Package 'DelayedEffect.Design'

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Title Sample Size and Power Calculations using the APPLE and SEPPLE Methods			
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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></bin.zhu@nih.gov></yongpark@pitt.edu></boguang.zhen@fda.hhs.gov></zhenzhen.>			
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="">.</doi:10.1002>			
Maintainer Zhenzhen Xu <zhenzhen.xu@fda.hhs.gov></zhenzhen.xu@fda.hhs.gov>			
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DelayedEffect.Design			
HR.APPLE			
N.APPLE			
pow.APPLE 5 pow.SEPPLE 6			
pow.sim.logrk			
Index 10			

2 HR.APPLE

DelayedEffect.Design Sample size and power calculations using APPLE and SEPPLE

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 SEPPLE 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),
- 2. Simulation-based Empirical Power calculation method based on Piecewise weighted Log-rank tEst (SEPPLE).

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.SEPPLE. 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 <bir>bin.zhu@nih.gov>

References

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

HR.APPLE

APPLE hazard ratio computation

Description

Perform the post-delay hazard ratio calculation given power and sample size 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

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

HR.APPLE 3

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
Α	Total enrollment duration
beta	Type II error rate; Power=1-beta
ар	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>, Yongsoek Park <yongpark@pitt.edu> and Bin Zhu
bin.zhu@nih.gov>

References

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

See Also

```
pow.APPLE, N.APPLE
```

Examples

4 N.APPLE

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

N. APPLE

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

```
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
Α	Total enrollment duration
beta	Type II error rate; Power=1-beta
ар	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>, Yongsoek Park <yongpark@pitt.edu> and Bin Zhu
bin.zhu@nih.gov>

pow.APPLE 5

References

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

See Also

```
pow.APPLE, HR.APPLE
```

Examples

```
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)
```

pow.APPLE

APPLE power computation

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

```
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
Α	Total enrollment duration
ар	Experimental-control allocation ratio. The default is 0.5.
alpha	Type I error rate (two-sided). The default is 0.05.

6 pow.SEPPLE

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 power

Author(s)

References

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

See Also

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

Examples

```
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

pow.SEPPLE 7

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
Α	Total enrollment duration
ар	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>, Yongsoek Park <yongpark@pitt.edu> and Bin Zhu <bir>bin.zhu@nih.gov>

References

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

See Also

```
pow.APPLE, pow.sim.logrk
```

8 pow.sim.logrk

Examples

```
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)
```

pow.sim.logrk

Simulated log-rank power computation

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

```
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
Α	Total enrollment duration
ар	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

pow.sim.logrk 9

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

Xu, Z., Zhen, B., Park, Y., & Zhu, B. (2017). Designing therapeutic cancer vaccine trials with delayed treatment effect. Statistics in medicine, 36(4), 592-605.

See Also

```
pow.APPLE, pow.SEPPLE
```

Examples

```
lambda1 <- NULL

t1 <- 183

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.SEPPLE, 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.SEPPLE, 2, 6, 6, 9
pow.sim.logrk, 2, 6, 7, 8
```