Package ‘DelayedEffect.Design’

September 1, 2017

Title Sample Size and Power Calculations using the APPLE and SEPPLE Methods

Version 0.0.4

Date 2017-09-01

Author Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen <Boguang.Zhen@fda.hhs.gov>, Yongsoek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

Description Provides sample size and power calculations when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject. The methods used are described in Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017) <doi:10.1002/sim.7157>.

Maintainer Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>

Imports msm, survival

License GPL-2

NeedsCompilation no

Repository CRAN

Date/Publication 2017-09-01 15:07:35 UTC

R topics documented:

DelayedEffect.Design .................................................. 2
HR.APPLE ................................................................. 2
N.APPLE ................................................................. 4
pow.APPLE .............................................................. 5
pow.SEPPLE ............................................................. 6
pow.sim.logrk ............................................................ 8

Index 10
**Description**

An R package for sample size and power calculation when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject using the APPLE and SEPLE methods based on the piecewise weighted log-rank test. For comparison, this package also performs the power calculation based on the regular log-rank test which ignores the existence of lag effect.

**Details**

The two new methods in this package for performing the sample size and power calculations are:

1. Analytic Power calculation method based on Piecewise weighted Log-rank tEst (APPLE),

See the reference for details of these methods and the piecewise weighted log-rank test. The functions for computing power corresponding to the above methods are `pow.APPLE` and `pow.SEPLE`. These can be compared to `pow.sim.logrk`, which computes the power from a simulation-based algorithm using the regular log-rank test which ignores the existence of lag effect.

This package also includes the function `n.APPLE` to back calculate the sample size given the power and hazard ratio, and the function `HR.APPLE` to back calculate the hazard ratio given the power and sample size, respectively, using the close-form APPLE method.

**Author(s)**

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen <Boguang.Zhen@fda.hhs.gov>, Yongsoek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

**References**


**Usage**

`HR.APPLE(lambda1, t1, p, N, tao, A, beta, ap=0.5, alpha=0.05)`
Arguments

- **lambda1**: Baseline hazard or NULL (see details)
- **t1**: Delayed duration or NULL (see details)
- **p**: Proportion of subjects who survive beyond the delayed period or NULL (see details)
- **N**: Sample size
- **tao**: Total study duration
- **A**: Total enrollment duration
- **beta**: Type II error rate; Power=1-beta
- **ap**: Experimental-control allocation ratio. The default is 0.5.
- **alpha**: Type I error rate (two-sided). The default is 0.05.

Details

APPLE is an acronym for:
Analytic Power calculation method based on Piecewise weighted Log-rank tEst. See the reference for details of this method.

Out of the three input parameters `lambda1`, `t1` and `p`, only two need to be specified, the remaining one will be computed internally from the formula `lambda1 = -log(p)/t1`. If all three are not NULL, then `lambda1` will be set to `-log(p)/t1` regardless of the user input value.

Value

The hazard ratio

Author(s)

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen<Boguang.Zhen@fda.hhs.gov>, Yong-soek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

References


See Also

`pow.APPLE, N.APPLE`

Examples

```r
lambda1 <- NULL
t1 <- 183
p <- 0.7
N <- 200
tao <- 365*3
A <- 365
```


```r
beta <- 0.2
HR.APPLE(lambda1, t1, p, N, tao, A, beta)
```

**APPLE sample size computation**

**Description**

Perform the sample size calculation given the power and post-delay hazard ratio using the closeform APPLE method based on the piecewise weighted log-rank test when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject.

**Usage**

```r
N.APPLE(lambda1, t1, p, HR, tao, A, beta, ap=0.5, alpha=0.05)
```

**Arguments**

- `lambda1`: Baseline hazard or NULL (see details)
- `t1`: Delayed duration or NULL (see details)
- `p`: Proportion of subjects who survive beyond the delayed period or NULL (see details)
- `HR`: Post-delay hazard ratio
- `tao`: Total study duration
- `A`: Total enrollment duration
- `beta`: Type II error rate; Power=1-beta
- `ap`: Experimental-control allocation ratio. The default is 0.5.
- `alpha`: Type I error rate (two-sided). The default is 0.05.

**Details**

APPLE is an acronym for:
Analytic Power calculation method based on Piecewise weighted Log-rank tEst. See the reference for details of this method.

Out of the three input parameters `lambda1`, `t1` and `p`, only two need to be specified, the remaining one will be computed internally from the formula `lambda1 = -log(p)/t1`. If all three are not NULL, then `lambda1` will be set to `-log(p)/t1` regardless of the user input value.

**Value**

The sample size

**Author(s)**

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen<Boguang.Zhen@fda.hhs.gov>, Yong-soek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>
References

See Also
pow.APPLE, HR.APPLE

Examples
```r
lambda1 <- NULL
t1 <- 183
p <- 0.7
HR <- 0.55
tao <- 365*3
A <- 365
beta <- 0.2
N.APPLE(lambda1, t1, p, HR, tao, A, beta)
```

Description
Perform the power calculation using the close-form APPLE method based on the piecewise weighted log-rank test when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject

Usage
```r
pow.APPLE(lambda1, t1, p, N, HR, tao, A, ap=0.5, alpha=0.05)
```

Arguments
- `lambda1`: Baseline hazard or NULL (see details)
- `t1`: Delayed duration or NULL (see details)
- `p`: Proportion of subjects who survive beyond the delayed period or NULL (see details)
- `N`: Sample size
- `HR`: Post-delay hazard ratio
- `tao`: Total study duration
- `A`: Total enrollment duration
- `ap`: Experimental-control allocation ratio. The default is 0.5.
- `alpha`: Type I error rate (two-sided). The default is 0.05.
Details

APPLE is an acronym for:
Analytic Power calculation method based on Piecewise weighted Log-rank tEst. See the reference for details of this method.

Out of the three input parameters \( \lambda_1 \), \( t_1 \) and \( p \), only two need to be specified, the remaining one will be computed internally from the formula \( \lambda_1 = -\log(p)/t_1 \). If all three are not NULL, then \( \lambda_1 \) will be set to \(-\log(p)/t_1\) regardless of the user input value.

Value

The power

Author(s)

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen<BoGuang.Zhen@fda.hhs.gov>, Yong-soek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

References


See Also

N.APPLE, HR.APPLE, pow.SEPPLE, pow.sim.logrk

Examples

```r
lambda1 <- NULL
t1 <- 183
p <- 0.7
N <- 200
HR <- 0.55
tao <- 365*3
A <- 365
pow.APPLE(lambda1, t1, p, N, HR, tao, A)
```

---

**pow.SEPPLE**

*SEPPLE power computation*

Description

Perform the power calculation using the numeric SEPPLE method based on the piecewise weighted log-rank test when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject.
Usage

pow.SEPPLE(lambda1, t1, p, N, HR, tao, A, ap=0.5, alpha=0.05, nsim=10000)

Arguments

lambda1  Baseline hazard or NULL (see details)
t1       Delayed duration or NULL (see details)
p        Proportion of subjects who survive beyond the delayed period or NULL (see details)
N        Sample size
HR       Post-delay hazard ratio
tao      Total study duration
A        Total enrollment duration
ap       Experimental-control allocation ratio. The default is 0.5.
alpha    Type I error rate (two-sided). The default is 0.05.
nsim     Number of simulations. The default is 10000.

Details

SEPPLE is an acronym for:
Simulation-based Empirical Power calculation method based on Piecewise weighted Log-rank tEst.
See the reference for details of this method.

Out of the three input parameters lambda1, t1 and p, only two need to be specified, the remaining one will be computed internally from the formula lambda1 = -log(p)/t1. If all three are not NULL, then lambda1 will be set to -log(p)/t1 regardless of the user input value.

Value

The power

Author(s)

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen<Boguang.Zhen@fda.hhs.gov>, Yong-soek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

References


See Also

pow.APPLE, pow.sim.logrk
Examples

```r
lambda1 <- NULL
t1 <- 183
p <- 0.7
N <- 200
HR <- 0.55
tao <- 365*3
A <- 365
pow.SEPPLE(lambda1, t1, p, N, HR, tao, A, nsim=1000)
```

Description

Perform the power calculation using a simulation-based method based on the regular log-rank test when the treatment time-lag effect is present and the lag duration is homogeneous across the individual subject.

Usage

```r
pow.sim.logrk(lambda1, t1, p, N, HR, tao, A, ap=0.5, alpha=0.05, nsim=10000)
```

Arguments

- `lambda1`: Baseline hazard or NULL (see details).
- `t1`: Delayed duration or NULL (see details).
- `p`: Proportion of subjects who survive beyond the delayed period or NULL (see details).
- `N`: Sample size.
- `HR`: Post-delay hazard ratio.
- `tao`: Total study duration.
- `A`: Total enrollment duration.
- `ap`: Experimental-control allocation ratio. The default is 0.5.
- `alpha`: Type I error rate (two-sided). The default is 0.05.
- `nsim`: Number of simulations. The default is 10000.

Details

Out of the three input parameters `lambda1`, `t1` and `p`, only two need to be specified, the remaining one will be computed internally from the formula `lambda1 = -log(p)/t1`. If all three are not NULL, then `lambda1` will be set to `-log(p)/t1` regardless of the user input value.

Value

The power.
Author(s)

Zhenzhen Xu <Zhenzhen.Xu@fda.hhs.gov>, Boguang Zhen <Boguang.Zhen@fda.hhs.gov>, Yong-soek Park <yongpark@pitt.edu> and Bin Zhu <bin.zhu@nih.gov>

References


See Also

pow.APPLE, pow.SEPPLE

Examples

```r
lambda1 <- NULL
t1 <- 1
p <- 0.7
N <- 200
HR <- 0.55
tao <- 365*3
A <- 365
pow.sim.logrk(lambda1, t1, p, N, HR, tao, A, nsim=1000)
```
Index

*Topic package
  DelayedEffect.Design, 2

*Topic power
  HR.APPLE, 2
  N.APPLE, 4
  pow.APPLE, 5
  pow.SEPPE, 6
  pow.sim.logrk, 8

DelayedEffect.Design, 2

HR.APPLE, 2, 2, 5, 6

N.APPLE, 2, 3, 4, 6

pow.APPLE, 2, 3, 5, 5, 7, 9
pow.SEPPE, 2, 6, 6, 9
pow.sim.logrk, 2, 6, 7, 8