

Package ‘AEBSD’

January 9, 2019

Title Calculate sample size of AEBSA and compare AEBSA with BS

Version 0.0.0.9000

Description This package provides sample size calculation of AEBSA for different test requirements and its comparison with BS.

Depends R (>= 3.5.2)

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0.9000

R topics documented:

posall	1
posint	2
Index	4

posall	<i>Sample Size of AEBSA for Positive and Overall</i>
--------	--

Description

Calculate minimum sample size needed of AEBSA for testing both treatment effect in biomarker positive and overall treatment effect, and its comparison with BS

Usage

```
posall(rtrue,raux,ppv,lam1e,lam0e,lam1c,lam0c,tau,raccrual,powerdesired,alpha, costs)
```

Arguments

rtrue	the prevalence rates of patients with positive true biomarker
raux	the prevalence rates of patients with positive auxiliary biomarker
lam1e	hazrd rate for biomarker-positive subpopulation in the experimental treatment group

lam0e	hazrd rate for biomarker-negative subpopulation in the experimental treatment group
lam1c	hazrd rate for biomarker-positive subpopulation in the control treatment group
lam0c	hazrd rate for biomarker-negative subpopulation in the control treatment group
tau	minimum follow-up time
raccrual	accrual rate
powerdesired	desired design power
alpha	type-I error (for each test)
costs	cost vector including costscr (screening cost), costtrt (average treatment cost), costfol (follow-up cost) and costtest (biomarker test cost) for each randomized patient

Value

(1) The probability of randomizing patients with positive and negative auxiliary variable; (2) Number of randomized patients for AEBSD (3) Screening number for AEBSD (4) Number of randomized patients for BSD (5) Patient ratio (6) Cost ratio (7) Screening ratio

posint	<i>Sample Size of AEBSD for Postive and Interaction</i>
--------	---

Description

Calculate minimum sample size needed of AEBSD for testing both treatment effect in biomarker positive and interaction effect, and its comparison with BSD

Usage

```
posint(rtrue,raux,ppv,lam1e,lam0e,lam1c,lam0c,tau,raccrual,powerdesired,alpha, costs)
```

Arguments

rtrue	the prevalence rates of patients with positive true biomarker
raux	the prevalence rates of patients with positive auxiliary biomarker
lam1e	hazrd rate for biomarker-positive subpopulation in the experimental treatment group
lam0e	hazrd rate for biomarker-negative subpopulation in the experimental treatment group
lam1c	hazrd rate for biomarker-positive subpopulation in the control treatment group
lam0c	hazrd rate for biomarker-negative subpopulation in the control treatment group
tau	minimum follow-up time
raccrual	accrual rate
powerdesired	desired design power
alpha	type-I error (for each test)
costs	cost vector including costscr (screening cost), costtrt (average treatment cost), costfol (follow-up cost) and costtest (biomarker test cost) for each randomized patient

Value

(1) The probability of randomizing patients with positive and negative auxiliary variable; (2) Number of randomized patients for AEBS (3) Screening number for AEBS (4) Number of randomized patients for BS (5) Patient ratio (6) Cost ratio (7) Screening ratio

Index

posall, [1](#)
posint, [2](#)