Package ‘factorial2x2’

April 27, 2020

Type Package

Title Design and Analysis of a 2x2 Factorial Trial

Version 0.2.0

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Depends R (>= 3.6.0), survival, stats, mvtnorm

Imports

License GPL-2

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

cor2x2 ................................................................. 2
crit2x2 ................................................................. 4
eventProb ............................................................. 7
cor2x2

Hazard ratios and correlations for the 2x2 statistics

Description

Computes the hazard ratios, confidence intervals, p-values, and correlations for the overall A, simple A, and simple AB logrank statistics.

Usage

cor2x2(time, event, indA, indB, covmat)

Arguments

time follow-up times
event event indicators (0/1)
indA treatment A indicators (0/1)
indB treatment B indicators (0/1)
covmat matrix of covariates; one row per subject. NOTE!! Factor variables must use 0/1 indicator variables

Details

This function computes (i) correlation between the overall A test and the simple A test (ii) correlation between the overall A test and the simple AB test (iii) correlation between the simple A and simple AB test. The correlation estimates are derived in Lin, Gong, Gallo, et al. (Biometrics 2016).
**Value**

- `loghrA`: overall A log hazard ratio
- `seA`: standard error of the overall A log hazard ratio
- `hrA`: overall A hazard ratio
- `ciA`: 95% confidence interval for overall A hazard ratio
- `pvalA`: two-sided p-value for overall A hazard ratio
- `loghra`: simple A log hazard ratio
- `sea`: standard error of the simple A log hazard ratio
- `hra`: simple A hazard ratio
- `cia`: 95% confidence interval for simple A hazard ratio
- `pvala`: two-sided p-value for simple A hazard ratio
- `loghrab`: simple AB log hazard ratio
- `seab`: standard error of the simple AB log hazard ratio
- `hrab`: simple AB hazard ratio
- `ciab`: 95% confidence interval for simple AB hazard ratio
- `pvalab`: two-sided p-value for simple AB hazard ratio
- `corAa`: correlation between the overall A and simple A test statistics
- `corAab`: correlation between the overall A and simple AB test statistics
- `coraab`: correlation between the simple A and simple AB test statistics

**References**


**Examples**

```r
# First load the simulated data variables. The "simdat" file is
# a 100-by-9 matrix which is loaded with the factorial2x2 package.
time <- simdat[, "time"]
event <- simdat[, "event"]
indA <- simdat[, "indA"]
indB <- simdat[, "indB"]
covmat <- simdat[, 6:10]

cor2x2(time, event, indA, indB, covmat)
# $loghrA
# [1] 0.05613844

# $seA
# [1] 0.4531521

# $hrA
# [1] 1.057744
```
Critical values for the Equal Allocation 3, Proportional Allocation 2, and Equal Allocation 2 procedures
Description

Computes the critical values for null hypotheses rejection and corresponding nominal two-sided significance levels for the Equal Allocation 3, Proportional Allocation 2, and Equal Allocation 2 procedures.

Usage

crit2x2(
corAa,
coraAab,
coraab,
dig = 2,
alpha = 0.05,
niter = 5,
abseps = 1e-05,
tol = 1e-04
)

Arguments

corAa     correlation between the overall A and simple A log hazard ratio estimates
coraAab   correlation between the overall A and simple AB log hazard ratio estimates
coraab    correlation between the simple A and simple AB log hazard ratio estimates
dig       number of decimal places to which we roundDown the critical value
alpha     two-sided familywise error level to control
niter     number of times we compute the critical values to average out the randomness from the pmvnorm function call
abseps    abseps setting in the pmvnorm function call
tol       tol setting in the uniroot function call

Details

This function computes the Dunnett-corrected critical values based on the asymptotic correlations of the overall A, simple A, and simple AB logrank statistics as described in Leifer, Troendle, et al. (2020) and are derived in Lin, Gong, et al. (2016) and Slud (1994). pmvnorm uses a random seed in its algorithm. To smooth out the randomness, pmvnorm is called niter times. The roundDown function is used in conjunction with the dig argument to insure that any rounding of the (negative) critical values will be done conservatively to control the familywise type I error at the desired level.

Value

critEA3        Equal Allocation 3 procedure's critical value for all three test statistics
sigEA3         two-sided nominal significance level corresponding to critEA3
critPA2A       Proportional Allocation 2 procedure's critical value for the overall A statistic
sigPA2A        two-sided nominal significance level corresponding to critPA2A
critPA2ab      Proportional Allocation 2 procedure's critical value for the simple AB statistic
crit2x2

sigPA2ab  two-sided nominal significance level corresponding to critPA2ab

critEA2  Equal Allocation 2 procedure’s critical value for the simple A and AB statistics

sigEA2  two-sided nominal significance level corresponding to critEA2

References


See Also

roundDown, eventProb, lgrkPower, strLgrkPower, pmvnorm

Examples

# Example 1: Compute the nominal significance levels for rejection using
# the asymptotic correlations derived in Slud (1994)
corAa <- 1/sqrt(2)
corAab <- 1/sqrt(2)
coraab <- 1/2
crit2x2(corAa, corAab, coraab, dig = 2, alpha = 0.05, niter = 5)
# critEA3
# [1] -2.32
# sigEA3
# [1] 0.02034088

# critPA2A
# [1] -2.13
# sigPA2A
# [1] 0.03317161

# critPA2ab
# [1] -2.24
# sigPA2ab
# [1] 0.02509092

# critEA2
# [1] -2.22
# sigEA2
# [1] 0.02641877

# Example 2: Compute the nominal critical values and significance levels for rejection
# using the estimated correlations for simdat.
eventProb

```
corAa  <-  0.6123399
corAab <-  0.5675396
coraab <-  0.4642737

crit2x2(corAa, corAab, coraab, dig = 2, alpha = 0.05, niter = 5)
# $critEA3
# [1] -2.34

# $critPA2A
# [1] -2.13

# $sigPA2A
# [1] 0.03317161

# $critPA2ab
# [1] -2.3

# $sigPA2ab
# [1] 0.02144822

# $sigEA3
# [1] 0.01928374

# $critEA2
# [1] -2.22

# $sigEA2
# [1] 0.02641877
```

eventProb  

*Calculate event probabilities*

**Description**

Calculates the event probabilities for each of the four factorial groups C, A, B, AB. The time unit is in years, but of course, any time unit could be used. Average event probabilities across various combinations of the groups are also calculated. The event times are assumed to be exponentially distributed. The censoring times are assumed to be uniformly distributed and independent of the event times.

**Usage**

```
eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)
```

**Arguments**

- `rateC`  
  group C one year event rate

- `hrA`  
  group A to group C hazard ratio

- `hrB`  
  group B to group C hazard ratio
hrAB          group AB to group C hazard ratio
mincens       minimum censoring time
maxcens       maximum censoring time

Value
hazC          group C’s exponential hazard rate
probC         event probability of the C group
probA         event probability of the A group
probB         event probability of the B group
probAB        event probability of the AB group
avgprob       average event probability across all factorial groups
probA_C       average event probability of the A and C groups
probAB_C      average event probability of the AB and C groups

Examples
# Corresponds to scenario 5 of Table 2 from Leifer, Troendle, et al. (2019).
rateC <- 0.0445
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4
eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)
# hazC
# [1] 0.04552052

# probC
# [1] 0.2446365

# probA
# [1] 0.201254

# probB
# [1] 0.201254

# probAB
# [1] 0.1831806

# avgprob
# [1] 0.2075813

# probAB_C
# [1] 0.2139086
fac2x2analyze

Description

Performs significance testing for the Proportional Allocation 2, Equal Allocation 3, Equal Allocation 2 procedures. Also reports the hazard ratios, 95% confidence intervals, p-values, nominal significance levels, and correlations for the overall and simple test statistics.

Usage

fac2x2analyze(time, event, indA, indB, covmat, alpha, dig = 2, niter = 5)

Arguments

time   follow-up times
event  event indicators (0/1)
indA   treatment A indicators (0/1)
indB   treatment B indicators (0/1)
covmat covariate matrix, must be non-NULL. Factor variables MUST use 0/1 dummy variables
alpha  two-sided familywise significance level
dig    number of decimal places to which we roundDown the critical value
niter  number of interations passed to crit2x2 function call

Details

For each of the three multiple testing procedures, the critical values for the overall A (respectively, simple A) logrank statistics may be slightly different from the overall B (respectively, simple B) logrank statistics. This is due to their slightly different correlations with each other (i.e., correlation between overall A and simple A, respectively, overall B and simple B, statistics) as well as with the simple AB statistic.

Value

loghraoverall  overall A log hazard ratio
seoverall  standard error of the overall A log hazard ratio
zstatAoverall  Z-statistic for the overall A log hazard ratio
pvalAoverall  two-sided p-value for the overall hazard ratio
hraoverall  overall A hazard ratio
ciAoverall  95% confidence interval for the overall A hazard ratio
loghraasimple  simple A log hazard ratio
seAsimple  standard error of the simple A log hazard ratio
ZstatAsimple Z-statistic for the simple A log hazard ratio
pvalAsimple two-sided p-value for the simple A hazard ratio
hrAsimple  simple A hazard ratio
ciAsimple  95% confidence interval for the simple A hazard ratio
loghrABsimple simple AB log hazard ratio
seABsimple standard error of the simple AB log hazard ratio
ZstatABsimple Z-statistic for the simple AB log hazard ratio
pvalABsimple two-sided p-value for the simple AB hazard ratio
hrABsimple  simple AB hazard ratio
ciABsimple  95% confidence interval for the simple AB hazard ratio
critEA3_A Equal Allocation 3’s critical value for the overall A simple A, and simple AB hypotheses
sigEA3_A Equal Allocation 3’s p-value rejection criterion for the overall A, simple A, and simple AB hypotheses
resultEA3_A Equal Allocation 3’s accept/reject decisions for the overall A, simple A, and simple AB hypotheses
critPA2overallA Proportional Allocation 2’s critical value for the overall A statistic
sigPA2overallA Proportional Allocation 2’s p-value rejection criterion for the overall A hypothesis
critPA2simpleAB Proportional Allocation 2’s critical value for the simple AB hypothesis
sigPA2simpleAB Proportional Allocation 2 procedure’s p-value rejection criterion for the simple AB hypothesis
resultPA2_A Proportional Allocation 2 procedure’s accept/reject decisions for the overall A and simple A hypotheses
critEA2_A Equal Allocation 2 procedure’s critical value for the simple A and simple AB hypotheses
sigEA2_A Equal Allocation 2 procedure’s p-value rejection criterion for the simple A and simple AB hypotheses
resultEA2_A Equal Allocation 2 procedure’s accept/reject decisions for the simple A and simple AB hypotheses
corAa correlation between the overall A and simple A logrank statistics
corAab correlation between the overall A and simple AB logrank statistics
coraab correlation between the simple A and simple AB logrank statistics

Author(s)
Eric Leifer, James Troendle
References


Examples

# First load the simulated data variables. The "simdataSub" file is a 100-by-9 matrix which is loaded with the factorial2x2 package.
time <- simdataSub[, "time"]
event <- simdataSub[, "event"]
indA <- simdataSub[, "indA"]
indB <- simdataSub[, "indB"]
covmat <- simdataSub[, 6:10]
fac2x2analyze(time, event, indA, indB, covmat, alpha = 0.05, niter = 5)

# $loghrA
# [1] 0.05613844

# $seA
# [1] 0.4531521

# $ZstatA
# [1] 0.1238843

# $pvalA
# [1] 0.9014069

# $hrA
# [1] 1.057744

# $ciA
# [1] 0.4351608 2.5710556

# $loghra
# [1] 0.1987329

# $sea
# [1] 0.6805458

# $Zstata
# [1] 0.2920198

# $pvala
# [1] 0.7702714

# $hra
# [1] 1.219856

# $cia
# [1] 0.3213781 4.6302116
# $loghrab
# [1] 0.2864932
# $seab
# [1] 0.6762458
# $Zstatab
# [1] 0.4236525
# $pvalab
# [1] 0.6718193
# $hrab
# [1] 1.331749
# $ciab
# [1] 0.3538265 5.0125010
# $critPA2A
# [1] -2.129
# $sigPA2A
# [1] 0.03325426
# $critPA2ab
# [1] -2.299
# $sigPA2ab
# [1] 0.02150494
# $result23
# [1] "accept overall A" "accept simple AB"
# $critEA3
# [1] -2.338
# $sigEA3
# [1] 0.01938725
# $result13
# [1] "accept overall A" "accept simple A" "accept simple AB"
# $critEA2
# [1] -2.216
# $sigEA2
# [1] 0.0266915
# $result12
# [1] "accept simple A" "accept simple AB"


## Description

Power for the Equal Allocation 3, Proportional Allocation 2, and Equal Allocation 2 procedures.

## Usage

```r
fac2x2design(
  n,
  rateC,
  hrA,
  hrB,
  hrAB,
  mincens,
  maxcens,
  dig = 2,
  alpha = 0.05,
  niter = 5,
  abseps = 0.001,
  corAa = 1/sqrt(2),
  corAab = 1/sqrt(2),
  coraab = 1/2
)
```

## Arguments

- `n` total sample size
- `rateC` group C one year event rate
- `hrA` group A to group C hazard ratio
- `hrB` group B to group C hazard ratio
- `hrAB` group AB to group C hazard ratio
- `mincens` minimum censoring time
- `maxcens` maximum censoring time
- `dig` number of decimal places to `roundDown` the critical value to
alpha  two-sided significance level
niter  number of times we call pmvnorm to average out its randomness
abseps  abseps setting in the pmvnorm call
corAA  correlation between the overall A and simple A log hazard ratio estimates
corAAB  correlation between the overall A and simple AB log hazard ratio estimates
coraab  correlation between the simple A and simple AB log hazard ratio estimates

Value

events  expected number of events
evtprob  event probabilities for the C, A, B, and AB groups, respectively
powerEA3overallA  Equal Allocation 3’s power to detect the overall A effect
powerEA3simpleA  Equal Allocation 3’s power to detect the simple A effect
powerEA3simpleAB  Equal Allocation 3’s power to detect the simple AB effect
powerEA3anyA  Equal Allocation 3’s power to detect the simple A or AB effects
powerPA2overallA  Proportional Allocation 2’s power to detect the overall A effect
powerPA2simpleAB  Proportional Allocation 2’s power to detect the simple AB effect
powerEA2simpleA  Equal Allocation 2’s power to detect the simple A effect
powerEA2simpleAB  Equal Allocation 2’s power to detect the simple AB effect
powerA  power to detect the overall A effect at the two-sided alpha level
powerB  power to detect the overall B effect at the two-sided alpha level

References


See Also
eventProb, crit2x2, lgrkPower, strLgrkPower, powerEA3, powerPA2, powerEA2
Examples

# Corresponds to scenario 4 in Table 2 from Leifer, Troendle, et al. (2019).

n <- 4600
rateC <- 0.0445
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4

fac2x2design(n, rateC, hrA, hrB, hrAB, mincens, maxcens, dig = 2, alpha = 0.05, niter = 1)

# $events
# [1] 954.8738

# $evtprob
# probC probA probB probAB
# 0.2446365 0.2012540 0.2012540 0.1831806

# $powerEA3overallA
# [1] 0.5861992

# $powerEA3simpleA
# [1] 0.5817954

# $powerEA3simplAB
# [1] 0.9071236

# $powerEA3anyA
# [1] 0.7060777

# $powerPA2overallA
# [1] 0.6582819

# $powerPA2simpleAB
# [1] 0.9197286

# $powerEA2simpleA
# [1] 0.6203837

# $powerEA2simpleAB
# [1] 0.9226679

# $powerA
# [1] 0.7182932

# $powerB
# [1] 0.7182932

lgrkPower

Unstratified (ordinary) logrank power
Description

Computes the power for the unstratified (ordinary) logrank statistic for two group comparison.

Usage

lgrkPower(hr, nevent, alpha = 0.05, rprob = 0.5)

Arguments

hr          hazard ratio
nevent      expected number of events
alpha       two-sided significance level
rprob       randomization probability

Details

Uses the formula at the bottom of p.317 from Schoenfeld (Biometrika, 1981) where the beta should be 1 - beta. The formula is modified to assume that values of the hazard ratio less than 1 correspond to treatment efficacy. We do this because we only want to include the probability of rejecting the null in favor of efficacy, not inferiority as well.

Value

power       logrank power

Author(s)

Eric Leifer, James Troendle

References


Examples

hr <- 0.5
nevent <- 98
lgrkPower(hr, nevent, alpha = 0.05, rprob = 0.5)
  # $power
  # [1] 0.9293463
**powerEA2**  
*Power of the Equal Allocation 2 procedure*

**Description**

Computes the Equal Allocation 2's procedure power to detect the simple A effect and the simple AB effect, respectively.

**Usage**

```r
powerEA2(n, hrA, hrAB, probA_C, probAB_C, crit12)
```

**Arguments**

- `n` total subjects with n/4 subjects in each of the C, A, B, and AB groups
- `hrA` group A to group C hazard ratio; hrA < 1 corresponds to group A superiority
- `hrAB` group AB to group C hazard ratio; hrAB < 1 corresponds to group AB superiority
- `probA_C` event probability averaged across the A and C groups
- `probAB_C` event probability averaged across the AB and C groups
- `crit12` logrank statistic critical value for both the simple A and simple AB effects

**Details**

For a 2-by-2 factorial design, this function computes the probability that either the simple A, respectively, simple AB logrank statistics reject their null hypotheses using a Dunnett-corrected `crit12` critical value. When the two-sided familywise type I error is 0.05, we may use `crit2x2` to compute `crit12 = -2.22` which corresponds to a 0.0264 two-sided significance level. This is described in Leifer, Troendle, et al. (2020).

**Value**

- `powerEA2simpleA` power to detect the simple A effect
- `powerEA2simpleAB` power to detect the simple AB effect

**References**


powerEA3

Description

Computes the Equal Allocation 3 procedure’s power to detect the overall A effect, the simple A effect, or the simple AB effect, respectively.

Usage

```r
powerEA3(
  n,
  hrA,
  hrB,
  hrAB,
  avgprob,
  probA_C,
  probAB_C,
  critEA2
)
```

Examples

# Corresponds to scenario 4 in Table 2 from Leifer, Troendle, et al. (2020).
rateC <- 0.0445 # one-year C group event rate
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4
evtprob <- eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)
probA_C <- evtprob$probA_C
probAB_C <- evtprob$probAB_C
corAa <- 1/sqrt(2)
corAab <- 1/sqrt(2)
coraab <- 1/2
dig <- 2
alpha <- 0.05
critEA2 <- crit2x2(corAa, corAab, coraab, dig, alpha)$critEA2
n <- 4600
powerEA2(n, hrA, hrAB, probA_C, probAB_C, critEA2)

# $powerEA2simpleA
# [1] 0.6203837

# $powerEA2simpleAB
# [1] 0.9226679
powerEA3

critEA3,
dig,
cormat12 = matrix(c(1, sqrt(0.5), sqrt(0.5), 1), byrow = T, nrow = 2),
niter = 5,
abseps = 0.001
)

Arguments

n total subjects with n/4 subjects in each of the C, A, B, and AB groups
hrA group A to group C hazard ratio; hrA < 1 corresponds to group A superiority
hrB group B to group C hazard ratio; hrA < 1 corresponds to group A superiority
hrAB group AB to group C hazard ratio; hrAB < 1 corresponds to group AB superiority
avgprob event probability averaged across the C, A, B, and AB groups
probAC event probability averaged across the A and C groups
probAB_C event probability averaged across the AB and C groups
critEA3 rejection critical value for the overall A, simple A, and simple AB logrank statistics
dig number of decimal places to roundDown the critical value to
cormat12 asymptotic correlation matrix for the overall A and simple A, respectively, simple AB logrank statistics
niter number of times we call pmvnorm to average out its randomness
abseps abseps setting in the pmvnorm call

Details

For a 2-by-2 factorial design, this function computes the probability that either the overall A or the simple A or the simple AB logrank statistics reject their null hypotheses at the Dunnet-corrected critEA3 critical value. As described in Leifer, Troendle, et al. (2019), the critEA3 = -2.32 critical value corresponds to controlling the familywise error of the Equal Allocation 3 procedure at the two-sided 0.05 significance level. The critical value -2.32 may be computed using the crit2x2 function. The pmvnorm function from the mvtnorm package is used to calculate the power for simultaneously detecting the overall and simple A effects. This is used to compute the power for detecting the overall A and/or simple A effects, which is computed as the sum of the powers for each of the effects minus the power for simultaneously detecting both effects. Since the power for simultaneously detecting both effects involves bivariate normal integration over an unbounded region in R^2, pmvnorm uses a random seed for these computations. Note that cRAN suggested we not include the random seed as an argument in this function. To smooth out the randomness, pmvnorm is called niter times and the average value over the niter calls is taken to be those powers.

Value

powerEA3overallA power to detect the overall A effect
powerEA3simpleA
  power to detect the simple A effect
powerEA3simpleAB
  power to detect the simple AB effect
powerEA3anyA
  power to detect either the overall A or simple A effects

References

See Also
crit2x2, lgrkPower, strLgrkPower, pmvnorm

Examples
# Corresponds to scenario 5 in Table 2 from Leifer, Troendle, et al. (2020).
rateC <- 0.0445
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4
evtprob <- eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)
avgprob <- evtprob$avgprob
probAB_C <- evtprob$probAB_C
probA_C <- evtprob$probA_C
dig <- 2
alpha <- 0.05
corAa <- 1/sqrt(2)
corAab <- 1/sqrt(2)
coraab <- 1/2
critEA3 <- crit2x2(corAa, corAab, coraab, dig, alpha)$critEA3
n <- 4600
powerEA3(n, hrA, hrB, hrAB, avgprob, probA_C, probAB_C,
critEA3, dig, cormat12 = matrix(c(1, sqrt(0.5), sqrt(0.5), 1), byrow = TRUE, nrow = 2), niter = 1, abseps = 1e-03)

# $powerEA3overallA
# [1] 0.5861992

# $powerEA3simpleA
# [1] 0.5817954

# $powerAB
# [1] 0.9071236
# $powerEA3anyA
# [1] 0.7060777

---

**powerPA2**  
*Power of the Proportional Allocation 2 procedure*

**Description**

Computes the Proportional Allocation 2 procedure’s power to detect the overall A effect or the simple AB effect, respectively.

**Usage**

```r
powerPA2(n, hrA, hrB, hrAB, avgprob, probAB_C, critPA2A, critPA2ab, dig)
```

**Arguments**

- `n`: total subjects with n/4 subjects in each of the C, A, B, and AB groups
- `hrA`: group A to group C hazard ratio; hrA < 1 corresponds to group A superiority
- `hrB`: group B to group C hazard ratio; hrA < 1 corresponds to group A superiority
- `hrAB`: group AB to group C hazard ratio; hrAB < 1 corresponds to group AB superiority
- `avgprob`: event probability averaged across the C, A, B, and AB groups
- `probAB_C`: event probability averaged across the AB and C groups
- `critPA2A`: rejection critical value for the overall A stratified logrank statistic
- `critPA2ab`: rejection critical value for the simple AB ordinary logrank statistic
- `dig`: number of decimal places to which we roundDown the critical value for the overall A test as calculated in `powerPA2` by `strLgrkPower`

**Details**

The Proportional Allocation 2 procedure uses a two-sided 2/3 * alpha significance level to test the overall A effect and the remaining Dunnett-corrected type 1 error to test the simple AB effect. When the familywise error is alpha = 0.05, this corresponds to a critical value `critPA2A` = -2.13. Then `crit2x2` is used to compute a critical value `critPA2ab` = -2.24 to test the simple AB effect. This corresponds to a two-sided 0.0251 significance level. This controls the asymptotic familywise type I error for the two hypothesis tests at the two-sided 0.05 level. This is because of the 1/sqrt(2) asymptotic correlation between the logrank test statistics for the overall A and simple AB effects (Slud, 1994). The overall A effect’s significance level 2/3 * 0.05 is prespecified and the simple AB effect’s significance level 0.0251 is computed using `crit2x2`.

**Value**

- `powerPA2overallA`: power to detect the overall A effect
- `powerPA2simpleAB`: power to detect the simple AB effect
Author(s)

Eric Leifer, James Troendle

References


See Also

crit2x2, eventProb, lgrkPower, strLgrkPower

Examples

# Corresponds to scenario 4 in Table 2 from Leifer, Troendle, et al. (2020).
rateC <- 0.0445 # one-year C group event rate
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4
evtprob <- eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)
avgprob <- evtprob$avgprob
probAB_C <- evtprob$probAB_C
dig <- 2
alpha <- 0.05
corAa <- 1/sqrt(2)
corAab <- 1/sqrt(2)
coraab <- 1/2
critvals <- crit2x2(corAa, corAab, coraab, dig, alpha)
critPA2A <- critvals$critPA2A
critPA2ab <- critvals$critPA2ab
n <- 4600
powerPA2(n, hrA, hrB, hrAB, avgprob, probAB_C, critPA2A, critPA2ab, dig)
# $powerPA2overallA
# [1] 0.6582819

# $powerPA2simpleAB
# [1] 0.9197286
roundDown

**Round down a negative number**

**Description**

Rounds a negative number to the nearest, more negative number to a specified decimal place.

**Usage**

```r
roundDown(x, dig)
```

**Arguments**

- `x` number to be rounded
- `dig` number of decimal places to be rounded

**Details**

`roundDown` is used to round a negative Z-statistic critical value, which has (infinitely) many significant digits, to the nearest `dig` decimal place which is more extreme than the critical value itself. This is done to preserve the desired type I error level.

**Examples**

```r
roundDown(-1.95456, 2)
# [1] -1.96
```

---

**simdat**

*Simulated 2x2 factorial trial data*

**Description**

A dataset mimicking data that might be obtained from a two-by-two factorial clinical trial. It is the first 100 rows of the data set `simdata`.

**Usage**

```r
data(simdat)
```

**Format**

A data frame with 100 rows and 10 variables
Details

- subjno subject ID
- time time to event or censoring
- event event indicator (1=event, 0=censoring)
- indA indicator of receiving treatment A (1=yes, 0=no)
- indB indicator of receiving treatment B (1=yes, 0=no)
- cvd history of cardiovascular disease (1=yes, 0=no)
- fac2-fac5 indicator variables for the 5 level factor variable

---

**simdata**  
*Simulated 2x2 factorial trial data*

Description

A dataset mimicking data that might be obtained from a two-by-two factorial clinical trial.

Usage

data(simdata)

Format

A data frame with 4600 rows and 10 variables

Details

- subjno subject ID
- time time to event or censoring
- event event indicator (1=event, 0=censoring)
- indA indicator of receiving treatment A (1=yes, 0=no)
- indB indicator of receiving treatment B (1=yes, 0=no)
- cvd history of cardiovascular disease (1=yes, 0=no)
- fac2-fac5 indicator variables for the 5 level factor variable
Simulated 2x2 factorial trial data

Description

A dataset mimicking data that might be obtained from a two-by-two factorial clinical trial. It is the first 100 rows of the data set simdata.

Usage

data(simdataSub)

Format

A data frame with 100 rows and 10 variables

Details

- subjno subject ID
- time time to event or censoring
- event event indicator (1=event, 0=censoring)
- indA indicator of receiving treatment A (1=yes, 0=no)
- indB indicator of receiving treatment B (1=yes, 0=no)
- cvd history of cardiovascular disease (1=yes, 0=no)
- fac2-fac5 indicator variables for the 5 level factor variable

Stratified (overall) logrank power

Description

Computes the power for the overall treatment A effect based on the stratified logrank test based on Slud (1994).

Usage

strLgrkPower(n, hrA, hrB, hrAB, avgprob, dig = 2, alpha = 0.05)
Arguments

- **n**: total subjects with \(n/4\) subjects in the C, A, B, and AB groups
- **hrA**: group A to group C hazard ratio
- **hrB**: group B to group C hazard ratio
- **hrAB**: group AB to group C hazard ratio
- **avgprob**: average event probability across the four groups as calculated by the function eventProb
- **dig**: number of decimal places to which we roundDown the critical value corresponding to \(\alpha\)
- **alpha**: two-sided significance level

Details

The roundDown function is used in conjunction with the dig argument to insure that any rounding of the (negative) critical values will be done conservatively to control the familywise type I error at the desired level.

Value

- **mean**: logrank mean value
- **power**: logrank power
- **nevent**: expected number of events

Author(s)

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References


See Also

roundDown, eventProb

Examples

```r
rateC <- 0.0445
hrA <- 0.80
hrB <- 0.80
hrAB <- 0.72
mincens <- 4.0
maxcens <- 8.4
avgprob <- eventProb(rateC, hrA, hrB, hrAB, mincens, maxcens)$avgprob
n <- 4600
```
strLgrkPower(n, hrA, hrB, hrAB, avgprob, dig = 2, alpha = 0.05)
# $mean
# [1] -2.537779

# $power
# [1] 0.7182932

# $nevent
# [1] 954.8738
Index

*Topic datasets
  simdat, 23
  simdata, 24
  simdataSub, 25

cor2x2, 2
crit2x2, 4, 14, 17, 20, 21

eventProb, 7, 14, 26

fac2x2analyze, 9
fac2x2design, 13

lgrkPower, 14, 15

powerEA2, 14, 17
powerEA3, 14, 18
powerPA2, 14, 21, 21

roundDown, 5, 9, 13, 19, 21, 23, 26

simdat, 23
simdata, 24
simdataSub, 25
strLgrkPower, 14, 21, 25