](#) returns `simon_pr` object.

## Slots

`frail` `numeric` scalar or `vector`, probabilities of frail (i.e., early termination) at given true response rate(s)  $p$ .

`reject` `numeric` scalar or `vector`, probabilities of success (to reject  $H_0$ ) at given true response rate(s)  $p$ .

`eN` `numeric` scalar or `vector`, expected sample size(s)  $E(n)$  at given true response rate(s)  $p$ .

`prob` `double` scalar or `vector`, true response rate(s)  $p$

## Examples

```
(x = clinfun::ph2simon(pu = .2, pa = .4, ep1 = .05, ep2 = .1))
simon_pr(prob = c(.2, .3, .4), object = x)
simon_pr.ph2simon4(prob = c(.2, .3, .4), r1 = 5L, n1 = 24L, r = 13L, n = 45L) # internal use
```

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