

Package ‘MIDN’

October 12, 2022

Type Package

Title Nearly Exact Sample Size Calculation for Exact Powerful
Nonrandomized Tests for Differences Between Binomial
Proportions

Version 1.0

Date 2016-10-18

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Description Implementation of the mid-n algorithms presented in
Wellek S (2015) <[DOI:10.1111/stan.12063](https://doi.org/10.1111/stan.12063)> Statistica Neerlandica 69, 358-373 for exact
sample size calculation for superiority trials with binary outcome.

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Depends BiasedUrn

NeedsCompilation no

Repository CRAN

Date/Publication 2016-10-28 11:31:15

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|--------------|---|
| MIDN-package | <i>Nearly exact sample size calculation for exact powerful nonrandomized tests for differences between binomial proportions</i> |
|--------------|---|

Description

Implementation of the mid-n algorithms presented in Wellek S (2015) *Statistica Neerlandica* 69, 358-373 for exact sample size calculation for superiority trials with binary outcome.

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References

Wellek S: Nearly exact sample size calculation for powerful nonrandomized tests for differences between binomial proportions. *Statistica Neerlandica* 69 (2015), 358-373.

Examples

```
result1 <- fisher_boschloo_midN(0.025,0.0001,0.95,0.8,0.8,2,1)
POWEX <- result1[5]
result1 # shows values of vector result1
POWEX # shows value of POWEX

result2 <- McNem_Score_midn(0.025,0.0001,0.585,0.315,0.9)
POWEX <- result2[3]
result2 # shows values of vector result2
POWEX # shows value of POWEX
```

| | |
|----------------------|---|
| fisher_boschloo_midN | <i>Nearly exact sample size calculation for the Fisher-Boschloo test for differences between independent binomial proportions</i> |
|----------------------|---|

Description

The function computes the exact sample sizes required in the randomized UMPU test and its conservative nonrandomized version for attaining prespecified power. In a final step, the mean of both quantities is output as an nearly exact value required in the Fisher-Boschloo test, a powerful non-randomized version of the exact Fisher-type test.

Usage

```
fisher_boschloo_midN(alpha, SW, p1, p2, POW0, mton_a, mton_b)
```

Arguments

| | |
|--------|---|
| alpha | target significance level |
| SW | step width for increasing p2 in the search for the size of a given critical region in the sample space of (X,Y) |
| p1 | true value of the responder rate for Population 1 |
| p2 | true value of the responder rate for Population 2 |
| POW0 | power to be obtained against the alternative (p1,p2) |
| mton_a | desired ratio of sample sizes: numerator |
| mton_b | desired ratio of sample sizes: denominator |

Value

| | |
|--------|--|
| mstart | initial value of 1st sample size |
| nstart | initial value of 2nd sample size |
| Mex | size of Sample 1 for randomized UMPU test |
| Nex | size of Sample 2 for randomized UMPU test |
| POWEX | power of randomized UMPU test attained with m=Mex,n=Nex |
| Mnr | size of Sample 1 for conservative nonrandomized Fisher-type test |
| Nnr | size of Sample 2 for conservative nonrandomized Fisher-type test |
| POWNR | power of conservative nonrandomized Fisher-type test attained with m=Mnr,n=Nnr |
| midN_m | nearly exact size of Sample 1 for Boschloo-Fisher test |
| midN_n | nearly exact size of Sample 2 for Boschloo-Fisher test |

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References

Wellek S: Nearly exact sample size calculation for powerful nonrandomized tests for differences between binomial proportions. *Statistica Neerlandica* 69 (2015), 358-373.

Examples

```
result1 <- fisher_boschloo_midN(0.025,0.0001,0.95,0.8,0.8,2,1)
POWEX <- result1[5]
result1 # shows values of vector result1
POWEX # shows value of POWEX
```

| | |
|------------------|--|
| McNem_Score_midn | <i>Nearly exact sample size calculation for the level-corrected score test for differences between binomial proportions estimated from paired data</i> |
|------------------|--|

Description

Again, the function computes the exact sample sizes required in the randomized UMPU test and its conservative nonrandomized counterpart for attaining prespecified power. However, in contrast to the parallel group setting, the midpoint of the interval between these two numbers shall now used as an nearly exact value of the number of pairs to be observed in the asymptotic test based on the score-statistic corrected for possible exceedances of the nominal significance level.

Usage

```
McNem_Score_midn(alpha, SW, ppl, pmi, POWO)
```

Arguments

| | |
|-------|--|
| alpha | target significance level, 1-sided |
| SW | width of search grid for determining the size of a given critical region in the sample space of N_+ [= number of pairs with $(X_i, Y_i) = (1, 0)$] and N_0 [= number of tied pairs] |
| ppl | true value of $\Pr[(X, Y) = (1, 0)]$ |
| pmi | true value of $\Pr[(X, Y) = (0, 1)]$ |
| POWO | power to be attained in the level-corrected score test against the alternative (ppl, pmi) |

Value

| | |
|--------|---|
| nstart | initial value for the iteration algorithm |
| Nex | sample size required in the exact randomized McNemar test |
| POWEX | power of the exact randomized McNemar test performed with Nex pairs |
| Nnr | sample size required in the conservative nonrandomized McNemar test |
| POWNR | power of the nonrandomized McNemar test performed with Nnr pairs |
| mid_n | midpoint of the interval [Nex, Nnr], rounded to the next integer |

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References

Wellek S: Nearly exact sample size calculation for powerful nonrandomized tests for differences between binomial proportions. *Statistica Neerlandica* 69 (2015), 358-373.

Examples

```
result2 <- McNem_Score_midn(0.025,0.0001,0.585,0.315,0.9)
POWEX <- result2[3]
result2 # shows values of vector result2
POWEX   # shows value of POWEX
```

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