Package 'EQUIVNONINF'

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Type Package

Title Testing for Equivalence and Noninferiority

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Description
Making available in R the complete set of programs accompanying S. Wellek's (2010) monograph "Testing Statistical Hypotheses of Equivalence and Noninferiority. Second Edition" (Chapman&Hall/CRC).

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Depends R (>= 3.0.0), stats, BiasedUrn

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Contents

`EQUIVNONINF-package` *Testing for equivalence and noninferiority*

Description

The package makes available in R the complete set of programs accompanying S. Wellek's (2010) monograph "Testing Statistical Hypotheses of Equivalence and Noninferiority. Second Edition" (Chapman&Hall/CRC).

Note

In order to keep execution time of all examples below the limit set by the CRAN administration, in a number of cases the function calls shown in the documentation contain specifications which are insufficient for real applications. This holds in particular true for the width sw of search grids, which should be chosen to be .001 or smaller. Similarly, the maximum number of interval halving steps to be carried out in finding maximally admissible significance levels should be set to values >= 10.

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2015.

Examples

```
bi2ste1(397,397,0.0,0.025,0.511,0.384)
bi2ste2(0.0,0.025,0.95,0.8,0.80,1.0)
```

`bi1st` *Critical constants and power of the UMP test for equivalence of a single binomial proportion to some given reference value*

Description

The function computes the critical constants defining the uniformly most powerful (randomized) test for the problem $p \leq p_1$ or $p \geq p_2$ versus $p_1 < p < p_2$, with p denoting the parameter of a binomial distribution from which a single sample of size n is available. In the output, one also finds the power against the alternative that the true value of p falls on the midpoint of the hypothetical equivalence interval (p_1, p_2).

Usage

```
bi1st(alpha,n,P1,P2)
```

Arguments

`alpha`	significance level
`n`	sample size
`P1`	lower limit of the hypothetical equivalence range for the binomial parameter p
`P2`	upper limit of the hypothetical equivalence range for p

Value

`alpha`	significance level
`n`	sample size
`P1`	lower limit of the hypothetical equivalence range for the binomial parameter p
`P2`	upper limit of the hypothetical equivalence range for p

`C1`	left-hand limit of the critical interval for the observed number X of successes
`C2`	right-hand limit of the critical interval for X
`GAM1`	probability of rejecting the null hypothesis when it turns out that $X = C_1$
`GAM2`	probability of rejecting the null hypothesis for $X = C_2$
`POWNONRD`	Power of the nonrandomized version of the test against the alternative $p = (p_1 + p_2)/2$
`POW`	Power of the randomized UMP test against the alternative $p = (p_1 + p_2)/2$

Author(s)

Stefan Wellek <stefan.wellek@zi-mannheim.de>
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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 4.3.

Examples

```
bi1st(.05,273,.65,.75)
```

`bi2aeq1` *Power of the exact Fisher type test for equivalence*

Description

The function computes exact values of the power of the randomized UMPU test for equivalence in the strict (i.e. two-sided) sense of two binomial distributions and the conservative nonrandomized version of that test. It is assumed that the samples being available from both distributions are independent.

Usage

```
bi2aeq1(m,n,rho1,rho2,alpha,p1,p2)
```

Arguments

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2

Value

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`POWNR`	Power of the nonrandomized version of the test
`POW`	Power of the randomized UMPU test

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.4.

Examples

```
bi2aeq1(302,302,0.6667,1.5,0.05,0.5,0.5)
```

`bi2aeq2` *Sample sizes for the exact Fisher type test for equivalence*

Description

The function computes minimum sample sizes required in the randomized UMPU test for equivalence of two binomial distributions with respect to the odds ratio. Computation is done under the side condition that the ratio m/n has some predefined value λ.

Usage

```
bi2aeq2(rho1,rho2,alpha,p1,p2,beta,qlambd)
```

Arguments

`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`beta`	target value of power
`qlambd`	sample size ratio m/n

Value

`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`beta`	target value of power
`qlambd`	sample size ratio m/n
`M`	minimum size of Sample 1
`N`	minimum size of Sample 2
`POW`	Power of the randomized UMPU test attained with the computed values of m,n

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.4.

Examples

```
bi2aeq2(0.5,2.0,0.05,0.5,0.5,0.60,1.0)
```

`bi2aeq3` *Determination of a maximally raised nominal significance level for the nonrandomized version of the exact Fisher type test for equivalence*

Description

The objective is to raise the nominal significance level as far as possible without exceeding the target significance level in the nonrandomized version of the test. The approach goes back to R.D. Boschloo (1970) who used the same technique for reducing the conservatism of the traditional nonrandomized Fisher test for superiority.

Usage

```
bi2aeq3(m,n,rho1,rho2,alpha,sw,tolrd,tol,maxh)
```

Arguments

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance from 0 and 1, respectively of the left- and right-most boundary point to be included in the search grid
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level

Details

It should be noted that, as the function of the nominal level, the size of the nonrandomized test is piecewise constant. Accordingly, there is a nondegenerate interval of "candidate" nominal levels serving the purpose. The limits of such an interval can be read from the output. In terms of execution time, bi2aeq3 is the most demanding program of the whole package.

Value

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio

`alpha`	significance level
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance from 0 and 1, respectively of the left- and right-most boundary point to be included in the search grid
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level
`ALPH_0`	current trial value of the raised nominal level searched for
`NHST`	number of interval-halving steps performed up to now
`SIZE`	size of the critical region corresponding to α_0

Author(s)

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References

Boschloo RD: Raised conditional level of significance for the 2 x 2- table when testing the equality of two probabilities. Statistica Neerlandica 24 (1970), 1-35.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.5.

Examples

```
bi2aeq3(50,50,0.6667,1.5000,0.05,0.01,0.000001,0.0001,5)
```

`bi2by_ni_del` *Objective Bayesian test for noninferiority in the two-sample setting with binary data and the difference of the two proportions as the parameter of interest*

Description

Implementation of the construction described on pp. 185-6 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
bi2by_ni_del(N1,N2,EPS,SW,NSUB,ALPHA,MAXH)
```

Arguments

`N1`	size of Sample 1
`N2`	size of sample 2
`EPS`	noninferiority margin to the difference of success probabilities
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`NSUB`	number of subintervals for partitioning the range of integration
`ALPHA`	target significance level
`MAXH`	maximum number of interval halving steps to be carried out in finding the maximally admissible nominal level

Details

The program uses 96-point Gauss-Legendre quadrature on each of the NSUB intervals into which the range of integration is partitioned.

Value

`N1`	size of Sample 1
`N2`	size of sample 2
`EPS`	noninferiority margin to the difference of success probabilities
`NSUB`	number of subintervals for partitioning the range of integration
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA0`	result of the search for the largest admissible nominal level
`SIZE0`	size of the critical region corresponding to α_0
`SIZE_UNC`	size of the critical region of the test at uncorrected nominal level

Author(s)

Stefan Wellek <stefan.wellek@zi-mannheim.de>
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References

Wellek S: Statistical methods for the analysis of two-armed non-inferiority trials with binary outcomes. Biometrical Journal 47 (2005), 48–61.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.3.

Examples

```
bi2by_ni_del(20,20,.10,.01,10,.05,5)
```

`bi2by_ni_OR` *Objective Bayesian test for noninferiority in the two-sample setting with binary data and the odds ratio as the parameter of interest*

Description

Implementation of the construction described on pp. 179–181 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
bi2by_ni_OR(N1,N2,EPS,SW,NSUB,ALPHA,MAXH)
```

Arguments

`N1`	size of sample 1
`N2`	size of sample 2
`EPS`	noninferiority margin to the deviation of the odds ratio from unity
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`NSUB`	number of subintervals for partitioning the range of integration
`ALPHA`	target significance level
`MAXH`	maximum number of interval halving steps to be carried out in finding the maximally admissible nominal level

Details

The program uses 96-point Gauss-Legendre quadrature on each of the NSUB intervals into which the range of integration is partitioned.

Value

`N1`	size of sample 1
`N2`	size of sample 2
`EPS`	noninferiority margin to the deviation of the odds ratio from unity
`NSUB`	number of subintervals for partitioning the range of integration
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA0`	result of the search for the largest admissible nominal level
`SIZE0`	size of the critical region corresponding to α_0
`SIZE_UNC`	size of the critical region of the test at uncorrected nominal level

Author(s)

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References

Wellek S: Statistical methods for the analysis of two-arm non-inferiority trials with binary outcomes. Biometrical Journal 47 (2005), 48–61.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.2.

Examples

```
bi2by_ni_OR(10,10,1/3,.0005,10,.05,12)
```

`bi2diffac` *Determination of a corrected nominal significance level for the asymptotic test for equivalence of two unrelated binomial proportions with respect to the difference δ of their population counterparts*

Description

The program computes the largest nominal significance level which can be substituted for the target level α without making the exact size of the asymptotic testing procedure larger than α.

Usage

```
bi2diffac(alpha,m,n,del1,del2,sw,tolrd,tol,maxh)
```

Arguments

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`del1`	absolute value of the lower limit of the hypothetical equivalence range for $p_1 - p_2$
`del2`	upper limit of the hypothetical equivalence range for $p_1 - p_2$
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance of the left- and right-most boundary point to be included in the search grid
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level

Value

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`del1`	absolute value of the lower limit of the hypothetical equivalence range for $p_1 - p_2$
`del2`	upper limit of the hypothetical equivalence range for $p_1 - p_2$
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance of the left- and right-most boundary point to be included in the search grid
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level
`NH`	number of interval-halving steps actually performed
`ALPH_0`	value of the raised nominal level obtained after NH steps
`SIZE0`	size of the critical region corresponding to α_0
`ERROR`	error indicator answering the question of whether or not the sufficient condition for the correctness of the result output by the program, was satisfied

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.6.

Examples

```
bi2diffac(0.05,20,20,0.40,0.40,0.1,1e-6,1e-4,3)
```

`bi2dipow` *Exact rejection probability of the asymptotic test for equivalence of two unrelated binomial proportions with respect to the difference of their expectations at any nominal level under an arbitrary parameter configuration*

Description

The program computes exact values of the rejection probability of the asymptotic test for equivalence in the sense of $-\delta_1 < p_1 - p_2 < \delta_2$, at any nominal level α_0. [The largest α_0 for which the test is valid in terms of the significance level, can be computed by means of the program bi2diffac.]

Usage

```
bi2dipow(alpha0,m,n,del1,del2,p1,p2)
```

Arguments

`alpha0`	nominal significance level
`m`	size of Sample 1
`n`	size of Sample 2
`del1`	absolute value of the lower limit of the hypothetical equivalence range for $p_1 - p_2$
`del2`	upper limit of the hypothetical equivalence range for $p_1 - p_2$
`p1`	true value of the success probability in Population 1
`p2`	true value of the success probability in Population 2

Value

`alpha0`	nominal significance level
`m`	size of Sample 1
`n`	size of Sample 2
`del1`	absolute value of the lower limit of the hypothetical equivalence range for $p_1 - p_2$
`del2`	upper limit of the hypothetical equivalence range for $p_1 - p_2$
`p1`	true value of the success probability in Population 1
`p2`	true value of the success probability in Population 2
`POWEX0`	exact rejection probability under (p_1, p_2) of the test at nominal level α_0 for equivalence of two binomial distributions with respect to the difference of the success probabilities
`ERROR`	error indicator answering the question of whether or not the sufficient condition for the correctness of the result output by the program, was satisfied

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.6.

Examples

```
bi2dipow(0.0228,50,50,0.20,0.20,0.50,0.50)
```

`bi2rlv1` *Power of the exact Fisher type test for relevant differences*

Description

The function computes exact values of the power of the randomized UMPU test for relevant differences between two binomial distributions and the conservative nonrandomized version of that test. It is assumed that the samples being available from both distributions are independent.

Usage

```
bi2rlv1(m,n,rho1,rho2,alpha,p1,p2)
```

Arguments

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2

Value

`m`	size of Sample 1
`n`	size of Sample 2
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`POWNR`	power of the nonrandomized version of the test
`POW`	power of the randomized UMPU test

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 11.3.3.

Examples

```
bi2rlv1(200,300,.6667,1.5,.05,.25,.10)
```

`bi2rlv2` *Sample sizes for the exact Fisher type test for relevant differences*

Description

The function computes minimum sample sizes required in the randomized UMPU test for relevant differences between two binomial distributions with respect to the odds ratio. Computation is done under the side condition that the ratio m/n has some predefined value λ.

Usage

```
bi2rlv2(rho1,rho2,alpha,p1,p2,beta,qlambd)
```

Arguments

`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`beta`	target value of power
`qlambd`	sample size ratio m/n

Value

`rho1`	lower limit of the hypothetical equivalence range for the odds ratio
`rho2`	upper limit of the hypothetical equivalence range for the odds ratio
`alpha`	significance level
`p1`	true success rate in Population 1
`p2`	true success rate in Population 2
`beta`	target value of power
`qlambd`	sample size ratio m/n
`M`	minimum size of Sample 1
`N`	minimum size of Sample 2
`POW`	power of the randomized UMPU test attained with the computed values of m, n

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References

Welleck S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 11.3.3.

Examples

```
bi2rlv2(.6667,1.5,.05,.70,.50,.50,2.0)
```

`bi2st` *Critical constants for the exact Fisher type UMPU test for equivalence of two binomial distributions with respect to the odds ratio*

Description

The function computes the critical constants defining the uniformly most powerful unbiased test for equivalence of two binomial distributions with parameters p_1 and p_2 in terms of the odds ratio. Like the ordinary Fisher type test of the null hypothesis $p_1 = p_2$, the test is conditional on the total number S of successes in the pooled sample.

Usage

```
bi2st(alpha,m,n,s,rho1,rho2)
```

Arguments

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`s`	observed total count of successes
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio $\varrho = \frac{p_1(1-p_2)}{p_2(1-p_1)}$
`rho2`	upper limit of the hypothetical equivalence range for ϱ

Value

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`s`	observed total count of successes
`rho1`	lower limit of the hypothetical equivalence range for the odds ratio $\varrho = \frac{p_1(1-p_2)}{p_2(1-p_1)}$
`rho2`	upper limit of the hypothetical equivalence range for ϱ
`C1`	left-hand limit of the critical interval for the number X of successes observed in Sample 1
`C2`	right-hand limit of the critical interval for X
`GAM1`	probability of rejecting the null hypothesis when it turns out that $X = C_1$
`GAM2`	probability of rejecting the null hypothesis for $X = C_2$

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.4.

Examples

```
bi2st(.05,225,119,171, 2/3, 3/2)
```

`bi2ste1` *Power of the exact Fisher type test for noninferiority*

Description

The function computes exact values of the power of the randomized UMPU test for one-sided equivalence of two binomial distributions and its conservative nonrandomized version. It is assumed that the samples being available from both distributions are independent.

Usage

```
bi2ste1(m, n, eps, alpha, p1, p2)
```

Arguments

`m`	size of Sample 1
`n`	size of Sample 2
`eps`	noninferiority margin to the odds ratio ϱ, defined to be the maximum acceptable deviation of the true value of ϱ from unity
`alpha`	significance level
`p1`	success rate in Population 1
`p2`	success rate in Population 2

Value

`m`	size of Sample 1
`n`	size of Sample 2
`eps`	noninferiority margin to the odds ratio ϱ, defined to be the maximum acceptable deviation of the true value of ϱ from unity
`alpha`	significance level
`p1`	success rate in Population 1
`p2`	success rate in Population 2
`POWNR`	power of the nonrandomized version of the test
`POW`	power of the randomized UMPU test

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, 6.6.1.

Examples

```
bi2ste1(106,107,0.5,0.05,0.9245,0.9065)
```

`bi2ste2` *Sample sizes for the exact Fisher type test for noninferiority*

Description

Sample sizes for the exact Fisher type test for noninferiority

Usage

```
bi2ste2(eps, alpha, p1, p2, bet, qlambd)
```

Arguments

`eps`	noninferiority margin to the odds ratio
`alpha`	significance level
`p1`	success rate in Population 1
`p2`	success rate in Population 2
`bet`	target power value
`qlambd`	sample size ratio m/n

Details

The program computes the smallest sample sizes m,n satisfying $m/n = \lambda$ required for ensuring that the power of the randomized UMPU test does not fall below β.

Value

`eps`	noninferiority margin to the odds ratio
`alpha`	significance level
`p1`	success rate in Population 1
`p2`	success rate in Population 2
`bet`	target power value

`qlambd`	sample size ratio m/n
`M`	minimum size of Sample 1
`N`	minimum size of Sample 2
`POW`	power of the randomized UMPU test attained with the computed values of m, n

Author(s)

Stefan Wellek <stefan.wellek@zi-mannheim.de>
Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, 6.6.1.

Examples

```
bi2ste2(0.5,0.05,0.9245,0.9065,0.80,1.00)
```

`bi2ste3` *Determination of a maximally raised nominal significance level for the nonrandomized version of the exact Fisher type test for noninferiority*

Description

The objective is to raise the nominal significance level as far as possible without exceeding the target significance level in the nonrandomized version of the test. The approach goes back to R.D. Boschloo (1970) who used the same technique for reducing the conservatism of the traditional nonrandomized Fisher test for superiority.

Usage

```
bi2ste3(m, n, eps, alpha, sw, tolrd, tol, maxh)
```

Arguments

`m`	size of Sample 1
`n`	size of Sample 2
`eps`	noninferiority margin to the odds ratio ϱ, defined to be the maximum acceptable deviation of the true value of ϱ from unity
`alpha`	target significance level
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance from 0 and 1, respectively, of the left- and right-most boundary point to be included in the search grid

`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval-halving steps to be carried out in finding the maximally raised nominal level

Details

It should be noted that, as the function of the nominal level, the size of the nonrandomized test is piecewise constant. Accordingly, there is a nondegenerate interval of "candidate" nominal levels serving the purpose. The limits of such an interval can be read from the output.

Value

`m`	size of Sample 1
`n`	size of Sample 2
`eps`	noninferiority margin to the odds ratio ϱ, defined to be the maximum acceptable deviation of the true value of ϱ from unity
`alpha`	target significance level
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tolrd`	horizontal distance from 0 and 1, respectively, of the left- and right-most boundary point to be included in the search grid
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval-halving steps to be carried out in finding the maximally raised nominal level
`ALPH_0`	current trial value of the raised nominal level searched for
`NHST`	number of interval-halving steps performed up to now
`SIZE`	size of the critical region corresponding to α_0

Author(s)

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References

Boschloo RD: Raised conditional level of significance for the 2 x 2- table when testing the equality of two probabilities. Statistica Neerlandica 24 (1970), 1-35.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, §6.6.2.

Examples

```
bi2ste3(50, 50, 1/3, 0.05, 0.05, 1e-10, 1e-8, 10)
```

`bi2wld_ni_del` *Function to compute corrected nominal levels for the Wald type (asymptotic) test for one-sided equivalence of two binomial distributions with respect to the difference of success rates*

Description

Implementation of the construction described on pp. 183-5 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
bi2wld_ni_del(N1,N2,EPS,SW,ALPHA,MAXH)
```

Arguments

`N1`	size of Sample 1
`N2`	size of Sample 2
`EPS`	noninferiority margin to the difference of success probabilities
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA`	target significance level
`MAXH`	maximum number of interval-halving steps

Details

The program computes the largest nominal significance level to be used for determining the critical lower bound to the Wald-type statistic for the problem of testing $H : p_1 \leq p_2 - \varepsilon$ versus $K : p_1 < p_2 - \varepsilon$.

Value

`N1`	size of Sample 1
`N2`	size of Sample 2
`EPS`	noninferiority margin to the difference of success probabilities
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA`	target significance level
`MAXH`	maximum number of interval-halving steps
`ALPHA0`	corrected nominal level
`SIZE0`	size of the critical region of the test at nominal level ALPHA0
`SIZE_UNC`	size of the test at uncorrected nominal level ALPHA
`ERR_IND`	indicator taking value 1 when it occurs that the sufficient condition allowing one to restrict the search for the maximum of the rejection probability under the null hypothesis to its boundary, fails to be satisfied; otherwise the indicator retains its default value 0.

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.6.3.

Examples

```
bi2wld_ni_del(25,25,.10,.01,.05,10)
```

`cf_reh_exact` *Exact confidence bounds to the relative excess heterozygosity (REH) exhibited by a SNP genotype distribution*

Description

Implementation of the interval estimation procedure described on pp. 305-6 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
cf_reh_exact(X1,X2,X3,alpha,SW,TOL,ITMAX)
```

Arguments

`X1`	count of homozygotes of the first kind [$\leftrightarrow$ genotype AA]
`X2`	count of heterozygotes [$\leftrightarrow$ genotype AB]
`X3`	count of homozygotes of the second kind [$\leftrightarrow$ genotype BB]
`alpha`	1 - confidence level
`SW`	width of the search grid for determining an interval covering the parameter point at which the conditional distribution function takes value α and $1-\alpha$, respectively
`TOL`	numerical tolerance to the deviation between the computed confidence limits and their exact values
`ITMAX`	maximum number of interval-halving steps

Details

The program exploits the structure of the family of all genotype distributions, which is 2-parameter exponential with $\log(REH)$ as one of these parameters.

Value

`X1`	count of homozygotes of the first kind [↔ genotype AA]
`X2`	count of heterozygotes [↔ genotype AB]
`X3`	count of homozygotes of the second kind [↔ genotype BB]
`alpha`	1 - confidence level
`SW`	width of the search grid for determining an interval covering the parameter point at which the conditional distribution function takes value α and $1-\alpha$, respectively
`TOL`	numerical tolerance to the deviation between the computed confidence limits and their exact values
`ITMAX`	maximum number of interval-halving steps
`C_l_exact`	exact conditional lower $(1-\alpha)$-confidence bound to REH
`C_r_exact`	exact conditional upper $(1-\alpha)$-confidence bound to REH

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S, Goddard KAB, Ziegler A: A confidence-limit-based approach to the assessment of Hardy-Weinberg equilibrium. Biometrical Journal 52 (2010), 253-270.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 9.4.3.

Examples

```
cf_reh_exact(34,118,96,.05,.1,1E-4,25)
```

`cf_reh_midp` *Mid-p-value - based confidence bounds to the relative excess heterozygosity (REH) exhibited by a SNP genotype distribution*

Description

Implementation of the interval estimation procedure described on pp. 306-7 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
cf_reh_midp(X1,X2,X3,alpha,SW,TOL,ITMAX)
```

Arguments

`X1`	count of homozygotes of the first kind [↔ genotype AA]
`X2`	count of heterozygotes [↔ genotype AB]
`X3`	count of homozygotes of the second kind [↔ genotype BB]
`alpha`	1 - confidence level
`SW`	width of the search grid for determining an interval covering the parameter point at which the conditional distribution function takes value α and $1-\alpha$, respectively
`TOL`	numerical tolerance to the deviation between the computed confidence limits and their exact values
`ITMAX`	maximum number of interval-halving steps

Details

The mid-p algorithm serves as a device for reducing the conservatism inherent in exact confidence estimation procedures for parameters of discrete distributions.

Value

`X1`	count of homozygotes of the first kind [↔ genotype AA]
`X2`	count of heterozygotes [↔ genotype AB]
`X3`	count of homozygotes of the second kind [↔ genotype BB]
`alpha`	1 - confidence level
`SW`	width of the search grid for determining an interval covering the parameter point at which the conditional distribution function takes value α and $1-\alpha$, respectively
`TOL`	numerical tolerance to the deviation between the computed confidence limits and their exact values
`ITMAX`	maximum number of interval-halving steps
`C_l_midp`	lower $(1-\alpha)$-confidence bound to REH based on conditional mid-p-values
`C_r_midp`	upper $(1-\alpha)$-confidence bound to REH based on conditional mid-p-values

Author(s)

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References

Agresti A: Categorical data Analysis (2nd edn). Hoboken, NJ: Wiley, Inc., 2002, Section 1.4.5.

Wellek S, Goddard KAB, Ziegler A: A confidence-limit-based approach to the assessment of Hardy-Weinberg equilibrium. Biometrical Journal 52 (2010), 253-270.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 9.4.3.

Examples

```
cf_reh_midp(137,34,8,.05,.1,1E-4,25)
```

`exp1st` *Critical constants and power against the null alternative of the UMP test for equivalence of the hazard rate of a single exponential distribution to some given reference value*

Description

The function computes the critical constants defining the uniformly most powerful test for the problem $\sigma \leq 1/(1+\varepsilon)$ or $\sigma \geq (1+\varepsilon)$ versus $1/(1+\varepsilon) < \sigma < (1+\varepsilon)$, with σ denoting the scale parameter [≡ reciprocal hazard rate] of an exponential distribution.

Usage

```
exp1st(alpha,tol,itmax,n,eps)
```

Arguments

`alpha`	significance level
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps
`n`	sample size
`eps`	margin determining the hypothetical equivalence range symmetrically on the log-scale

Value

`alpha`	significance level
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps
`n`	sample size
`eps`	margin determining the hypothetical equivalence range symmetrically on the log-scale
`IT`	number of iteration steps performed until reaching the stopping criterion corresponding to TOL
`C1`	left-hand limit of the critical interval for $T = \sum_{i=1}^{n} X_i$
`C2`	right-hand limit of the critical interval for $T = \sum_{i=1}^{n} X_i$
`ERR1`	deviation of the rejection probability from α under $\sigma = 1/(1+\varepsilon)$
`POW0`	power of the randomized UMP test against the alternative $\sigma = 1$

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 4.2.

Examples

```
exp1st(0.05,1.0e-10,100,80,0.3)
```

`fstretch`	*Critical constants and power of the UMPI (uniformly most powerful invariant) test for dispersion equivalence of two Gaussian distributions*

Description

The function computes the critical constants defining the optimal test for the problem $\sigma^2/\tau^2 \leq \varrho_1$ or $\sigma^2/\tau^2 \geq \varrho_2$ versus $\varrho_1 < \sigma^2/\tau^2 < \varrho_2$, with (ϱ_1, ϱ_2) as a fixed nonempty interval around unity.

Usage

```
fstretch(alpha,tol,itmax,ny1,ny2,rho1,rho2)
```

Arguments

`alpha`	significance level
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps
`ny1`	number of degrees of freedom of the estimator of σ^2
`ny2`	number of degrees of freedom of the estimator of τ^2
`rho1`	lower equivalence limit to σ^2/τ^2
`rho2`	upper equivalence limit to σ^2/τ^2

Value

`alpha`	significance level
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps
`ny1`	number of degrees of freedom of the estimator of σ^2

`ny2`	number of degrees of freedom of the estimator of τ^2
`rho1`	lower equivalence limit to σ^2/τ^2
`rho2`	upper equivalence limit to σ^2/τ^2
`IT`	number of iteration steps performed until reaching the stopping criterion corresponding to TOL
`C1`	left-hand limit of the critical interval for $$T = \frac{n-1}{m-1} \sum_{i=1}^{m} (X_i - \overline{X})^2 / \sum_{j=1}^{n-1} (Y_j - \overline{Y})^2$$
`C2`	right-hand limit of the critical interval for $$T = \frac{n-1}{m-1} \sum_{i=1}^{m} (X_i - \overline{X})^2 / \sum_{j=1}^{n-1} (Y_j - \overline{Y})^2$$
`ERR`	deviation of the rejection probability from α under $\sigma^2/\tau^2 = \varrho_1$
`POW0`	power of the UMPI test against the alternative $\sigma^2/\tau^2 = 1$

Note

If the two independent samples under analysis are from exponential rather than Gaussian distributions, the critical constants computed by means of fstretch with $\nu_1 = 2m$, $\nu_2 = 2n$, can be used for testing for equivalence with respect to the ratio of hazard rates. The only difference is that the ratio of sample means rather than variances has to be used as the test statistic then.

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.5.

Examples

```
fstretch(0.05, 1.0e-10, 50,40,45,0.5625,1.7689)
```

`gofhwex` *Critical constants of the exact UMPU test for approximate compatibility of a SNP genotype distribution with the Hardy-Weinberg model*

Description

The function computes the critical constants defining the uniformly most powerful unbiased test for equivalence of the population distribution of the three genotypes distinguishable in terms of a single nucleotide polymorphism (SNP), to a distribution being in Hardy-Weinberg equilibrium (HWE). The test is conditional on the total count S of alleles of the kind of interest, and the parameter θ, in terms of which equivalence shall be established, is defined by $\theta = \frac{\pi_2^2}{\pi_1(1-\pi_1-\pi_2)}$, with π_1 and π_2 denoting the population frequence of homozygotes of the 1st kind and heterozygotes, respectively.

Usage

```
gofhwex(alpha,n,s,del1,del2)
```

Arguments

`alpha`	significance level
`n`	number of genotyped individuals
`s`	observed count of alleles of the kind of interest
`del1`	absolute value of the lower equivalence limit to $\theta/4-1$
`del2`	upper equivalence limit to $\theta/4-1$

Value

`alpha`	significance level
`n`	number of genotyped individuals
`s`	observed count of alleles of the kind of interest
`del1`	absolute value of the lower equivalence limit to $\theta/4-1$
`del2`	upper equivalence limit to $\theta/4-1$
`C1`	left-hand limit of the critical interval for the observed number X_2 of heterozygotes
`C2`	right-hand limit of the critical interval for the observed number X_2
`GAM1`	probability of rejecting the null hypothesis when it turns out that $X_2 = C_1$
`GAM2`	probability of rejecting the null hypothesis for $X_2 = C_2$

Author(s)

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References

Wellek S: Tests for establishing compatibility of an observed genotype distribution with Hardy-Weinberg equilibrium in the case of a biallelic locus. Biometrics 60 (2004), 694-703.

Goddard KAB, Ziegler A, Wellek S: Adapting the logical basis of tests for Hardy-Weinberg equilibrium to the real needs of association studies in human and medical genetics. Genetic Epidemiology 33 (2009), 569-580.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 9.4.2.

Examples

```
gofhwex(0.05,475,429,1-1/1.96,0.96)
```

`gofhwex_1s` *Critical constants of the exact UMPU test for absence of a substantial deficit of heterozygotes as compared with a HWE-compliant SNP genotype distribution [noninferiority version of the test implemented by means of gofhwex]*

Description

The function computes the critical constants defining the UMPU test for one-sided equivalence of the population distribution of a SNP, to a distribution being in Hardy-Weinberg equilibrium (HWE). A substantial deficit of heterozygotes is defined to occur when the true value of the parametric function $\omega = \frac{\pi_2/2}{\sqrt{\pi_1 \pi_3}}$ [called relative excess heterozygosity (REH)] falls below unity by more than some given margin δ_0.
Like its two-sided counterpart [see the description of the R function gofhwex], the test is conditional on the total count S of alleles of the kind of interest.

Usage

```
gofhwex_1s(alpha,n,s,del0)
```

Arguments

`alpha`	significance level
`n`	number of genotyped individuals
`s`	observed count of alleles of the kind of interest
`del0`	noninferiority margin for ω, which has to satisfy $\omega > 1-\delta_0$ under the alternative hypothesis to be established

Value

`alpha`	significance level
`n`	number of genotyped individuals
`s`	observed count of alleles of the kind of interest
`del0`	noninferiority margin for ω, which has to satisfy $\omega > 1-\delta_0$ under the alternative hypothesis to be established
`C`	left-hand limit of the critical interval for the observed number X_2 of heterozygotes
`GAM`	probability of rejecting the null hypothesis when it turns out that $X_2 = C$

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, pp. 300-302.

Examples

```
gofhwex_1s(0.05,133,65,1-1/1.96)
```

`gofind_t` *Establishing approximate independence in a two-way contingency table: Test statistic and critical bound*

Description

The function computes all quantities required for carrying out the asymptotic test for approximate independence of two categorial variables derived in $\S$ 9.2 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
gofind_t(alpha,r,s,eps,xv)
```

Arguments

`alpha`	significance level
`r`	number of rows of the contingency table under analysis
`s`	number of columns of the contingency table under analysis
`eps`	margin to the Euclidean distance between the vector π of true cell probabilities and the associated vector of products of marginal totals
`xv`	row vector of length $r \cdot s$ whose $(i-1)s+j$-th component is the entry in cell (i,j) of the $r \times s$ contingency table under analysis $i = 1,\ldots,r$, $j = 1,\ldots,s$.

Value

`n`	size of the sample to which the input table relates
`alpha`	significance level
`r`	number of rows of the contingency table under analysis
`s`	number of columns of the contingency table under analysis
`eps`	margin to the Euclidean distance between the vector π of true cell probabilities and the associated vector of products of marginal totals
`X(r,s)`	observed cell counts
`DSQ_OBS`	observed value of the squared Euclidean distance
`VN`	square root of the estimated asymtotic variance of $\sqrt{n}DSQ\_OBS$
`CRIT`	upper critical bound to $\sqrt{n}DSQ\_OBS$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 9.2.

Examples

```
xv <- c(8, 13, 15, 6,  19, 21, 31, 7)
gofind_t(0.05,2,4,0.15,xv)
```

`gofsimpt` *Establishing goodness of fit of an observed to a fully specified multinomial distribution: test statistic and critical bound*

Description

The function computes all quantities required for carrying out the asymptotic test for goodness rather than lack of fit of an observed to a fully specified multinomial distribution derived in § 9.1 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
gofsimpt(alpha,n,k,eps,x,pio)
```

Arguments

`alpha`	significance level
`n`	sample size
`k`	number of categories
`eps`	margin to the Euclidean distance between the vectors π and π_0 of true and hypothesized cell probabilities
`x`	vector of length k with the observed cell counts as components
`pio`	prespecified vector of cell probabilities

Value

`alpha`	significance level
`n`	sample size
`k`	number of categories
`eps`	margin to the Euclidean distance between the vectors π and π_0 of true and hypothesized cell probabilities
`X(1,K)`	observed cell counts
`PI0(1,K)`	hypothecized cell probabilities
`DSQPIH_0`	observed value of the squared Euclidean distance
`VN_N`	square root of the estimated asymtotic variance of $\sqrt{n}DSQPIH\_0$
`CRIT`	upper critical bound to $\sqrt{n}DSQPIH\_0$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 9.1.

Examples

```
x<- c(17,16,25,9,16,17)
pio <- rep(1,6)/6
gofsimpt(0.05,100,6,0.15,x,pio)
```

`mawi` *Mann-Whitney test for equivalence of two continuous distributions of arbitrary shape: test statistic and critical upper bound*

Description

Implementation of the asymptotically distribution-free test for equivalence of two continuous distributions in terms of the Mann-Whitney-Wilcoxon functional. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition, § 6.2.

Usage

```
mawi(alpha,m,n,eps1_,eps2_,x,y)
```

Arguments

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+ - 1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+ - 1/2$
`x`	row vector with the m observations making up Sample1 as components
`y`	row vector with the n observations making up Sample2 as components

Details

Notation: π_+ stands for the Mann-Whitney functional defined by $\pi_+ = P[X > Y]$, with $X \sim F \equiv$ cdf of Population 1 being independent of $Y \sim G \equiv$ cdf of Population 2.

Value

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+ - 1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+ - 1/2$
`W+`	observed value of the U-statistics estimator of π_+
`SIGMAH`	square root of the estimated asymtotic variance of W_+
`CRIT`	upper critical bound to $\|W_+ - 1/2 - (\varepsilon_2' - \varepsilon_1')/2\|/\hat{\sigma}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S: A new approach to equivalence assessment in standard comparative bioavailability trials by means of the Mann-Whitney statistic. Biometrical Journal 38 (1996), 695-710.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.2.

Examples

```
x <- c(10.3,11.3,2.0,-6.1,6.2,6.8,3.7,-3.3,-3.6,-3.5,13.7,12.6)
y <- c(3.3,17.7,6.7,11.1,-5.8,6.9,5.8,3.0,6.0,3.5,18.7,9.6)
mawi(0.05,12,12,0.1382,0.2602,x,y)
```

`mcnasc_ni` *Determination of a corrected nominal significance level for the asymptotic test for noninferiority in the McNemar setting*

Description

The program computes the largest nominal significance level which can be substituted for the target level α without making the exact size of the asymptotic testing procedure larger than α.

Usage

```
mcnasc_ni(alpha,n,del0,sw,tol,maxh)
```

Arguments

`alpha`	significance level
`n`	sample size
`del0`	absolute value of the noninferiority margin for $\delta := p_{10} - p_{01}$, with p_{10} and p_{01} denoting the probabilities of discordant pairs of both kinds
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level

Value

`alpha`	significance level
`n`	sample size
`del0`	absolute value of the noninferiority margin for $\delta := p_{10} - p_{01}$, with p_{10} and p_{01} denoting the probabilities of discordant pairs of both kinds
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPH_0`	value of the corrected nominal level obtained after nh steps
`SIZE_UNC`	exact size of the rejection region of the test at uncorrected nominal level α
`SIZE0`	exact size of the rejection region of the test at nominal level α_0
`NH`	number of interval-halving steps actually performed

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.2.3.

Examples

```
mcnasc_ni(0.05,50,0.05,0.05,0.0001,5)
```

`mcnby_ni` *Bayesian test for noninferiority in the McNemar setting with the difference of proportions as the parameter of interest*

Description

The program determines through iteration the largest nominal level α_0 such that comparing the posterior probability of the alternative hypothesis $K_1 : \delta > -\delta_0$ to the lower bound $1-\alpha_0$ generates a critical region whose size does not exceed the target significance level α. In addition, exact values of the power against specific parameter configurations with $\delta = 0$ are output.

Usage

```
mcnby_ni(N,DEL0,K1,K2,K3,NSUB,SW,ALPHA,MAXH)
```

Arguments

`N`	sample size
`DEL0`	noninferiority margin to the difference of the parameters of the marginal binomial distributions under comparison
`K1`	Parameter 1 of the Dirichlet prior for the family of trinomial distributions
`K2`	Parameter 2 of the Dirichlet prior for the family of trinomial distributions
`K3`	Parameter 3 of the Dirichlet prior for the family of trinomial distributions
`NSUB`	number of subintervals for partitioning the range of integration
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA`	target significance level
`MAXH`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level

Details

The program uses 96-point Gauss-Legendre quadrature on each of the NSUB intervals into which the range of integration is partitioned.

Value

`N`	sample size
`DEL0`	noninferiority margin to the difference of the parameters of the marginal binomial distributions under comparison
`K1`	Parameter 1 of the Dirichlet prior for the family of trinomial distributions
`K2`	Parameter 2 of the Dirichlet prior for the family of trinomial distributions
`K3`	Parameter 3 of the Dirichlet prior for the family of trinomial distributions
`NSUB`	number of subintervals for partitioning the range of integration
`SW`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPHA`	target significance level
`MAXH`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level
`ALPHA0`	result of the search for the largest admissible nominal level
`SIZE0`	size of the critical region corresponding to α_0
`SIZE_UNC`	size of the critical region of test at uncorrected nominal level α
`POW`	power against 7 different parameter configurations with $\delta = 0$

Author(s)

Stefan Wellek <stefan.wellek@zi-mannheim.de>
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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.2.3.

Examples

```
mcnby_ni(25,.10,.5,.5,.5,10,.05,.05,5)
```

`mcnby_ni_pp` *Computation of the posterior probability of the alternative hypothesis of noninferiority in the McNemar setting, given a specific point in the sample space*

Description

Evaluation of the integral on the right-hand side of Equation (5.24) on p. 88 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
mcnby_ni_pp(N,DEL0,N10,N01)
```

Arguments

`N`	sample size
`DEL0`	noninferiority margin to the difference of the parameters of the marginal binomial distributions under comparison
`N10`	count of pairs with $(X, Y) = (1, 0)$
`N01`	count of pairs with $(X, Y) = (0, 1)$

Details

The program uses 96-point Gauss-Legendre quadrature on each of 10 subintervals into which the range of integration is partitioned.

Value

`N`	sample size
`DEL0`	noninferiority margin to the difference of the parameters of the marginal binomial distributions under comparison
`N10`	count of pairs with $(X, Y) = (1, 0)$
`N01`	count of pairs with $(X, Y) = (0, 1)$
`PPOST`	posterior probability of the alternative hypothesis $K_1 : \delta > -\delta_0$ with respect to the noninformative prior determined according to Jeffrey's rule

Note

The program uses Equation (5.24) of Wellek S (2010) corrected for a typo in the middle line which must read

$$\int_{\delta_0}^{(1+\delta_0)/2} \Big[B\big(n_{01}+1/2, n-n_{01}+1\big)\; p_{01}^{n_{01}-1/2}(1-p_{01})^{n-n_{01}}$$

.

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.2.3.

Examples

```
mcnby_ni_pp(72,0.05,4,5)
```

`mcnemasc` *Determination of a corrected nominal significance level for the asymptotic test for equivalence of two paired binomial proportions with respect to the difference of their expectations (McNemar setting)*

Description

The program computes the largest nominal significance level which can be substituted for the target level α without making the exact size of the asymptotic testing procedure larger than α.

Usage

```
mcnemasc(alpha,n,del0,sw,tol,maxh)
```

Arguments

`alpha`	significance level
`n`	sample size
`del0`	upper limit set to $\lvert p_{10} - p_{01}\rvert$ under the alternative hypothesis of equivalence, with p_{10} and p_{01} denoting the probabilities of discordant pairs of both kinds
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`tol`	upper bound to the absolute difference between size and target level below which the search for a corrected nominal level terminates
`maxh`	maximum number of interval halving steps to be carried out in finding the maximally raised nominal level

Value

`alpha`	significance level
`n`	sample size
`del0`	upper limit set to $\|p_{10} - p_{01}\|$ under the alternative hypothesis of equivalence, with p_{10} and p_{01} denoting the probabilities of discordant pairs of both kinds
`sw`	width of the search grid for determining the maximum of the rejection probability on the common boundary of the hypotheses
`ALPH_0`	value of the corrected nominal level obtained after nh steps
`NH`	number of interval-halving steps actually performed
`ERROR`	error indicator messaging "!!!!!" if the sufficient condition for the correctness of the result output by the program was found violated

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.2.2.

Examples

```
mcnemasc(0.05,50,0.20,0.05,0.0005,5)
```

`mcnempow` *Exact rejection probability of the asymptotic test for equivalence of two paired binomial proportions with respect to the difference of their expectations (McNemar setting)*

Description

The program computes exact values of the rejection probability of the asymptotic test for equivalence in the sense of $-\delta_0 < p_{10} - p_{01} < \delta_0$, at any nominal level α. [The largest α for which the test is valid in terms of the significance level, can be computed by means of the program mcnemasc.]

Usage

```
mcnempow(alpha,n,del0,p10,p01)
```

Arguments

`alpha`	nominal significance level
`n`	sample size
`del0`	upper limit set to $\vert\delta\vert$ under the alternative hypothesis of equivalence
`p10`	true value of $P[X = 1, Y = 0]$
`p01`	true value of $P[X = 0, Y = 1]$

Value

`alpha`	nominal significance level
`n`	sample size
`del0`	upper limit set to $\vert\delta\vert$ under the alternative hypothesis of equivalence
`p10`	true value of $P[X = 1, Y = 0]$
`p01`	true value of $P[X = 0, Y = 1]$
`POW`	exact rejection probability of the asymptotic McNemar test for equivalence at nominal level α
`ERROR`	error indicator messaging "!!!!!" if the sufficient condition for the correctness of the result output by the program was found violated

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, p.84.

Examples

```
mcnempow(0.024902,50,0.20,0.30,0.30)
```

`mwtie_fr` *Analogue of mwtie_xy for settings with grouped data*

Description

Implementation of the asymptotically distribution-free test for equivalence of discrete distributions from which grouped data are obtained. Hypothesis formulation is in terms of the Mann-Whitney-Wilcoxon functional generalized to the case that ties between observations from different distributions may occur with positive probability. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition, p.155.

Usage

```
mwtie_fr(k,alpha,m,n,eps1_,eps2_,x,y)
```

Arguments

`k`	total number of grouped values which can be distinguished in the pooled sample
`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`x`	row vector with the m observations making up Sample1 as components
`y`	row vector with the n observations making up Sample2 as components

Details

Notation: π_+ and π_0 stands for the functional defined by $\pi_+ = P[X > Y]$ and $\pi_0 = P[X = Y]$, respectively, with $X \sim F \equiv$ cdf of Population 1 being independent of $Y \sim G \equiv$ cdf of Population 2.

Value

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`WXY_TIE`	observed value of the U-statistics – based estimator of $\pi_+/(1-\pi_0)$
`SIGMAH`	square root of the estimated asymtotic variance of $W_+/(1-W_0)$
`CRIT`	upper critical bound to $\lvert W_+/(1-W_0)-1/2-(\varepsilon_2'-\varepsilon_1')/2\rvert/\hat{\sigma}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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References

Wellek S, Hampel B: A distribution-free two-sample equivalence test allowing for tied observations. Biometrical Journal 41 (1999), 171-186.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.4.

Examples

```
x <- c(1,1,3,2,2,3,1,1,1,2,1,2,2,2,1,2,1,3,2,1,2,1,1,1,1,1,1,1,1,1,1,2,1,3,1,3,2,1,1,
       2,1,2,1,1,2,2,1,2,1,1,1,1,1,2,2,1,2,2,1,3,1,2,1,1,2,2,1,2,2,1,1,1,3,2,1,1,1,2,1,
       3,3,3,1,2,1,2,2,1,1,1,2,2,1,1,2,1,1,2,3,1,3,2,1,1,1,1,2,2,2,1,1,2,2,3,2,1,2,1,1,
       2,2,1,2,2,2,1,1,2,3,2,1,3,2,1,1,1,2,2,2,2,1,2,2,1,1,1,1,2,1,1,1,2,1,2,2,1,2,2,2,
       2,1,1,2,1,2,2,1,1,1,1,3,1,1,2,2,1,1,1,2,2,2,1,2,3,2,2,1,2,1,2,1,1,2,1,2,2,1,1,1,
       2,2,2,2)
y <- c(2,1,2,2,1,1,2,2,2,1,1,2,1,3,3,1,1,1,1,1,1,2,2,3,1,1,1,3,1,1,1,1,1,1,1,2,2,3,2,1,
       2,2,2,1,2,1,1,2,2,1,2,1,1,1,1,2,1,2,1,1,3,1,1,1,2,2,2,1,1,1,1,2,1,2,1,1,2,2,2,2,
       2,1,1,1,3,2,2,2,1,2,3,1,2,1,1,1,2,1,3,3,1,2,2,2,2,2,2,1,2,1,1,1,1,2,2,1,1,1,1,2,
       1,3,1,1,2,1,2,1,2,2,2,1,2,2,2,1,1,1,2,1,2,1,2,1,1,1,2,1,2,2,1,1,1,1,2,2,3,1,3,1,
       1,2,2,2,1,1,1,1,2,1,1,3,2,2,3,1,2,2,1,1,2,1,1,2,1,2,2,1,2,1,2,2,2,1,1,1,1,1,1,1,
       1,1,1,2,1,3,2,2,1,1,1,2,2,1,1,2,1,2,1,2,2,2,1,2,3,1,1,2,1,2,2,1,1,1,1,2,2,2,1,1,
       3,2,1,2,2,2,1,1,1,2,1,2,2,1,2,1,1,2)
mwtie_fr(3,0.05,204,258,0.10,0.10,x,y)
```

`mwtie_xy` *Distribution-free two-sample equivalence test for tied data: test statistic and critical upper bound*

Description

Implementation of the asymptotically distribution-free test for equivalence of discrete distributions in terms of the Mann-Whitney-Wilcoxon functional generalized to the case that ties between observations from different distributions may occur with positive probability. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition, § 6.4.

Usage

```
mwtie_xy(alpha,m,n,eps1_,eps2_,x,y)
```

Arguments

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`x`	row vector with the m observations making up Sample1 as components
`y`	row vector with the n observations making up Sample2 as components

Details

Notation: π_+ and π_0 stands for the functional defined by $\pi_+ = P[X > Y]$ and $\pi_0 = P[X = Y]$, respectively, with $X \sim F \equiv$ cdf of Population 1 being independent of $Y \sim G \equiv$ cdf of Population 2.

Value

`alpha`	significance level
`m`	size of Sample 1
`n`	size of Sample 2
`eps1_`	absolute value of the left-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`eps2_`	right-hand limit of the hypothetical equivalence range for $\pi_+/(1-\pi_0)-1/2$
`WXY_TIE`	observed value of the U-statistics – based estimator of $\pi_+/(1-\pi_0)$
`SIGMAH`	square root of the estimated asymtotic variance of $W_+/(1-W_0)$
`CRIT`	upper critical bound to $\lvert W_+/(1-W_0)-1/2-(\varepsilon_2'-\varepsilon_1')/2\rvert/\hat{\sigma}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S, Hampel B: A distribution-free two-sample equivalence test allowing for tied observations. Biometrical Journal 41 (1999), 171-186.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.4.

Examples

```
x <- c(1,1,3,2,2,3,1,1,1,2)
y <- c(2,1,2,2,1,1,2,2,2,1,1,2)
mwtie_xy(0.05,10,12,0.10,0.10,x,y)
```

`postmys` *Bayesian posterior probability of the alternative hypothesis in the setting of the one-sample t-test for equivalence*

Description

Evaluation of the integral appearing on the right-hand side of equation (3.6) on p. 38 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition

Usage

```
postmys(n,dq,sd,eps1,eps2,tol)
```

Arguments

`n`	sample size
`dq`	mean within-pair difference observed in the sample under analysis
`sd`	square root of the sample variance of the within-pair differences
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for δ/σ_D
`eps2`	right-hand limit of the hypothetical equivalence range for δ/σ_D
`tol`	tolerance for the error induced through truncating the range of integration on the right

Details

The program uses 96-point Gauss-Legendre quadrature.

Value

`n`	sample size
`dq`	mean within-pair difference observed in the sample under analysis
`sd`	square root of the sample variance of the within-pair differences
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for δ/σ_D
`eps2`	right-hand limit of the hypothetical equivalence range for δ/σ_D
`tol`	tolerance for the error induced through truncating the range of integration on the right
`PPOST`	posterior probability of the set of all (δ, σ_D) such that $-\varepsilon_1 < \delta/\sigma_D < \varepsilon_2$

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 3.2.

Examples

```
postmys(23,0.16,3.99,0.5,0.5,1e-6)
```

`powsign` *Nonconditional power of the UMPU sign test for equivalence and its nonrandomized counterpart*

Description

The program computes for each possible value of the number n_0 of zero observations the power conditional on $N_0 = n_0$ and averages these conditional power values with respect to the distribution of N_0. Equivalence is defined in terms of the logarithm of the ratio p_+/p_-, where p_+ and p_- denotes the probability of obtaining a positive and negative sign, respectively.

Usage

```
powsign(alpha,n,eps1,eps2,poa)
```

Arguments

`alpha`	significance level
`n`	sample size
`eps1`	absolute value of the lower limit of the hypothetical equivalence range for $\log(p_+/p_-)$.
`eps2`	upper limit of the hypothetical equivalence range for $\log(p_+/p_-)$.
`poa`	probability of a tie under the alternative of interest

Value

`alpha`	significance level
`n`	sample size
`eps1`	absolute value of the lower limit of the hypothetical equivalence range for $\log(p_+/p_-)$.
`eps2`	upper limit of the hypothetical equivalence range for $\log(p_+/p_-)$.
`poa`	probability of a tie under the alternative of interest
`POWNONRD`	power of the nonrandomized version of the test against the alternative $p_+ = p_- = (1 - p_\circ)/2$
`POW`	power of the randomized UMPU test against the alternative $p_+ = p_- = (1 - p_\circ)/2$

Note

A special case of the test whose power is computed by this program, is the exact conditional equivalence test for the McNemar setting (cf. Wellek 2010, pp. 76-77).

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.1.

Examples

```
powsign(0.06580,50,0.847298,0.847298,0.26)
```

`pow_abe` *Confidence innterval inclusion test for average bioequivalence: exact power against an arbitrary specific alternative*

Description

Evaluation of the integral on the right-hand side of equation (10.11) of p. 317 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition

Usage

```
pow_abe(m,n,alpha,del_0,del,sig)
```

Arguments

`m`	sample size in sequence group T(est)/R(eference)
`n`	sample size in sequence group R(eference)/T(est)
`alpha`	significance level
`del_0`	equivalence margin to the absolute value of the log-ratio μ_T^* and μ_R^* of the formulation effects
`del`	assumed true value of $\lvert\log(\mu_T^*/\mu_R^*)\rvert$, with $0 \le \delta < \delta_0$
`sig`	theoretical standard deviation of the log within-subject bioavailability ratios in each sequence group

Details

The program uses 96-point Gauss-Legendre quadrature.

Value

`m`	sample size in sequence group T(est)/R(eference)
`n`	sample size in sequence group R(eference)/T(est)
`alpha`	significance level
`del_0`	equivalence margin to the absolute value of the log-ratio μ_T^* and μ_R^* of the formulation effects
`del`	assumed true value of $\lvert\log(\mu_T^*/\mu_R^*)\rvert$, with $0 \le \delta < \delta_0$
`POW_ABE`	power of the interval inclusion test for average bioequivalence against the specific alternative given by (δ, σ)

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 10.2.1.

Examples

```
pow_abe(12,13,0.05,log(1.25),log(1.25)/2,0.175624)
```

`po_pbibe` *Bayesian posterior probability of the alternative hypothesis of probability-based individual bioequivalence (PBIBE)*

Description

Implementation of the algorithm presented in § 10.3.3 of Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition.

Usage

```
po_pbibe(n,eps,pio,zq,s,tol,sw,ihmax)
```

Arguments

`n`	sample size
`eps`	equivalence margin to an individual log-bioavailability ratio
`pio`	prespecified lower bound to the probability of obtaining an individual log-bioavailability ratio falling in the equivalence range $(-\varepsilon, \varepsilon)$
`zq`	mean log-bioavailability ratio observed in the sample under analysis
`s`	square root of the sample variance of the log-bioavailability ratios
`tol`	maximum numerical error allowed for transforming the hypothesis of PBIBE into a region in the parameter space of the log-normal distribution assumed to underlie the given sample of individual bioavailability ratios
`sw`	step width used in the numerical procedure yielding results at a level of accuracy specified by the value chosen for tol
`ihmax`	maximum number of interval halving steps to be carried out in finding the region specified in the parameter space according to the criterion of PBIBE

Details

The program uses 96-point Gauss-Legendre quadrature.

Value

`n`	sample size
`eps`	equivalence margin to an individual log-bioavailability ratio
`pio`	prespecified lower bound to the probability of obtaining an individual log-bioavailability ratio falling in the equivalence range $(-\varepsilon, \varepsilon)$
`zq`	mean log-bioavailability ratio observed in the sample under analysis
`s`	square root of the sample variance of the log-bioavailability ratios
`tol`	maximum numerical error allowed for transforming the hypothesis of PBIBE into a region in the parameter space of the log-normal distribution assumed to underlie the given sample of individual bioavailability ratios
`sw`	step width used in the numerical procedure yielding results at a level of accuracy specified by the value chosen for tol
`ihmax`	maximum number of interval halving steps to be carried out in finding the region specified in the parameter space according to the criterion of PBIBE
`PO_PBIBE`	posterior probability of the alternative hypothesis of PBIBE

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References

Wellek S: Bayesian construction of an improved parametric test for probability-based individual bioequivalence. Biometrical Journal 42 (2000), 1039-52.

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 10.3.3.

Examples

```
po_pbibe(20,0.25,0.75,0.17451,0.04169, 10e-10,0.01,100)
```

`sgnrk` *Signed rank test for equivalence of an arbitrary continuous distribution of the intraindividual differences in terms of the probability of a positive sign of a Walsh average: test statistic and critical upper bound*

Description

Implementation of the paired-data analogue of the Mann-Whitney-Wilcoxon test for equivalence of continuous distributions. The continuity assumption relates to the intraindividual differences D_i. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition,§ 5.4.

Usage

```
sgnrk(alpha,n,qpl1,qpl2,d)
```

Arguments

`alpha`	significance level
`n`	sample size
`qpl1`	lower equivalence limit q'_+ to the target functional q_+
`qpl2`	upper equivalence limit q''_+ to the target functional q_+
`d`	row vector with the intraindividual differences for all n pairs as components

Details

q_+ is the probability of getting a positive sign of the so-called Walsh-average of a pair of within-subject differences and can be viewed as a natural paired-observations analogue of the Mann-Whitney functional $\pi_+ = P[X > Y]$.

Value

`alpha`	significance level
`n`	sample size
`qpl1`	lower equivalence limit q'_+ to the target functional q_+
`qpl2`	upper equivalence limit q''_+ to the target functional q_+
`U_pl`	observed value of the U-statistics estimator of q_+
`SIGMAH`	square root of the estimated asymtotic variance of U_+
`CRIT`	upper critical bound to $\big\|U_+ - \big(q'_+ + q''_+\big)/2\big\|/\hat{\sigma}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Author(s)

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Peter Ziegler <peter.ziegler@zi-mannheim.de>

References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.4.

Examples

```
d <- c(-0.5,0.333,0.667,1.333,1.5,-2.0,-1.0,-0.167,1.667,0.833,-2.167,-1.833,
       4.5,-7.5,2.667,3.333,-4.167,5.667,2.333,-2.5)
sgnrk(0.05,20,0.2398,0.7602,d)
```

`srktie_d` *Generalized signed rank test for equivalence for tied data: test statistic and critical upper bound*

Description

Implementation of a generalized version of the signed-rank test for equivalence allowing for arbitrary patterns of ties between the within-subject differences. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition, § 5.5.

Usage

```
srktie_d(n,alpha,eps1,eps2,d)
```

Arguments

`n`	sample size
`alpha`	significance level
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`eps2`	right-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`d`	row vector with the intraindividual differences for all n pairs as components

Details

Notation: q_+ and q_0 stands for the functional defined by $q_+ = P[D_i + D_j > 0]$ and $q_0 = P[D_i + D_j = 0]$, respectively, with D_i and D_j as the intraindividual differences observed in two individuals independently selected from the underlying bivariate population.

Value

`n`	sample size
`alpha`	significance level
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`eps2`	right-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`U_pl`	observed value of the U-statistics estimator of q_+
`U_0`	observed value of the U-statistics estimator of q_0
`UAS_PL`	observed value of $U_+/(1-U_0)$
`TAUHAS`	square root of the estimated asymtotic variance of $\sqrt{n}U_+/(1-U_0)$
`CRIT`	upper critical bound to $\sqrt{n}\lvert U_+/(1-U_0)-1/2-(\varepsilon_2-\varepsilon_1)/2\rvert/\hat{\tau}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

Note

The function srktie_d can be viewed as the paired-data analogue of mwtie_xy

Author(s)

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.5.

Examples

```
d <- c(0.8,0.2,0.0,-0.1,-0.3,0.3,-0.1,0.4,0.6,0.2,0.0,-0.2,-0.3,0.0,0.1,0.3,-0.3,
       0.1,-0.2,-0.5,0.2,-0.1,0.2,-0.1)
srktie_d(24,0.05,0.2602,0.2602,d)
```

`srktie_m` *Analogue of srktie_d for settings where the distribution of intraindividual differences is concentrated on a finite lattice*

Description

Analogue of the function srktie_d tailored for settings where the distribution of the within-subject differences is concentrated on a finite lattice. For details see Wellek S (2010) Testing statistical hypotheses of equivalence and noninferiority. Second edition, pp.112-3.

Usage

```
srktie_m(n,alpha,eps1,eps2,w,d)
```

Arguments

`n`	sample size
`alpha`	significance level
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`eps2`	right-hand limit of the hypothetical equivalence range for $q_+/(1-q_0)-1/2$
`w`	span of the lattice in which the intraindividual differences take their values
`d`	row vector with the intraindividual differences for all n pairs as components

Details

Notation: q_+ and q_0 stands for the functional defined by $q_+ = P[D_i + D_j > 0]$ and $q_0 = P[D_i + D_j = 0]$, respectively, with D_i and D_j as the intraindividual differences observed in two individuals independently selected from the underlying bivariate population.

Value

`n`	sample size
`alpha`	significance level
`eps1`	absolute value of the left-hand limit of the hypothetical equivalence range for $q_+/(1-q_0) - 1/2$
`eps2`	right-hand limit of the hypothetical equivalence range for $q_+/(1-q_0) - 1/2$
`w`	span of the lattice in which the intraindividual differences take their values
`U_pl`	observed value of the U-statistics estimator of q_+
`U_0`	observed value of the U-statistics estimator of q_0
`UAS_PL`	observed value of $U_+/(1-U_0)$
`TAUHAS`	square root of the estimated asymtotic variance of $\sqrt{n}U_+/(1-U_0)$
`CRIT`	upper critical bound to $\sqrt{n}\lvert U_+/(1-U_0) - 1/2 - (\varepsilon_2 - \varepsilon_1)/2\rvert/\hat{\tau}$
`REJ`	indicator of a positive [=1] vs negative [=0] rejection decision to be taken with the data under analysis

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, pp. 112-114.

Examples

```
d <- c(0.8,0.2,0.0,-0.1,-0.3,0.3,-0.1,0.4,0.6,0.2,0.0,-0.2,-0.3,0.0,0.1,0.3,-0.3,
       0.1,-0.2,-0.5,0.2,-0.1,0.2,-0.1)
srktie_m(24,0.05,0.2602,0.2602,0.1,d)
```

`tt1st` *Critical constants and power against the null alternative of the one-sample t-test for equivalence with an arbitrary, maybe nonsymmetric choice of the limits of the equivalence range*

Description

The function computes the critical constants defining the uniformly most powerful invariant test for the problem $\delta/\sigma_D \leq \theta_1$ or $\delta/\sigma_D \geq \theta_2$ versus $\theta_1 < \delta/\sigma_D < \theta_2$, with (θ_1, θ_2) as a fixed nondegenerate interval on the real line. In addition, tt1st outputs the power against the null alternative $\delta = 0$.

Usage

```
tt1st(n,alpha,theta1,theta2,tol,itmax)
```

Arguments

`n`	sample size
`alpha`	significance level
`theta1`	lower equivalence limit to δ/σ_D
`theta2`	upper equivalence limit to δ/σ_D
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps

Value

`n`	sample size
`alpha`	significance level
`theta1`	lower equivalence limit to δ/σ_D
`theta2`	upper equivalence limit to δ/σ_D
`IT`	number of iteration steps performed until reaching the stopping criterion corresponding to TOL
`C1`	left-hand limit of the critical interval for the one-sample t-statistic
`C2`	right-hand limit of the critical interval for the one-sample t-statistic
`ERR1`	deviation of the rejection probability from α under $\delta/\sigma_D = \theta_1$
`ERR2`	deviation of the rejection probability from α under $\delta/\sigma_D = \theta_2$
`POW0`	power of the UMPI test against the alternative $\delta = 0$

Note

If the output value of ERR2 is NA, the deviation of the rejection probability at the right-hand boundary of the hypothetical equivalence interval from α is smaller than the smallest real number representable in R.

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 5.3.

Examples

```
tt1st(36,0.05, -0.4716,0.3853,1e-10,50)
```

`tt2st` *Critical constants and power against the null alternative of the two-sample t-test for equivalence with an arbitrary, maybe nonsymmetric choice of the limits of the equivalence range*

Description

The function computes the critical constants defining the uniformly most powerful invariant test for the problem $(\xi - \eta)/\sigma \leq -\varepsilon_1$ or $(\xi - \eta)/\sigma \geq \varepsilon_2$ versus $-\varepsilon_1 < (\xi - \eta)/\sigma < \varepsilon_2$, with ξ and η denoting the expected values of two normal distributions with common variance σ^2 from which independent samples are taken. In addition, tt2st outputs the power against the null alternative $\xi = \eta$.

Usage

```
tt2st(m,n,alpha,eps1,eps2,tol,itmax)
```

Arguments

`m`	size of the sample from $\mathcal{N}(\xi, \sigma^2)$
`n`	size of the sample from $\mathcal{N}(\eta, \sigma^2)$
`alpha`	significance level
`eps1`	absolute value of the lower equivalence limit to $(\xi - \eta)/\sigma$
`eps2`	upper equivalence limit to $(\xi - \eta)/\sigma$
`tol`	tolerable deviation from α of the rejection probability at either boundary of the hypothetical equivalence interval
`itmax`	maximum number of iteration steps

Value

`m`	size of the sample from $\mathcal{N}(\xi, \sigma^2)$
`n`	size of the sample from $\mathcal{N}(\eta, \sigma^2)$
`alpha`	significance level
`eps1`	absolute value of the lower equivalence limit to $(\xi - \eta)/\sigma$
`eps2`	upper equivalence limit to $(\xi - \eta)/\sigma$
`IT`	number of iteration steps performed until reaching the stopping criterion corresponding to TOL
`C1`	left-hand limit of the critical interval for the two-sample t-statistic
`C2`	right-hand limit of the critical interval for the two-sample t-statistic
`ERR1`	deviation of the rejection probability from α under $(\xi - \eta)/\sigma = -\varepsilon_1$
`ERR2`	deviation of the rejection probability from α under $(\xi - \eta)/\sigma = \varepsilon_2$
`POW0`	power of the UMPI test against the alternative $\xi = \eta$

Note

If the output value of ERR2 is NA, the deviation of the rejection probability at the right-hand boundary of the hypothetical equivalence interval from α is smaller than the smallest real number representable in R.

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References

Wellek S: Testing statistical hypotheses of equivalence and noninferiority. Second edition. Boca Raton: Chapman & Hall/CRC Press, 2010, § 6.1.

Examples

```
tt2st(12,12,0.05,0.50,1.00,1e-10,50)
```

Index