Package ‘contingencytables’

December 12, 2022

Title Statistical Analysis of Contingency Tables

Version 1.0.4

Description Provides functions to perform statistical inference of data organized in contingency tables. This package is a companion to the ``Statistical Analysis of Contingency Tables" book by Fagerland et al. <ISBN 9781466588172>.

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.2

URL `https://contingencytables.com/`

BugReports `https://github.com/ocbe-uio/contingencytables/issues`

Imports MASS, boot

Suggests testthat

NeedsCompilation no

Author Morten Wang Fagerland [aut],
Stian Lydersen [ctb],
Petter Laake [ctb],
Waldir Leoncio [cre],
Ole Christian Lingjærde [trl]

Maintainer Waldir Leoncio <`w.l.netto@medisin.uio.no`>

Repository CRAN

Date/Publication 2022-12-12 11:00:02 UTC

R topics documented:

`.onAttach` *Prints welcome message on package load*

Description

Prints package version number and welcome message on package load

Usage

```
.onAttach(libname, pkgname)
```

Arguments

`libname`	library location. See `?base::.onAttach` for details
`pkgname`	package name. See `?base::.onAttach` for details

`Adjusted_inv_sinh_CI_OR_2x2`

The adjusted inverse hyperbolic sine confidence interval for the odds ratio

---

Description

The adjusted inverse hyperbolic sine confidence interval for the odds ratio.

Described in Chapter 4 "The 2x2 Table"

Usage

```
Adjusted_inv_sinh_CI_OR_2x2(
  n,
  psi1 = 0.45,
  psi2 = 0.25,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`psi1`	pseudo-frequency (should be > 0)
`psi2`	pseudo-frequency (should be > 0)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013)
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Adjusted_inv_sinh_CI_OR_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Adjusted_inv_sinh_CI_OR_2x2(n)
```

`Adjusted_inv_sinh_CI_ratio_2x2`

The adjusted inverse hyperbolic sine confidence interval for the ratio of probabilities

---

Description

The adjusted inverse hyperbolic sine confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Adjusted_inv_sinh_CI_ratio_2x2(
  n,
  psi1 = 0,
  psi2 = 0,
  psi3 = 0,
  psi4 = 1,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`psi1`	pseudo-frequency
`psi2`	pseudo-frequency
`psi3`	pseudo-frequency
`psi4`	pseudo-frequency
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Adjusted_inv_sinh_CI_ratio_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Adjusted_inv_sinh_CI_ratio_2x2(n)
```

`Adjusted_log_CI_2x2` *The adjusted log confidence interval for the ratio of probabilities*

Description

The adjusted log confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Adjusted_log_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Adjusted_log_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Adjusted_log_CI_2x2(n)
```

`AgrestiCaffo_CI_2x2` *The Agresti-Caffo confidence interval for the difference between probabilities*

Description

The Agresti-Caffo confidence interval for the difference between probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
AgrestiCaffo_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
AgrestiCaffo_CI_2x2(n = matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE))
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
AgrestiCaffo_CI_2x2(n = matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE))
```

`AgrestiCoull_CI_1x2` *The Agresti-Coull confidence interval for the binomial probability*

Description

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
AgrestiCoull_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Agresti A, Coull BA (1998) Approximate is better than "exact" for interval estimation of binomial proportions. The American Statistician; 52:119-126

See Also

Wald_CI_1x2

Examples

```
# The number of 1st order male births (Singh et al. 2010)
AgrestiCoull_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
AgrestiCoull_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
AgrestiCoull_CI_1x2(X = 103, n = 167)
# Example: The number of 4th order male births (Singh et al. 2010)
AgrestiCoull_CI_1x2(X = 33, n = 45)
# Example: Ligarden et al. (2010)
AgrestiCoull_CI_1x2(X = 13, n = 16)
```

`Arcsine_CI_1x2` *Arcsine confidence interval*

Description

The Arcsine confidence interval for the binomial probability (with Anscombe variance stabilizing transformation) Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Arcsine_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Anscombe FJ (1948) The transformation of Poisson, binomial and negative binomial data. Biometrika; 35:246-254

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Arcsine_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Arcsine_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Arcsine_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Arcsine_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Arcsine_CI_1x2(X = 13, n = 16)
```

`BaptistaPike_exact_conditional_CI_2x2` *The Baptista-Pike exact conditional confidence interval for the odds ratio*

Description

The Baptista-Pike exact conditional confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
BaptistaPike_exact_conditional_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
n1 <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
n2 <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
n3 <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
n4 <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
BaptistaPike_exact_conditional_CI_2x2(n1)
BaptistaPike_exact_conditional_CI_2x2(n2)
BaptistaPike_exact_conditional_CI_2x2(n3)
BaptistaPike_exact_conditional_CI_2x2(n4)
```

`BaptistaPike_midP_CI_2x2`
The Baptista-Pike mid-P confidence interval for the odds ratio

---

Description

The Baptista-Pike mid-P confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
BaptistaPike_midP_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
n1 <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
n2 <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
n3 <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
n4 <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
BaptistaPike_midP_CI_2x2(n1)
BaptistaPike_midP_CI_2x2(n2)
BaptistaPike_midP_CI_2x2(n3)
BaptistaPike_midP_CI_2x2(n4)
```

`Bhapkar_test_paired_cxc`
The Bhapkar test for marginal homogeneity

Description

The Bhapkar test for marginal homogeneity

Described in Chapter 9 "The Paired cxc Table"

Usage

```
Bhapkar_test_paired_cxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
Bhapkar_test_paired_cxc(n)
```

`Blaker_exact_CI_1x2` *The Blaker exact confidence interval*

Description

The Blaker exact confidence interval for the binomial probability Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Blaker_exact_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Blaker H (2000) Confidence curves and improved exact confidence intervals for discrete distributions. The Canadian Journal of Statistics; 28:783-798

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Blaker_exact_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Blaker_exact_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Blaker_exact_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Blaker_exact_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Blaker_exact_CI_1x2(X = 13, n = 16)
```

`Blaker_exact_test_1x2` *The Blaker exact test*

Description

The Blaker exact test for the binomial probability (pi) H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided) Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Blaker_exact_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

The two-sided p-value

References

Blaker H (2000) Confidence curves and improved exact confidence intervals for discrete distributions. The Canadian Journal of Statistics; 28:783-798

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Blaker_exact_test_1x2(X = 250, n = 533, pi0 = 0.513)
# The number of 2nd order male births (Singh et al. 2010)
Blaker_exact_test_1x2(X = 204, n = 412, pi0 = 0.513)
# The number of 3rd order male births (Singh et al. 2010)
Blaker_exact_test_1x2(X = 103, n = 167, pi0 = 0.513)
# The number of 4th order male births (Singh et al. 2010)
Blaker_exact_test_1x2(X = 33, n = 45, pi0 = 0.513)
# Ligarden et al. (2010)
Blaker_exact_test_1x2(X = 13, n = 16, pi0 = 0.5)
```

`Blaker_midP_CI_1x2` *The Blaker mid-P confidence interval for the binomial probability*

Description

The Blaker mid-P confidence interval for the binomial probability Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Blaker_midP_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Blaker H (2000) Confidence curves and improved exact confidence intervals for discrete distributions. The Canadian Journal of Statistics; 28:783-798

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Blaker_midP_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Blaker_midP_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Blaker_midP_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Blaker_midP_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Blaker_midP_CI_1x2(X = 13, n = 16)
```

`Blaker_midP_test_1x2` *The Blaker mid-P test*

Description

The Blaker mid-P test for the binomial probability (pi) H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided) Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Blaker_midP_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (F = no, T = yes)

Value

The two-sided mid-P value

References

Blaker H (2000) Confidence curves and improved exact confidence intervals for discrete distributions. The Canadian Journal of Statistics; 28:783-798

Examples

```
# Example: The number of 1st order male births (Singh et al. 2010)
Blaker_midP_test_1x2(X = 250, n = 533, pi0 = 0.513)
# Example: The number of 2nd order male births (Singh et al. 2010)
Blaker_midP_test_1x2(X = 204, n = 412, pi0 = 0.513)
# Example: The number of 3rd order male births (Singh et al. 2010)
Blaker_midP_test_1x2(X = 103, n = 167, pi0 = 0.513)
# Example: The number of 4th order male births (Singh et al. 2010)
Blaker_midP_test_1x2(X = 33, n = 45, pi0 = 0.513)
# Example: Ligarden et al. (2010)
Blaker_midP_test_1x2(X = 13, n = 16, pi0 = 0.5)
```

`BonettPrice_hybrid_Wilson_score_CI_CC_paired_2x2` *The Bonett-Price hybrid Wilson score confidence interval for the ratio of paired probabilities*

Description

The Bonett-Price hybrid Wilson score confidence interval for the ratio of paired probabilities

with continuity correction

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
BonettPrice_hybrid_Wilson_score_CI_CC_paired_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
BonettPrice_hybrid_Wilson_score_CI_CC_paired_2x2(n)

# Complete response before and after consolidation therapy (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
BonettPrice_hybrid_Wilson_score_CI_CC_paired_2x2(n)
```

`BonettPrice_hybrid_Wilson_score_CI_paired_2x2` *The Bonett-Price hybrid Wilson score confidence interval for the ratio of paired probabilities*

Description

The Bonett-Price hybrid Wilson score confidence interval for the ratio of paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
BonettPrice_hybrid_Wilson_score_CI_paired_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
n <- rbind(c(1, 1), c(7, 12))
BonettPrice_hybrid_Wilson_score_CI_paired_2x2(n)
# Complete response before and after consolidation therapy (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
BonettPrice_hybrid_Wilson_score_CI_paired_2x2(n)
```

`Bonferroni_type_CIs_paired_cxc` *Bonferroni-type confidence intervals for differences of marginal probabilities*

Description

Bonferroni-type confidence intervals for differences of marginal probabilities

Described in Chapter 9 "The Paired kxk Table"

Usage

```
Bonferroni_type_CIs_paired_cxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
Bonferroni_type_CIs_paired_cxc(n)
```

`Bonferroni_type_CIs_rxc` *The Bonferroni-type simultaneous confidence intervals for the differences pi_1|i - pi_1|j*

Description

The Bonferroni-type simultaneous confidence intervals for the differences pi_1|i - pi_1|j

Described in Chapter 7 "The rxc Table"

Usage

```
Bonferroni_type_CIs_rxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 vector)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Example: Treatment for ear infection
n <- rbind(c(40, 25), c(54, 7), c(63, 10))
Bonferroni_type_CIs_rxc(n)
```

`Brant_test_2xc` *The Brant test for the proportional odds assumption*

Description

The Brant test for the proportional odds assumption

Described in Chapter 6 "The Ordered 2xc Table"

Usage

```
Brant_test_2xc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2xc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing the probability, the statistic and the degrees of freedom

Examples

```
# The Adolescent Placement Study (Fontanella et al., 2008)
n <- rbind(c(8, 28, 72, 126), c(46, 73, 69, 86))
Brant_test_2xc(n)

# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
Brant_test_2xc(n)
```

`BreslowDay_homogeneity_test_stratified_2x2`
The Breslow-Day test of homogeneity of odds ratios over strata

---

Description

The Breslow-Day test of homogeneity of odds ratios over strata with

Tarone correction

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
BreslowDay_homogeneity_test_stratified_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower bound, upper bound and differences of the statistic

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
BreslowDay_homogeneity_test_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
BreslowDay_homogeneity_test_stratified_2x2(n)
```

`Chacko_test_1xc` *The Chacko test for order-restriction*

Description

Described in Chapter 3, "The 1xc Table and the Multinomial Distribution", Chacko (1966) derived a test based on the Pearson chi-square statistic to test the hypothesis that the categories of a multinomial variable with c possible outcomes have a natural ordering. The test statistic is asymptotically chi-squared distributed.

Usage

```
Chacko_test_1xc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`printresults`	display results (F = no, T = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom.

References

Chacko, V. J. (1966). Modified chi-square test for ordered alternatives. Sankhyā: The Indian Journal of Statistics, Series B, 185-190.

Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL.

Examples

```
# Hypothetical experiment
Chacko_test_1xc(n = c(1, 4, 3, 11, 9))
```

`chap1` *Chapter 1: Introduction*

Description

There are no functions for Chapter 1 (Introduction), only from Chapters 2 to 10.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap10` *Chapter 10: Stratified 2x2 Tables and Meta-Analysis*

Description

These are the functions related to chapter 10:

1. BreslowDay_homogeneity_test_stratified_2x2
2. CochranMantelHaenszel_test_stratified_2x2
3. Cochran_Q_test_stratified_2x2
4. InverseVariance_estimate_stratified_2x2
5. ML_estimates_and_CIs_stratified_2x2
6. MantelHaenszel_estimate_stratified_2x2
7. Pearson_LR_homogeneity_test_stratified_2x2
8. Pearson_LR_test_common_effect_stratified_2x2
9. Peto_homogeneity_test_stratified_2x2
10. Peto_OR_estimate_stratified_2x2
11. RBG_test_and_CI_stratified_2x2
12. Wald_test_and_CI_common_diff_stratified_2x2
13. Wald_test_and_CI_common_ratio_stratified_2x2
14. Woolf_test_and_CI_stratified_2x2
15. stratified_2x2_tables

Note

You can also print the list above with `list_functions(10)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap2` *Chapter 2: The 1x2 Table and the Binomial Distribution*

Description

These are the functions related to chapter 2:

1. AgrestiCoull_CI_1x2
2. Arcsine_CI_1x2
3. Wald_CI_1x2
4. Blaker_exact_CI_1x2
5. Blaker_exact_test_1x2
6. Blaker_midP_CI_1x2
7. Blaker_midP_test_1x2
8. ClopperPearson_exact_CI_1x2
9. ClopperPearson_midP_CI_1x2
10. Exact_binomial_test_1x2
11. Jeffreys_CI_1x2
12. LR_CI_1x2
13. LR_test_1x2
14. MidP_binomial_test_1x2
15. Score_test_1x2
16. Score_test_CC_1x2
17. Wald_CI_CC_1x2
18. Wilson_score_CI_1x2
19. Wilson_score_CI_CC_1x2
20. the_1x2_table_CIs
21. Wald_test_1x2
22. Wald_test_CC_1x2
23. the_1x2_table_tests

Note

You can also print the list above with `list_functions(2)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap3` *Chapter 3: The 1xc Table and the Multinomial Distribution*

Description

These are the functions related to chapter 3:

1. Chacko_test_1xc
2. Exact_multinomial_test_1xc
3. Gold_Wald_CIs_1xc
4. Goodman_Wald_CIs_1xc
5. Goodman_Wald_CIs_for_diffs_1xc
6. Goodman_Wilson_score_CIs_1xc
7. LR_test_1xc
8. MidP_multinomial_test_1xc
9. Pearson_chi_squared_test_1xc
10. QuesenberryHurst_Wilson_score_CIs_1xc
11. the_1xc_table_CIs
12. the_1xc_table_tests

Note

You can also print the list above with `list_functions(3)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

chap4 *Chapter 4: The 2x2 Table*

Description

These are the functions related to chapter 4:

1. Adjusted_inv_sinh_CI_OR_2x2
2. Adjusted_inv_sinh_CI_ratio_2x2
3. Adjusted_log_CI_2x2
4. AgrestiCaffo_CI_2x2
5. Wald_CI_2x2
6. BaptistaPike_exact_conditional_CI_2x2
7. BaptistaPike_midP_CI_2x2
8. Cornfield_exact_conditional_CI_2x2
9. Cornfield_midP_CI_2x2
10. Fisher_exact_test_2x2
11. Exact_unconditional_test_2x2
12. Fisher_midP_test_2x2
13. Gart_adjusted_logit_CI_2x2
14. Independence_smoothed_logit_CI_2x2
15. Inv_sinh_CI_OR_2x2
16. Inv_sinh_CI_ratio_2x2
17. Katz_log_CI_2x2
18. Koopman_asymptotic_score_CI_2x2
19. LR_test_2x2
20. Mee_asymptotic_score_CI_2x2
21. MiettinenNurminen_asymptotic_score_CI_difference_2x2
22. MiettinenNurminen_asymptotic_score_CI_OR_2x2
23. MiettinenNurminen_asymptotic_score_CI_ratio_2x2
24. MOVER_R_Wilson_CI_OR_2x2
25. MOVER_R_Wilson_CI_ratio_2x2
26. Newcombe_hybrid_score_CI_2x2
27. Pearson_chi_squared_test_2x2
28. Pearson_chi_squared_test_CC_2x2
29. PriceBonett_approximate_Bayes_CI_2x2
30. Wald_CI_CC_2x2
31. Woolf_logit_CI_2x2

32. Uncorrected_asymptotic_score_CI_2x2
33. Z_unpooled_test_2x2
34. the_2x2_table_CIs_difference
35. the_2x2_table_CIs_OR
36. the_2x2_table_CIs_ratio
37. the_2x2_table_tests

Note

You can also print the list above with `list_functions(4)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap5` *Chapter 5: The Ordered rx2 Table*

Description

These are the functions related to chapter 5:

1. CochranArmitage_CI_rx2
2. CochranArmitage_exact_cond_midP_tests_rx2
3. CochranArmitage_MH_tests_rx2
4. Exact_cond_midP_unspecific_ordering_rx2
5. Pearson_LR_tests_unspecific_ordering_rx2
6. the_rx2_table
7. Trend_estimate_CI_tests_rx2

Note

You can also print the list above with `list_functions(5)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap6` *Chapter 6: The Ordered 2xc Table*

Description

These are the functions related to chapter 6:

1. Brant_test_2xc
2. Cumulative_models_for_2xc
3. Exact_cond_midP_linear_rank_tests_2xc
4. ClopperPearson_exact_CI_1x2_beta_version
5. Exact_cond_midP_unspecific_ordering_rx2
6. MantelHaenszel_test_2xc
7. Pearson_LR_tests_cum_OR_2xc
8. Score_test_for_effect_in_the_probit_model_2xc
9. the_2xc_table

Note

You can also print the list above with `list_functions(6)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap7` *Chapter 7: The rxc Table*

Description

These are the functions related to chapter 7:

1. Bonferroni_type_CIs_rxc
2. Cumulative_models_for_rxc
3. Exact_cond_midP_tests_rxc
4. FisherFreemanHalton_asymptotic_test_rxc
5. gamma_coefficient_rxc_bca
6. gamma_coefficient_rxc

7. JonckheereTerpstra_test_rxc
8. Kendalls_tau_b_rxc
9. Kendalls_tau_b_rxc_bca
10. KruskalWallis_asymptotic_test_rxc
11. linear_by_linear_test_rxc
12. Pearson_correlation_coefficient_rxc
13. Pearson_correlation_coefficient_rxc_bca
14. Pearson_LR_tests_rxc
15. Pearson_residuals_rxc
16. Scheffe_type_CIs_rxc
17. Spearman_correlation_coefficient_rxc
18. Spearman_correlation_coefficient_rxc_bca
19. the_rxc_table

Note

You can also print the list above with `list_functions(7)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap8` *Chapter 8: The Paired 2x2 Table*

Description

These are the functions related to chapter 8:

1. BonettPrice_hybrid_Wilson_score_CI_CC_paired_2x2
2. BonettPrice_hybrid_Wilson_score_CI_paired_2x2
3. ClopperPearson_exact_CI_1x2_beta_version
4. McNemar_asymptotic_test_CC_paired_2x2
5. McNemar_asymptotic_test_paired_2x2
6. McNemar_exact_cond_test_paired_2x2
7. McNemar_exact_unconditional_test_paired_2x2
8. McNemar_midP_test_paired_2x2
9. Tang_asymptotic_score_CI_paired_2x2

10. Tango_asymptotic_score_CI_paired_2x2
11. MOVER_Wilson_score_CI_paired_2x2
12. Newcombe_square_and_add_CI_paired_2x2
13. Transformed_Blaker_exact_CI_paired_2x2
14. Transformed_Clopper_Pearson_exact_CI_paired_2x2
15. Transformed_Clopper_Pearson_midP_CI_paired_2x2
16. Transformed_Wilson_score_CI_paired_2x2
17. Wald_CI_diff_paired_2x2
18. Wald_CI_diff_CC_paired_2x2
19. Wald_CI_AgrestiMin_paired_2x2
20. Wald_CI_BonettPrice_paired_2x2
21. Wald_CI_OR_Laplace_paired_2x2
22. Wald_CI_OR_paired_2x2
23. Wald_CI_ratio_paired_2x2
24. the_paired_2x2_table_CIs_difference
25. the_paired_2x2_table_CIs_OR
26. the_paired_2x2_table_CIs_ratio
27. the_paired_2x2_table_tests

Note

You can also print the list above with `list_functions(8)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`chap9` *Chapter 9: The Paired cxc Table*

Description

These are the functions related to chapter 9:

1. Bhapkar_test_paired_cxc
2. Bonferroni_type_CIs_paired_cxc
3. FleissEveritt_test_paired_cxc
4. FleissLevinPaik_test_paired_cxc

5. McNemarBowker_test_paired_cxc
6. Scheffe_type_CIs_paired_cxc
7. Score_test_and_CI_marginal_mean_scores_paired_cxc
8. Stuart_test_paired_cxc
9. Wald_test_and_CI_marginal_mean_ranks_paired_cxc
10. Wald_test_and_CI_marginal_mean_scores_paired_cxc
11. the_paired_cxc_table_nominal
12. the_paired_cxc_table_ordinal

Note

You can also print the list above with `list_functions(9)`.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`ClopperPearson_exact_CI_1x2`

The Clopper-Pearson exact confidence interval

Description

The Clopper-Pearson exact confidence interval for the binomial probability Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
ClopperPearson_exact_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95#' CIs
`printresults`	display results (F = no, T = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
ClopperPearson_exact_CI_1x2(X = 13, n = 16)
```

`ClopperPearson_exact_CI_1x2_beta_version` *The Clopper-Pearson exact confidence interval for the binomial probability (beta version)*

Description

The Clopper-Pearson exact confidence interval for the binomial probability

(defined via the beta distribution)

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
ClopperPearson_exact_CI_1x2_beta_version(
  X,
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

References

Brown LD, Cai T, DasGupta A (2001) Interval estimation for a binomial proportion. Statistical Science; 16:101-133

See Also

ClopperPearson_exact_CI_1x2

Examples

```
# The number of 1st order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2_beta_version(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2_beta_version(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2_beta_version(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
ClopperPearson_exact_CI_1x2_beta_version(X = 33, n = 45)
# Ligarden et al. (2010)
ClopperPearson_exact_CI_1x2_beta_version(X = 13, n = 16)
```

`ClopperPearson_midP_CI_1x2` *The Clopper-Pearson mid-P confidence interval*

Description

The Clopper-Pearson mid-P confidence interval for the binomial probability Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
ClopperPearson_midP_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010)
ClopperPearson_midP_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
ClopperPearson_midP_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
ClopperPearson_midP_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
ClopperPearson_midP_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
ClopperPearson_midP_CI_1x2(X = 13, n = 16)
```

`CochranArmitage_CI_rx2` *The Cochran-Armitage confidence interval for trend in the linear model*

Description

The Cochran-Armitage confidence interval for trend in the linear model

Described in Chapter 5 "The Ordered rx2 Table"

Usage

```
CochranArmitage_CI_rx2(n, a, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`a`	scores assigned to the rows
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# Alcohol consumption and malformations (Mills and Graubard, 1987)
n <- rbind(c(48, 17066), c(38, 14464), c(5, 788), c(1, 126), c(1, 37))
a <- c(1, 2, 3, 4, 5)
CochranArmitage_CI_rx2(n, a)

# Elevated troponin T levels in stroke patients (Indredavik et al., 2008)
n <- rbind(c(8, 53), c(10, 48), c(11, 100), c(22, 102), c(6, 129))
```

```
a <- c(1, 2, 3, 4, 5)
CochranArmitage_CI_rx2(n, a)
```

`CochranArmitage_exact_cond_midP_tests_rx2` *The Cochran-Armitage exact conditional and mid-P tests*

Description

The Cochran-Armitage exact conditional and mid-P tests

Described in Chapter 5 "The Ordered rx2 Table"

Usage

```
CochranArmitage_exact_cond_midP_tests_rx2(n, a, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`a`	scores assigned to the rows
`printresults`	display results

Value

A data frame containing the two-sided, twice-the-smallest tail P-value and the mid-P value

Examples

```
## Not run:
# Alcohol consumption and malformations (Mills and Graubard, 1987)
n <- rbind(c(48, 17066), c(38, 14464), c(5, 788), c(1, 126), c(1, 37))
a <- c(1, 2, 3, 4, 5)
CochranArmitage_exact_cond_midP_tests_rx2(n, a)

## End(Not run)

# Elevated troponin T levels in stroke patients (Indredavik et al., 2008)
n <- rbind(c(8, 53), c(10, 48), c(11, 100), c(22, 102), c(6, 129))
a <- c(1, 2, 3, 4, 5)
CochranArmitage_exact_cond_midP_tests_rx2(n, a)
```

`CochranArmitage_MH_tests_rx2` *The Cochran-Armitage, modified Cochran-Armitage, and Mantel-Haenszel tests for trend*

Description

Described in Chapter 5 "The Ordered rx2 Table"

Usage

```
CochranArmitage_MH_tests_rx2(n, a, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`a`	scores assigned to the rows
`printresults`	display results

Value

A list containing observed statistics and p-values

Examples

```
# Alcohol consumption and malformations (Mills and Graubard, 1987)
n <- rbind(c(48, 17066), c(38, 14464), c(5, 788), c(1, 126), c(1, 37))
a <- c(1, 2, 3, 4, 5)
CochranArmitage_MH_tests_rx2(n, a)

# Elevated troponin T levels in stroke patients (Indredavik et al., 2008)
n <- rbind(c(8, 53), c(10, 48), c(11, 100), c(22, 102), c(6, 129))
a <- c(1, 2, 3, 4, 5)
CochranArmitage_MH_tests_rx2(n, a)
```

`CochranMantelHaenszel_test_stratified_2x2` *The Cochran-Mantel-Haenszel test of a common odds ratio*

Description

The Cochran-Mantel-Haenszel test of a common odds ratio

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
CochranMantelHaenszel_test_stratified_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
CochranMantelHaenszel_test_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
CochranMantelHaenszel_test_stratified_2x2(n)
```

`Cochran_Q_test_stratified_2x2` *The Cochran Q test of homogeneity of effects over strata*

Description

The Cochran Q test of homogeneity of effects over strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Cochran_Q_test_stratified_2x2(
  n,
  link = "linear",
  estimatetype = "MH",
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`estimatetype`	Mantel-Haenszel or inverse variance estimate ('MH' or 'IV')
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Cochran_Q_test_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Cochran_Q_test_stratified_2x2(n)
```

`contingencytables` *Statistical Analysis of Contingency tables*

Description

Statistical Analysis of Contingency Tables is an invaluable tool for statistical inference in contingency tables. It covers effect size estimation, confidence intervals, and hypothesis tests for the binomial and the multinomial distributions, unpaired and paired 2x2 tables, rxc tables, ordered rx2 and 2xc tables, paired cxc tables, and stratified tables. This package provides functions that accompany the "Statistical Analysis of Contingency Tables" book by Fagerland et. al. <ISBN 9781466588172>.

References

- Fagerland MW, Lydersen S, Laake P (2017) Statistical Analysis of Contingency Tables. Chapman & Hall/CRC, Boca Raton, FL
- https://contingencytables.com/
- https://www.routledge.com/Statistical-Analysis-of-Contingency-Tables/Fagerland-Lydersen-Laake/p/book/978146658

`Cornfield_exact_conditional_CI_2x2` *The Cornfield exact conditional confidence interval for the odds ratio*

Description

The Cornfield exact conditional confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Cornfield_exact_conditional_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
Cornfield_exact_conditional_CI_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
Cornfield_exact_conditional_CI_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
Cornfield_exact_conditional_CI_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
Cornfield_exact_conditional_CI_2x2(n)
```

`Cornfield_midP_CI_2x2` *The Cornfield mid-P confidence interval for the odds ratio*

Description

The Cornfield mid-P confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Cornfield_midP_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
Cornfield_midP_CI_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
Cornfield_midP_CI_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
Cornfield_midP_CI_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
Cornfield_midP_CI_2x2(n)
```

`Cumulative_models_for_2xc`

Cumulative logit and probit models

Description

Cumulative logit and probit models

Described in Chapter 6 "The Ordered 2xc Table"

Usage

```
Cumulative_models_for_2xc(
  n,
  linkfunction = "logit",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2xc matrix)
`linkfunction`	either "logit" or "probit"
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing the results of statistical tests for the goodness-of-fit of a proportional odds model, the effect in a proportional odds model and the effect parameter beta in the proportional odds model.

Examples

```
# The Adolescent Placement Study (Fontanella et al., 2008)
n <- rbind(c(8, 28, 72, 126), c(46, 73, 69, 86))
Cumulative_models_for_2xc(n)

# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
Cumulative_models_for_2xc(n)
```

`Cumulative_models_for_rxc`

Cumulative logit and probit models

Description

Cumulative logit and probit models

Described in Chapter 7 "The rxc Table"

Usage

```
Cumulative_models_for_rxc(
  n,
  linkfunction = "logit",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (an rxc matrix)
`linkfunction`	either "logit" or "probit"
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the results of statistical tests for the goodness-of-fit of a proportional odds model, the effect in a proportional odds model and row comparisons

Examples

```
# Psychiatric diag. vs BMI with hyperkinetic disorders
# as reference category (Table 7.5)
n <- rbind(
  c(19, 130, 64), c(3, 55, 23), c(8, 102, 36), c(6, 14, 1), c(5, 21, 12), c(7, 26, 18)
)
Cumulative_models_for_rxc(n)

# LBW vs psych. morbidity with control as reference category (Table 7.6)
n <- rbind(c(51, 7, 6), c(22, 4, 12), c(24, 9, 10))
Cumulative_models_for_rxc(n)
```

`Exact_binomial_test_1x2` *The exact binomial test for the binomial probability (pi)*

Description

H_0 pi = pi0 vs H_A: pi ~= pi0 (two-sided)

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Exact_binomial_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (F = no, T = yes)

Value

The two-sided, twice-the-smallest tail p-value

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Exact_binomial_test_1x2(X = 250, n = 533, pi0 = 0.513)
# The number of 2nd order male births (Singh et al. 2010)
Exact_binomial_test_1x2(X = 204, n = 412, pi0 = 0.513)
# The number of 3rd order male births (Singh et al. 2010)
Exact_binomial_test_1x2(X = 103, n = 167, pi0 = 0.513)
# The number of 4th order male births (Singh et al. 2010)
Exact_binomial_test_1x2(X = 33, n = 45, pi0 = 0.513)
```

```
# Ligarden et al. (2010)
Exact_binomial_test_1x2(X = 13, n = 16, pi0 = 0.5)
```

`Exact_cond_midP_linear_rank_tests_2xc`

Exact conditional and mid-P linear rank tests

Description

Exact conditional and mid-P linear rank tests

Described in Chapter 6 "The Ordered 2xc Table"

Usage

```
Exact_cond_midP_linear_rank_tests_2xc(n, b = 0, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2xc matrix)
`b`	scores assigned to the columns (if b=0, midranks will be used as scores)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing the two-sided, twice-the-smallest tail P-value and the mid-P value

Examples

```
## Not run:
# The Adolescent Placement Study (Fontanella et al., 2008)
n <- rbind(c(8, 28, 72, 126), c(46, 73, 69, 86))
Exact_cond_midP_linear_rank_tests_2xc(n)

## End(Not run)

# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
Exact_cond_midP_linear_rank_tests_2xc(n)
```

`Exact_cond_midP_tests_rxc` *Exact conditional and mid-P tests for the rxc table*

Description

Exact conditional and mid-P tests for the rxc table: the Fisher-Freeman-Halton, Pearson, likelihood ratio, Kruskal-Wallis, linear-by-linear, and Jonckheere-Terpstra tests.

Described in Chapter 7 "The rxc Table"

Usage

```
Exact_cond_midP_tests_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing exact p-values and mid-p values

Note

Works only for 3x2 and 3x3 tables

Examples

```
# Treatment for ear infection (Table 7.3)
n <- rbind(c(40, 25), c(54, 7), c(63, 10))
Exact_cond_midP_tests_rxc(n)
# Low birth weight vs psychiatric morbitidy (Table 7.6)
## Not run:
n <- matrix(c(22, 4, 12, 24, 9, 10, 51, 7, 6), ncol = 3, byrow = TRUE)
Exact_cond_midP_tests_rxc(n)

## End(Not run)
```

`Exact_cond_midP_unspecific_ordering_rx2` *The exact conditional and mid-P tests for unspecific ordering*

Description

The exact conditional and mid-P tests for unspecific ordering. May also be used for 2xc tables, after flipping rows and columns (i.e. if n is a 2xc table, call this function with n' (the transpose of n) as the first argument).

Described in Chapter 5 "The Ordered rx2 Table"

Usage

```
Exact_cond_midP_unspecific_ordering_rx2(
  n,
  direction,
  statistic = "Pearson",
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`direction`	the direction of the success probabilities ("increasing" or "decreasing")
`statistic`	the Pearson test statistic ("Pearson") or the likelihood ratio test statistic ("LR"). Can also be used for cumulative ORs in 2xc tables with "PearsonCumOR" or "LRCumOR".
`printresults`	display results (0 = no, 1 = yes)

Value

A data frame containing the two-sided exact P-value and the mid-P value

Examples

```
# Chapter 6: Postoperative nausea (Lydersen et al., 2012a)
n <- t(rbind(c(14, 10, 3, 2), c(11, 7, 8, 4)))
Exact_cond_midP_unspecific_ordering_rx2(n, "decreasing")
## Not run:
Exact_cond_midP_unspecific_ordering_rx2(n, "decreasing", "PearsonCumOR")

## End(Not run)
```

`Exact_multinomial_test_1xc` *The exact multinomial test for multinomial probabilities*

Description

The exact multinomial test for multinomial probabilities

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Exact_multinomial_test_1xc(n, pi0, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`pi0`	given probabilities (a 1xc vector)
`printresults`	display results (F = no, T = yes)

Value

probability value

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
## Not run:
Exact_multinomial_test_1xc(n = c(276, 380, 118), pi0 = c(0.402, 0.479, 0.119))

## End(Not run)
# subset of 10 patients
Exact_multinomial_test_1xc(n = c(6, 1, 3), pi0 = c(0.402, 0.479, 0.119))
```

`Exact_unconditional_test_2x2` *Exact unconditional test for association in 2x2 tables*

Description

Exact unconditional test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
Exact_unconditional_test_2x2(
  n,
  statistic = "Pearson",
  gamma = 1e-04,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`statistic`	'Pearson' (Suissa-Shuster test default), 'LR' (likelihood ratio), ' unpooled' (unpooled Z), or 'Fisher' (Fisher-Boschloo test)
`gamma`	parameter for the Berger and Boos procedure (default=0.0001 gamma=0: no adj)
`printresults`	display results (F = no, T = yes)

Value

Fisher's exact test statistic

Note

Somewhat crude code with maximization over a simple partition of the nuisance parameter space into 'num_pi_values' equally spaced values (default: 1000). The number may be changed below. This method could be improved with a better algorithm for the maximization however, it works well for most purposes. Try 'showplot=TRUE' to get an indication of the precision. A refinement of the maximization can be done with a manual restriction of the parameter space.

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
Exact_unconditional_test_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
Exact_unconditional_test_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
Exact_unconditional_test_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
Exact_unconditional_test_2x2(n)
```

`FisherFreemanHalton_asymptotic_test_rxc`

The Fisher-Freeman-Halton asymptotic test for unordered rxc tables

---

Description

The Fisher-Freeman-Halton asymptotic test for unordered rxc tables

Described in Chapter 7 "The rxc Table"

Usage

```
FisherFreemanHalton_asymptotic_test_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Note

May not give results for all tables, due to overflow

Examples

```
# Treatment for ear infection (van Balen et al., 2003)
n <- rbind(c(40, 25), c(54, 7), c(63, 10))
FisherFreemanHalton_asymptotic_test_rxc(n)
```

`Fisher_exact_test_2x2` *The Fisher exact test for association in 2x2 tables*

Description

The Fisher exact test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
Fisher_exact_test_2x2(n, statistic = "Pearson", printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`statistic`	'hypergeometric' (i.e. Fisher-Irwin; default), 'Pearson', or 'LR' (likelihood ratio)
`printresults`	display results (F = no, T = yes)

Value

probability value

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
Fisher_exact_test_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
Fisher_exact_test_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
Fisher_exact_test_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
Fisher_exact_test_2x2(n)
```

`Fisher_midP_test_2x2` *The Fisher mid-P test for association in 2x2 tables*

Description

The Fisher mid-P test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
Fisher_midP_test_2x2(n, statistic = "hypergeometric", printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`statistic`	'hypergeometric' (i.e. Fisher-Irwin default), 'Pearson', or 'LR' (likelihood ratio)
`printresults`	display results (F = no, T = yes)

Value

probability value

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
Fisher_midP_test_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
Fisher_midP_test_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
Fisher_midP_test_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
Fisher_midP_test_2x2(n)
```

`FleissEveritt_test_paired_cxc`

The Fleiss-Everitt version of the Stuart test for marginal homogeneity

---

Description

The Fleiss-Everitt version of the Stuart test for marginal homogeneity

Described in Chapter 9 "The Paired cxc Table"

Usage

```
FleissEveritt_test_paired_cxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# From Table 13.6, page 382, of Fleiss et al. (2003)
n <- rbind(c(35, 5, 0), c(15, 20, 5), c(10, 5, 5))
FleissEveritt_test_paired_cxc(n)
```

`FleissLevinPaik_test_paired_cxc`

The Fleiss-Levin-Paik test for three-level ordinal outcomes

Description

The Fleiss-Levin-Paik test for three-level ordinal outcomes

Described in Chapter 9 "The Paired cxc Table"

Usage

```
FleissLevinPaik_test_paired_cxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# Pretherapy susceptability of pathogens *without the N / A category*
# (Peterson et al., 2007)
n <- rbind(c(596, 18, 6), c(0, 2, 0), c(0, 0, 42))
FleissLevinPaik_test_paired_cxc(n)
```

`gamma_coefficient_rxc` *The gamma coefficient*

Description

The gamma coefficient

Described in Chapter 7 "The rxc Table"

Usage

```
gamma_coefficient_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

a list containing the gamma coefficient, the number of concordant pairs and the number of discordant pairs

Examples

```
## Not run:
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
gamma_coefficient_rxc_bca(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
gamma_coefficient_rxc_bca(n)
```

```
# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
gamma_coefficient_rxc_bca(n)

## End(Not run)
```

`gamma_coefficient_rxc_bca` *The gamma coefficient with the bias-corrected and accelerated boostrap confidence interval*

Description

The gamma coefficient with the bias-corrected and accelerated boostrap confidence interval

Described in Chapter 7 "The rxc Table"

Usage

```
gamma_coefficient_rxc_bca(n, nboot = 10000, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`nboot`	number of bootstrap samples
`alpha`	the nominal significance level, used to compute a 100(1-alpha) confidence interval
`printresults`	display results (FALSE = no, TRUE = yes)

Value

a list with the gamma coefficient and the confidence interval limits

Examples

```
## Not run:
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
gamma_coefficient_rxc_bca(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
```

```
)
gamma_coefficient_rxc_bca(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
gamma_coefficient_rxc_bca(n)

## End(Not run)
```

`Gart_adjusted_logit_CI_2x2`

The Gart adjusted logit confidence interval for the odds ratio

---

Description

The Gart adjusted logit confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Gart_adjusted_logit_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Gart_adjusted_logit_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Gart_adjusted_logit_CI_2x2(n)
```

`Gold_Wald_CIs_1xc` *The Gold Wald simultaneous intervals for the multinomial probabilities*

Description

The Gold Wald simultaneous intervals for the multinomial probabilities (with Scheffe adjustment)

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Gold_Wald_CIs_1xc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
Gold_Wald_CIs_1xc(n = c(276, 380, 118))
```

`Goodman_Wald_CIs_1xc` *The Goodman Wald simultaneous intervals for the multinomial probabilities*

Description

The Goodman Wald simultaneous intervals for the multinomial probabilities

(with Bonferroni adjustment)

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Goodman_Wald_CIs_1xc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
Goodman_Wald_CIs_1xc(n = c(276, 380, 118))
```

`Goodman_Wald_CIs_for_diffs_1xc` *The Goodman Wald simultaneous intervals for the differences between the*

Description

The Goodman Wald simultaneous intervals for the differences between the

multinomial probabilities (with Scheffe or Bonferroni adjustment)

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Goodman_Wald_CIs_for_diffs_1xc(
  n,
  alpha = 0.05,
  adjustment = "Bonferroni",
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`adjustment`	Scheffe or Bonferroni adjustment ("Scheffe" or "Bonferroni")
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
Goodman_Wald_CIs_for_diffs_1xc(n = c(276, 380, 118))
```

`Goodman_Wilson_score_CIs_1xc`

The Goodman Wilson score simultaneous intervals for the multinomial probabilities

---

Description

The Goodman Wilson score simultaneous intervals for the multinomial probabilities

(with Bonferroni adjustment)

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Goodman_Wilson_score_CIs_1xc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
Goodman_Wilson_score_CIs_1xc(n = c(276, 380, 118))
```

`Independence_smoothed_logit_CI_2x2` *The Independence-smoothed logit confidence interval for the odds ratio*

Description

The Independence-smoothed logit confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Independence_smoothed_logit_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Independence_smoothed_logit_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Independence_smoothed_logit_CI_2x2(n)
```

`InverseVariance_estimate_stratified_2x2` *The inverse variance estimate of the overall effect across strata*

Description

The inverse variance estimate of the overall effect across strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
InverseVariance_estimate_stratified_2x2(n, link = "logit", printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`printresults`	display results (FALSE = no, TRUE = yes)

Value

a list respectively containing the inverse variance estimate of the overall effect (`estimate`), the stratum-specific effect estimates (`psihat`) and the weights (`v`).

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
InverseVariance_estimate_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
InverseVariance_estimate_stratified_2x2(n)
```

`Inv_sinh_CI_OR_2x2` *The inverse hyperbolic sine confidence interval for the odds ratio*

Description

The inverse hyperbolic sine confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Inv_sinh_CI_OR_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Inv_sinh_CI_OR_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Inv_sinh_CI_OR_2x2(n)
```

`Inv_sinh_CI_ratio_2x2` *The inverse hyperbolic sine confidence interval for the ratio of probabilities*

Description

The inverse hyperbolic sine confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Inv_sinh_CI_ratio_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Inv_sinh_CI_ratio_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Inv_sinh_CI_ratio_2x2(n)
```

`Jeffreys_CI_1x2` *Jeffreys confidence interval for the binomial probability*

Description

Jeffreys confidence interval for the binomial probability

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Jeffreys_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 <- yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Jeffreys_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Jeffreys_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Jeffreys_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Jeffreys_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Jeffreys_CI_1x2(X = 13, n = 16)
```

`JonckheereTerpstra_test_rxc`

The Jonckheere-Terpstra test for association

Description

The Jonckheere-Terpstra test for association

Described in Chapter 7 "The rxc Table"

Usage

```
JonckheereTerpstra_test_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`printresults`	display results (0 = no, 1 = yes)

Value

a list containing the standard normalized Jonckheere-Terpstra test statistic

Examples

```
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
JonckheereTerpstra_test_rxc(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
JonckheereTerpstra_test_rxc(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
JonckheereTerpstra_test_rxc(n)
```

`Katz_log_CI_2x2` *The Katz log confidence interval for the ratio of probabilities*

Description

The Katz log confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Katz_log_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Katz_log_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Katz_log_CI_2x2(n)
```

`Kendalls_tau_b_rxc` *Kendall's tau-b with confidence interval based on the Fieller standard deviation*

Description

Kendall's tau-b with confidence interval based on the Fieller standard deviation

Described in Chapter 7 "The rxc Table"

Usage

```
Kendalls_tau_b_rxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`alpha`	the nominal significance level, used to compute a 100(1-alpha)% confidence interval
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the statistic and the confindence interval limits

Examples

```
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
Kendalls_tau_b_rxc(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Kendalls_tau_b_rxc(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Kendalls_tau_b_rxc(n)
```

`Kendalls_tau_b_rxc_bca`

Kendall's tau-b with the bias-corrected and accelerated boostrap confidence interval

Description

Kendall's tau-b with the bias-corrected and accelerated boostrap confidence interval

Described in Chapter 7 "The rxc Table"

Usage

```
Kendalls_tau_b_rxc_bca(n, nboot = 10000, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`nboot`	number of bootstrap samples
`alpha`	the nominal significance level, used to compute a 100(1-alpha) confidence interval
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing the statistic and the confindence interval limits

Examples

```
## Not run:
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
Kendalls_tau_b_rxc_bca(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Kendalls_tau_b_rxc_bca(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Kendalls_tau_b_rxc_bca(n)

## End(Not run)
```

`Koopman_asymptotic_score_CI_2x2` *The Koopman asymptotic score confidence interval for the ratio of probabilities*

Description

The Koopman asymptotic score confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Koopman_asymptotic_score_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Note

This versions uses the score test statistic of the Miettinen-Nurminen interval without the variance correction term.

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Koopman_asymptotic_score_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Koopman_asymptotic_score_CI_2x2(n)
```

`KruskalWallis_asymptotic_test_rxc` *The Kruskal-Wallis asymptotic test for singly ordered rxc tables*

Description

The Kruskal-Wallis asymptotic test for singly ordered rxc tables

Described in Chapter 7 "The rxc Table"

Usage

```
KruskalWallis_asymptotic_test_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rxc matrix)
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Low birth weight vs psychiatric morbitidy (Table 7.6)
n <- rbind(c(22, 4, 12), c(24, 9, 10), c(51, 7, 6))
KruskalWallis_asymptotic_test_rxc(n)

# Psychiatric diag. vs BMI (Table 7.5)
n <- matrix(
  c(3, 55, 23, 8, 102, 36, 6, 14, 1, 5, 21, 12, 19, 130, 64, 7, 26, 18),
  ncol = 3, byrow = TRUE
)
KruskalWallis_asymptotic_test_rxc(n)
```

`linear_by_linear_test_rxc` *The linear-by-linear test for association*

Description

The linear-by-linear test for association

Described in Chapter 7 "The rxc Table"

Usage

```
linear_by_linear_test_rxc(
  n,
  a = seq_len(ncol(n)),
  b = seq_len(nrow(n)),
  printresults = TRUE
)
```

Arguments

`n`	the observed table (an rxc matrix)
`a`	scores assigned to the rows
`b`	scores assigned to the columns
`printresults`	display results (0 = no, 1 = yes)

Value

a list containing the linear-by-linear test statistic

Examples

```
#' # Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
linear_by_linear_test_rxc(n)

## Not run:
# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
linear_by_linear_test_rxc(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
linear_by_linear_test_rxc(n)

## End(Not run)
```

`list_functions` *List functions from a chapter*

Description

Complements the `?chapX` command by printing a list of functions related to a particular chapter `X` on the R console.

Usage

```
list_functions(chap_num)
```

Arguments

`chap_num`	Number of book chapter (from 2 to 10)

Value

List of functions from that chapter

Author(s)

Waldir Leoncio

`LR_CI_1x2` *The likelihood ratio confidence interval for the binomial probability*

Description

The likelihood ratio confidence interval for the binomial probability. Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
LR_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010)
LR_CI_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
LR_CI_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
LR_CI_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
LR_CI_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
LR_CI_1x2(X = 13, n = 16)
```

`LR_test_1x2` *The likelihood ratio test for the binomial probability (pi)*

Description

The likelihood ratio test for the binomial probability (pi) H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided). Described in Chapter 2 "The 1x2 Table and the Binomial Distribution".

Usage

```
LR_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# The number of 1st order male births (Singh et al. 2010, adapted)
LR_test_1x2(X = 250, n = 533, pi0 = .5)
# The number of 2nd order male births (Singh et al. 2010, adapted)
LR_test_1x2(X = 204, n = 412, pi0 = .5)
# The number of 3rd order male births (Singh et al. 2010, adapted)
LR_test_1x2(X = 103, n = 167, pi0 = .5)
# The number of 4th order male births (Singh et al. 2010, adapted)
LR_test_1x2(X = 33, n = 45, pi0 = .5)
# Ligarden et al. (2010, adapted)
LR_test_1x2(X = 13, n = 16, pi0 = .5)
```

`LR_test_1xc` *The likelihood ratio test for multinomial probabilities*

Description

The likelihood ratio test for multinomial probabilities

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
LR_test_1xc(n, pi0, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`pi0`	given probabilities (a 1xc vector)
`printresults`	display results (F = no, T = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
LR_test_1xc(n = c(276, 380, 118), pi0 = c(0.402, 0.479, 0.119))
# subset of 10 patients
LR_test_1xc(n = c(6, 1, 3), pi0 = c(0.402, 0.479, 0.119))
```

`LR_test_2x2` *The likelihood ratio test for association in 2x2 tables*

Description

The likelihood ratio test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
LR_test_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A vector containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
n <- rbind(c(3, 1), c(1, 3)) # Example: A lady tasting a cup of tea
LR_test_2x2(n)
n <- rbind(c(7, 27), c(1, 33)) # Example: Perondi et al. (2004)
LR_test_2x2(n)
n <- rbind(c(9, 4), c(4, 10)) # Example: Lampasona et al. (2013)
LR_test_2x2(n)
n <- rbind(c(0, 16), c(15, 57)) # Example: Ritland et al. (2007)
LR_test_2x2(n)
```

`MantelHaenszel_estimate_stratified_2x2` *The Mantel-Haenszel estimate of the overall effect across strata*

Description

The Mantel-Haenszel estimate of the overall effect across strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
MantelHaenszel_estimate_stratified_2x2(n, link = "logit", printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`printresults`	display results (FALSE = no, TRUE = yes)

Value

a list respectively containing the inverse variance estimate of the overall effect (`estimate`), the stratum-specific effect estimates (`psihat`) and the weights (`w`).

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
MantelHaenszel_estimate_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
MantelHaenszel_estimate_stratified_2x2(n)
```

`MantelHaenszel_test_2xc`
The Mantel-Haenszel test of association with column scores

Description

The Mantel-Haenszel test of association with column scores

Described in Chapter 6 "The Ordered 2xc Table"

Usage

```
MantelHaenszel_test_2xc(n, b = 0, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2xc matrix)
`b`	scores assigned to the columns (if b=0, midranks will be used as scores)
`printresults`	display results (0 = no, 1 = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
MantelHaenszel_test_2xc(n)
b <- 0
```

`McNemarBowker_test_paired_cxc`
The McNemar-Bowker test for marginal symmetry

Description

The McNemar-Bowker test for marginal symmetry

Described in Chapter 9 "The Paired cxc Table"

Usage

```
McNemarBowker_test_paired_cxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
McNemarBowker_test_paired_cxc(n)
```

`McNemar_asymptotic_test_CC_paired_2x2`
The McNemar asymptotic test with continuity correction

Description

The McNemar asymptotic test with continuity correction

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
McNemar_asymptotic_test_CC_paired_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

The McNemar test statistic with continuity correction (`Z`) and the reference distribution (standard normal, `P`)

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
McNemar_asymptotic_test_CC_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
```

```
McNemar_asymptotic_test_CC_paired_2x2(n)

# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
McNemar_asymptotic_test_CC_paired_2x2(n)
```

`McNemar_asymptotic_test_paired_2x2` *The McNemar asymptotic test*

Description

The McNemar asymptotic test

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
McNemar_asymptotic_test_paired_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

The McNemar test statistic with continuity correction (`Z`) and the reference distribution (standard normal, `P`)

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
McNemar_asymptotic_test_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
McNemar_asymptotic_test_paired_2x2(n)

# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
McNemar_asymptotic_test_paired_2x2(n)
```

`McNemar_exact_cond_test_paired_2x2`

The McNemar exact conditional test

Description

The McNemar exact conditional test

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
McNemar_exact_cond_test_paired_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

The exact p-value based on the binomial distribution

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
McNemar_exact_cond_test_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
McNemar_exact_cond_test_paired_2x2(n)

# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
McNemar_exact_cond_test_paired_2x2(n)
```

`McNemar_exact_unconditional_test_paired_2x2` *The McNemar exact unconditional test*

Description

The McNemar exact unconditional test

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
McNemar_exact_unconditional_test_paired_2x2(
  n,
  gamma = 1e-04,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`gamma`	parameter for the Berger and Boos procedure (default=0.0001; gamma=0: no adj)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

The T version of the test statistic (not the Z one)

Note

Somewhat crude code with maximization over a simple partition of the nuisance parameter space into 'num_pi_values' equally spaced values (default: 1000). The number may be changed below. This method could be improved with a better algorithm for the maximization; however, it works well for most purposes. Try `showplot=1` to get an indication of the precision. A refinement of the maximization can be done with a manual restriction of the parameter space.

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
McNemar_exact_unconditional_test_paired_2x2(n)

## Not run:
# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
```

```
McNemar_exact_unconditional_test_paired_2x2(n)

## End(Not run)

# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
McNemar_exact_unconditional_test_paired_2x2(n)
```

`McNemar_midP_test_paired_2x2` *The McNemar mid-P test*

Description

The McNemar mid-P test

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
McNemar_midP_test_paired_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

probability value

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
McNemar_midP_test_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
McNemar_midP_test_paired_2x2(n)

# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
McNemar_midP_test_paired_2x2(n)
```

`Mee_asymptotic_score_CI_2x2` *The Mee asymptotic score confidence interval for the difference between probabilities*

Description

The Mee asymptotic score confidence interval for the difference between probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Mee_asymptotic_score_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Mee_asymptotic_score_CI_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Mee_asymptotic_score_CI_2x2(n)
```

`MidP_binomial_test_1x2` *The mid-P binomial test for the binomial probability (pi)*

Description

The mid-P binomial test for the binomial probability (pi) H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided) Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
MidP_binomial_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

probability value

Examples

```
# The number of 1st order male births (Singh et al. 2010, adapted)
MidP_binomial_test_1x2(X = 250, n = 533, pi0 = .5)
# The number of 2nd order male births (Singh et al. 2010, adapted)
MidP_binomial_test_1x2(X = 204, n = 412, pi0 = .5)
# The number of 3rd order male births (Singh et al. 2010, adapted)
MidP_binomial_test_1x2(X = 103, n = 167, pi0 = .5)
# The number of 4th order male births (Singh et al. 2010, adapted)
MidP_binomial_test_1x2(X = 33, n = 45, pi0 = .5)
# Ligarden et al. (2010, adapted)
MidP_binomial_test_1x2(X = 13, n = 16, pi0 = .5)
```

`MidP_multinomial_test_1xc` *The mid-P multinomial test for multinomial probabilities*

Description

The mid-P multinomial test for multinomial probabilities

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
MidP_multinomial_test_1xc(n, pi0, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`pi0`	given probabilities (a 1xc vector)
`printresults`	display results (F = no, T = yes)

Value

probability value

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
## Not run:
MidP_multinomial_test_1xc(n = c(276, 380, 118), pi0 = c(0.402, 0.479, 0.119))

## End(Not run)
# subset of 10 patients
MidP_multinomial_test_1xc(n = c(6, 1, 3), pi0 = c(0.402, 0.479, 0.119))
```

`MiettinenNurminen_asymptotic_score_CI_difference_2x2`

The Mietinen-Nurminen asymptotic score confidence interval for the

---

Description

The Mietinen-Nurminen asymptotic score confidence interval for the

difference between probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
MiettinenNurminen_asymptotic_score_CI_difference_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_difference_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_difference_2x2(n)
```

`MiettinenNurminen_asymptotic_score_CI_OR_2x2`
The Miettinen-Nurminen asymptotic score CI for the odds ratio

---

Description

The Miettinen-Nurminen asymptotic score confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
MiettinenNurminen_asymptotic_score_CI_OR_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome
# (Lampasona et al., 2013)
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_OR_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_OR_2x2(n)
```

`MiettinenNurminen_asymptotic_score_CI_ratio_2x2` *The Miettinen-Nurminen asymptotic score confidence interval for the ratio of probabilities*

Description

The Miettinen-Nurminen asymptotic score confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
MiettinenNurminen_asymptotic_score_CI_ratio_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_ratio_2x2(n)
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
MiettinenNurminen_asymptotic_score_CI_ratio_2x2(n)
```

`ML_estimates_and_CIs_stratified_2x2`

Maximum likelihood estimates with CIs of the grouping and strata effects

---

Description

Maximum likelihood estimates with CIs of the grouping and strata effects

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
ML_estimates_and_CIs_stratified_2x2(
  n,
  link = "log",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the maximum likelihood estimates

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
ML_estimates_and_CIs_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
ML_estimates_and_CIs_stratified_2x2(n)
```

`MOVER_R_Wilson_CI_OR_2x2` *The MOVER-R Wilson confidence interval for the odds ratio*

Description

The MOVER-R Wilson confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
MOVER_R_Wilson_CI_OR_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, 1T= yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
MOVER_R_Wilson_CI_OR_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
MOVER_R_Wilson_CI_OR_2x2(n)
```

`MOVER_R_Wilson_CI_ratio_2x2` *The MOVER-R Wilson confidence interval for the ratio of probabilities*

Description

The MOVER-R Wilson confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
MOVER_R_Wilson_CI_ratio_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
MOVER_R_Wilson_CI_ratio_2x2(matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE))

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
MOVER_R_Wilson_CI_ratio_2x2(matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE))
```

`MOVER_Wilson_score_CI_paired_2x2` *The MOVER Wilson score confidence interval for the ratio of paired probabilities*

Description

The MOVER Wilson score confidence interval for the ratio of paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
MOVER_Wilson_score_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T= yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
n <- rbind(c(1, 1), c(7, 12))
MOVER_Wilson_score_CI_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- matrix(c(59, 6, 16, 80), 2, byrow = TRUE)
MOVER_Wilson_score_CI_paired_2x2(n)
```

`Newcombe_hybrid_score_CI_2x2` *The Newcombe hybrid score confidence interval for the difference between probabilities*

Description

The Newcombe hybrid score confidence interval for the difference between probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Newcombe_hybrid_score_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Newcombe_hybrid_score_CI_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Newcombe_hybrid_score_CI_2x2(n)
```

`Newcombe_square_and_add_CI_paired_2x2` *The Newcombe square-and-add confidence interval for the difference*

Description

The Newcombe square-and-add confidence interval for the difference between paired probabilities.

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Newcombe_square_and_add_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Newcombe_square_and_add_CI_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- matrix(c(59, 6, 16, 80), 2, byrow = TRUE)
Newcombe_square_and_add_CI_paired_2x2(n)
```

`Pearson_chi_squared_test_1xc` *The Pearson chi-squared test for multinomial probabilities*

Description

The Pearson chi-squared test for multinomial probabilities

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
Pearson_chi_squared_test_1xc(n, pi0, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`pi0`	given probabilities (a 1xc vector)
`printresults`	display results (F = no, T = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
Pearson_chi_squared_test_1xc(n = c(276, 380, 118), pi0 = c(0.402, 0.479, 0.119))
# subset of 10 patients
Pearson_chi_squared_test_1xc(n = c(6, 1, 3), pi0 = c(0.402, 0.479, 0.119))
```

`Pearson_chi_squared_test_2x2`
The Pearson chi-squared test for association in 2x2 tables

Description

The Pearson chi-squared test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
Pearson_chi_squared_test_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Example: A lady tasting a cup of tea
n <- rbind(c(3, 1), c(1, 3))
Pearson_chi_squared_test_2x2(n)

# Example: Perondi et al. (2004)
n <- rbind(c(7, 27), c(1, 33))
Pearson_chi_squared_test_2x2(n)

# Example: Lampasona et al. (2013)
n <- rbind(c(9, 4), c(4, 10))
Pearson_chi_squared_test_2x2(n)

# Example: Ritland et al. (2007)
n <- rbind(c(0, 16), c(15, 57))
Pearson_chi_squared_test_2x2(n)
```

`Pearson_chi_squared_test_CC_2x2`
The Pearson chi-squared test for association in 2x2 tables

Description

The Pearson chi-squared test for association in 2x2 tables

with continuity correction

Described in Chapter 4 "The 2x2 Table"

Usage

```
Pearson_chi_squared_test_CC_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Example: A lady tasting a cup of tea
n <- rbind(c(3, 1), c(1, 3))
Pearson_chi_squared_test_CC_2x2(n)

# Example: Perondi et al. (2004)
```

```
n <- rbind(c(7, 27), c(1, 33))
Pearson_chi_squared_test_CC_2x2(n)

# Example: Lampasona et al. (2013)
n <- rbind(c(9, 4), c(4, 10))
Pearson_chi_squared_test_CC_2x2(n)

# Example: Ritland et al. (2007)
n <- rbind(c(0, 16), c(15, 57))
Pearson_chi_squared_test_CC_2x2(n)
```

`Pearson_correlation_coefficient_rxc` *The Pearson correlation coefficient*

Description

The Pearson correlation coefficient

Described in Chapter 7 "The rxc Table"

Usage

```
Pearson_correlation_coefficient_rxc(
  n,
  a = seq_len(nrow(n)),
  b = seq_len(ncol(n)),
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (an rxc matrix)
`a`	scores assigned to the rows
`b`	scores assigned to the columns
`alpha`	the nominal significance level, used to compute a 100(1-alpha) confidence interval
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing the statistic and the confindence interval limits

Examples

```
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
Pearson_correlation_coefficient_rxc(n)
## Not run:
# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Pearson_correlation_coefficient_rxc(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Pearson_correlation_coefficient_rxc(n)

## End(Not run)
```

`Pearson_correlation_coefficient_rxc_bca` *The Pearson correlation coefficient with the bias-corrected and accelerated*

Description

The Pearson correlation coefficient with the bias-corrected and accelerated

boostrap confidence interval

Described in Chapter 7 "The rxc Table"

Usage

```
Pearson_correlation_coefficient_rxc_bca(
  n,
  nboot = 10000,
  a = seq_len(nrow(n)),
  b = seq_len(ncol(n)),
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (an rxc matrix)
`nboot`	number of bootstrap samples
`a`	scores assigned to the rows
`b`	scores assigned to the columns
`alpha`	the nominal significance level, used to compute a 100(1-alpha) confidence interval
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the statistic and the confindence interval limits

Examples

```
## Not run:
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
Pearson_correlation_coefficient_rxc_bca(n)

# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Pearson_correlation_coefficient_rxc_bca(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Pearson_correlation_coefficient_rxc_bca(n)

## End(Not run)
```

`Pearson_LR_homogeneity_test_stratified_2x2` *The Pearson chi-squared and likelihood ratio tests for homogeneity over strata*

Description

The Pearson chi-squared and likelihood ratio tests for homogeneity over strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Pearson_LR_homogeneity_test_stratified_2x2(
  n,
  link = "logit",
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the test statistic and the degrees of freedom for the likelihood ratio and the Pearson chi-squared tests

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Pearson_LR_homogeneity_test_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Pearson_LR_homogeneity_test_stratified_2x2(n)
```

`Pearson_LR_tests_cum_OR_2xc` *The Pearson chi-squared and likelihood ratio tests for cumulative ORs in 2xc tables*

Description

The Pearson chi-squared and likelihood ratio tests for cumulative ORs in 2xc tables

Described in Chapter 6 "The Ordered 2xc Table"

Usage

```
Pearson_LR_tests_cum_OR_2xc(n, direction = "decreasing", printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2xc matrix)
`direction`	the direction of column probabilities ("increasing" or "decreasing")
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing the two-sided p-value and the test statistic for the likelihood ratio and the Pearson chi-squared tests

Examples

```
# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
Pearson_LR_tests_cum_OR_2xc(n)
```

`Pearson_LR_tests_rxc` *The Pearson chi-squared and likelihood ratio tests for association in rxc tables*

Description

The Pearson chi-squared and likelihood ratio tests for association in rxc tables

Described in Chapter 7 "The rxc Table"

Usage

```
Pearson_LR_tests_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rxc matrix)
`printresults`	display results

Value

A list containing the two-sided p-value, the test statistic and the degrees of freedom for the likelihood ratio and the Pearson chi-squared tests

Examples

```
# Examples from Chapter 5 (ordered rx2 tables)


## Alcohol consumption and malformations (Mills and Graubard, 1987):

n <- matrix(
  c(48, 17066, 38, 14464, 5, 788, 1, 126, 1, 37),
  byrow = TRUE, ncol = 2
)
Pearson_LR_tests_rxc(n)

## Elevated troponin T levels in stroke patients (Indredavik et al., 2008):

n <- matrix(c(8, 53, 10, 48, 11, 100, 22, 102, 6, 129), byrow = TRUE, ncol = 2)
Pearson_LR_tests_rxc(n)


# Examples from Chapter 6 (ordered 2xc tables)
## The Adolescent Placement Study (Fontanella et al., 2008):

n <- matrix(c(8, 28, 72, 126, 46, 73, 69, 86), byrow = TRUE, ncol = 4)
Pearson_LR_tests_rxc(n)

## Postoperative nausea (Lydersen et al., 2012a):

n <- matrix(c(14, 10, 3, 2, 11, 7, 8, 4), byrow = TRUE, ncol = 4)
Pearson_LR_tests_rxc(n)


# Examples from Chapter 7 (unordered rxc tables)

## Treatment for ear infection (van Balen et al., 2003):

n <- matrix(c(40, 25, 54, 7, 63, 10), byrow = TRUE, ncol = 2)
Pearson_LR_tests_rxc(n)

## Psychiatric diagnoses vs PA (Mangerud et al., 2004):
n <- matrix(
  c(62, 21, 97, 48, 10, 12, 30, 7, 132, 78, 34, 17),
  byrow = TRUE, ncol = 2
)
Pearson_LR_tests_rxc(n)

## Psychiatric diag. vs BMI (Mangerud et al., 2004):
n <- matrix(
  c(3, 55, 23, 8, 102, 36, 6, 14, 1, 5, 21, 12, 19, 130, 64, 7, 26, 18),
  byrow = TRUE, ncol = 3
)
Pearson_LR_tests_rxc(n)
```

`Pearson_LR_tests_unspecific_ordering_rx2`

The Pearson chi-squared and likelihood ratio tests for unspecific ordering in rx2 tables

---

Description

The Pearson chi-squared and likelihood ratio tests for unspecific ordering in rx2 tables. Described in Chapter 5 "The Ordered rx2 Table". May also be used for 2xc tables, after flipping rows and columns (i.e. if n is a 2xc table, call this function with n' (the transpose of n) as the first argument).

Usage

```
Pearson_LR_tests_unspecific_ordering_rx2(n, direction, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`direction`	the direction of the success probabilities ("increasing" or "decreasing")
`printresults`	display results

Value

A list containing the two-sided p-value and the test statistic for the likelihood ratio and the Pearson chi-squared tests

Examples

```
# Chapter 5: Alcohol consumption and malformations (Mills and Graubard, 1987)
n <- matrix(
  c(48, 17066, 38, 14464, 5, 788, 1, 126, 1, 37),
  byrow = TRUE, ncol = 2
)
Pearson_LR_tests_unspecific_ordering_rx2(n, "increasing")

# Chapter 5: Elevated troponin T levels in stroke patients (Indredavik et al., 2008)
n <- matrix(c(8, 53, 10, 48, 11, 100, 22, 102, 6, 129), byrow = TRUE, ncol = 2)
Pearson_LR_tests_unspecific_ordering_rx2(n, "decreasing")

# Chapter 6: Postoperative nausea (Lydersen et al., 2012a)
n <- t(matrix(c(14, 10, 3, 2, 11, 7, 8, 4), byrow = TRUE, ncol = 4))
Pearson_LR_tests_unspecific_ordering_rx2(n, "decreasing")
```

`Pearson_LR_test_common_effect_stratified_2x2` *The Pearson chi-squared and likelihood ratio tests of a common difference*

Description

The Pearson chi-squared and likelihood ratio tests of a common difference

between probabilities (link = 'linear'), ratio of probabilities (link =

'log'), or odds ratio (link = 'logit')

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Pearson_LR_test_common_effect_stratified_2x2(
  n,
  link = "logit",
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`link`	the link function ('linear', 'log', or 'logit')
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the test statistic and the degrees of freedom for the likelihood ratio and the Pearson chi-squared tests

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Pearson_LR_test_common_effect_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
```

```
Pearson_LR_test_common_effect_stratified_2x2(n)
```

`Pearson_residuals_rxc` *The Pearson residuals and the standardized Pearson residuals*

Description

The Pearson residuals and the standardized Pearson residuals

Described in Chapter 7 "The rxc Table"

Usage

```
Pearson_residuals_rxc(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing matrices of the Pearson residuals and the standardized Pearson residuals

Examples

```
# Treatment for ear infection (van Balen et al., 2003)
n <- matrix(c(40, 25, 54, 7, 63, 10), ncol = 2, byrow = TRUE)
Pearson_residuals_rxc(n)

# Psychiatric diagnoses vs PA (Mangerud et al., 2004)
n <- matrix(
  c(62, 21, 97, 48, 10, 12, 30, 7, 132, 78, 34, 17),
  ncol = 2, byrow = TRUE
)
Pearson_residuals_rxc(n)

# Psychiatric diag. vs BMI (Mangerud et al., 2004)
n <- rbind(
  c(3, 55, 23), c(8, 102, 36), c(6, 14, 1),
  c(5, 21, 12), c(19, 130, 64), c(7, 26, 18)
)
Pearson_residuals_rxc(n)
```

`Peto_homogeneity_test_stratified_2x2` *The Peto test for homogeneity of odds ratios over strata*

Description

The Peto test for homogeneity of odds ratios over strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Peto_homogeneity_test_stratified_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the statistic and the degrees of freedom

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Peto_homogeneity_test_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Peto_homogeneity_test_stratified_2x2(n)
```

`Peto_OR_estimate_stratified_2x2`

The Peto estimate of the common odds ratio across strata

Description

The Peto estimate of the common odds ratio across strata

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Peto_OR_estimate_stratified_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the Peto odds ratio estimate, its conditional expectation (from the hypergeometric distribution) and the variance

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Peto_OR_estimate_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Peto_OR_estimate_stratified_2x2(n)
```

`PriceBonett_approximate_Bayes_CI_2x2` *The Price-Bonett approximate Bayes confidence interval for the ratio of probabilities*

Description

The Price-Bonett approximate Bayes confidence interval for the ratio of probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
PriceBonett_approximate_Bayes_CI_2x2(
  n,
  a = 1.25,
  b = 2.5,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`a, b`	parameters of the beta distribution
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
PriceBonett_approximate_Bayes_CI_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
PriceBonett_approximate_Bayes_CI_2x2(n)
```

`QuesenberryHurst_Wilson_score_CIs_1xc`
The Quesenberry-Hurst Wilson score simultaneous intervals for the multinomial probabilities

---

Description

The Quesenberry-Hurst Wilson score simultaneous intervals for the multinomial probabilities (with Scheffe adjustment)

Described in Chapter 3 "The 1xc Table and the Multinomial Distribution"

Usage

```
QuesenberryHurst_Wilson_score_CIs_1xc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
QuesenberryHurst_Wilson_score_CIs_1xc(n = c(276, 380, 118))
```

`RBG_test_and_CI_stratified_2x2`
The RBG test and CI for a common odds ratio

Description

The RBG test and CI for a common odds ratio

(A Wald-type test and CI based on the Mantel-Haenszel estimate)

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
RBG_test_and_CI_stratified_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value (`P`), the Wald test statistic (`Z`), the confidence limits (`L` and `U`), the Mantel-Haenszel overall estimate (`thetahatMH`) and the standard error (`SElog`).

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
RBG_test_and_CI_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
RBG_test_and_CI_stratified_2x2(n)
```

`Scheffe_type_CIs_paired_cxc` *ScheffE-type confidence intervals for differences of marginal probabilities*

Description

ScheffE-type confidence intervals for differences of marginal probabilities

Described in Chapter 9 "The Paired kxk Table"

Usage

```
Scheffe_type_CIs_paired_cxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
Scheffe_type_CIs_paired_cxc(n)
```

`Scheffe_type_CIs_rxc` *The ScheffE-type simultaneous confidence intervals for the differences pi_1|i - pi_1|j*

Description

The ScheffE-type simultaneous confidence intervals for the differences pi_1|i - pi_1|j

Described in Chapter 7 "The rxc Table"

Usage

```
Scheffe_type_CIs_rxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (an rx2 vector)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Example: Treatment for ear infection
n <- rbind(c(40, 25), c(54, 7), c(63, 10))
Scheffe_type_CIs_rxc(n)
```

`Score_test_1x2` *The score test for the binomial probability (pi)*

Description

The score test for the binomial probability (pi) H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided) Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Score_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing the two-sided p-value and the score test statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010, adapted)
Score_test_1x2(X = 250, n = 533, pi0 = .5)
# The number of 2nd order male births (Singh et al. 2010, adapted)
Score_test_1x2(X = 204, n = 412, pi0 = .5)
# The number of 3rd order male births (Singh et al. 2010, adapted)
Score_test_1x2(X = 103, n = 167, pi0 = .5)
# The number of 4th order male births (Singh et al. 2010, adapted)
Score_test_1x2(X = 33, n = 45, pi0 = .5)
# Ligarden et al. (2010, adapted)
Score_test_1x2(X = 13, n = 16, pi0 = .5)
```

`Score_test_and_CI_marginal_mean_scores_paired_cxc` *Score test and CI marginal mean scores paired CxC*

Description

The score test and confidence interval for the difference between marginal mean scores Described in Chapter 9 "The Paired cxc Table"

Usage

```
Score_test_and_CI_marginal_mean_scores_paired_cxc(
  n,
  a,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a cxc matrix)
`a`	scores assigned to the outcome categories
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A list containing the two-sided p-value, the score test statistic, the confidence limits and the estimate of the difference between marginal mean scores

Examples

```
# A comparison between serial and retrospective measurements
# (Fischer et al., 1999)
n <- rbind(
  c(1, 0, 1, 0, 0),
  c(0, 2, 8, 4, 4),
  c(1, 1, 31, 14, 11),
  c(1, 0, 15, 9, 12),
  c(0, 0, 2, 1, 3)
)
a <- c(8, 3.5, 0, -3.5, -8)
Score_test_and_CI_marginal_mean_scores_paired_cxc(n, a)
```

`Score_test_CC_1x2` *The score test with continuity correction for the*

Description

The score test with continuity correction for the binomial probability (pi). H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided). Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Score_test_CC_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

X	the number of successes
n	the total number of observations
pi0	a given probability
printresults	display results (0 = no, 1 = yes)

Value

A vector containing the two-sided p-value and the score test statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010, adapted)
Score_test_CC_1x2(X = 250, n = 533, pi0 = .5)
# The number of 2nd order male births (Singh et al. 2010, adapted)
Score_test_CC_1x2(X = 204, n = 412, pi0 = .5)
# The number of 3rd order male births (Singh et al. 2010, adapted)
Score_test_CC_1x2(X = 103, n = 167, pi0 = .5)
# The number of 4th order male births (Singh et al. 2010, adapted)
Score_test_CC_1x2(X = 33, n = 45, pi0 = .5)
# Ligarden et al. (2010, adapted)
Score_test_CC_1x2(X = 13, n = 16, pi0 = .5)
```

`Score_test_for_effect_in_the_probit_model_2xc`

Score test for effect in the cumulative probit model

Description

The score test for effect in the cumulative probit model described in Chapter 6 "The Ordered 2xc Table"

Usage

```
Score_test_for_effect_in_the_probit_model_2xc(
  n,
  alphahat0,
  printresults = TRUE
)
```

Arguments

n	the observed counts (a 2xc matrix)
alphahat0	a column vector with c-1 estimated coefficients (`alpha_j`) under the null hypothesis (`beta = 0`)
printresults	display results (F = no, T = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Note

Must give the alphahats under the null hypothesis as input, because Matlab does not calculate an intercept-only probit model (and this may apply to R code as well). alphahat0 can be calculated in, for instance, Stata.

Examples

```
# The Adolescent Placement Study (Fontanella et al., 2008)
n <- rbind(c(8, 28, 72, 126), c(46, 73, 69, 86))
alphahat0 <- c(-1.246452, -0.5097363, 0.2087471)
Score_test_for_effect_in_the_probit_model_2xc(n, alphahat0)

# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
alphahat0 <- c(-0.1923633, 0.5588396, 1.271953)
Score_test_for_effect_in_the_probit_model_2xc(n, alphahat0)
```

`Spearman_correlation_coefficient_rxc`

The Spearman correlation coefficient

Description

The Spearman correlation coefficient

Described in Chapter 7 "The rxc Table"

Usage

```
Spearman_correlation_coefficient_rxc(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (an rxc matrix)
`alpha`	the nominal significance level, used to compute a 100(1-alpha)# confidence interval
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the Spearman correlation coefficient, and the Fieller and Bonett-Wright confidence intervals

Examples

```
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
Spearman_correlation_coefficient_rxc(n)
## Not run:
# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Spearman_correlation_coefficient_rxc(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Spearman_correlation_coefficient_rxc(n)

## End(Not run)
```

`Spearman_correlation_coefficient_rxc_bca` *The Spearman correlation coefficient with the bias-corrected and accelerated*

Description

The Spearman correlation coefficient with the bias-corrected and accelerated

boostrap confidence interval

Described in Chapter 7 "The rxc Table"

Usage

```
Spearman_correlation_coefficient_rxc_bca(
  n,
  nboot = 10000,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (an rxc matrix)
`nboot`	number of bootstrap samples

`alpha`	the nominal significance level, used to compute a 100(1-alpha) confidence interval
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the statistic and the confindence interval limits

Examples

```
## Not run:
# Colorectal cancer (Table 7.7)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)

Spearman_correlation_coefficient_rxc_bca(n)
# Breast Tumor (Table 7.8)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  ncol = 5, byrow = TRUE
)
Spearman_correlation_coefficient_rxc_bca(n)

# Self-rated health (Table 7.9)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  ncol = 4, byrow = TRUE
)
Spearman_correlation_coefficient_rxc_bca(n)

## End(Not run)
```

`stratified_2x2_tables` *Stratified 2x2 tables*

Description

Stratified 2x2 tables

Usage

```
stratified_2x2_tables(n, alpha = 0.05)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs

Value

A string of "-". This function should be called for its printed output

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
stratified_2x2_tables(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
stratified_2x2_tables(n)
```

`Stuart_test_paired_cxc`

The Stuart test for marginal homogeneity

Description

The Stuart test for marginal homogeneity

Described in Chapter 9 "The Paired cxc Table"

Usage

```
Stuart_test_paired_cxc(n, printresults = TRUE)
```

Arguments

`n`	the observed table (a cxc matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the probability, the statistic and the degrees of freedom

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
Stuart_test_paired_cxc(n)
```

`Tango_asymptotic_score_CI_paired_2x2`

The Tango asymptotic score confidence interval for the difference between paired probabilities

---

Description

The Tango asymptotic score confidence interval for the difference between paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Tango_asymptotic_score_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Tango_asymptotic_score_CI_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Tango_asymptotic_score_CI_paired_2x2(n)
```

`Tang_asymptotic_score_CI_paired_2x2`

The Tang asymptotic score confidence interval for the ratio of paired probabilities

---

Description

The Tang asymptotic score confidence interval for the ratio of paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Tang_asymptotic_score_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Tang_asymptotic_score_CI_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Tang_asymptotic_score_CI_paired_2x2(n)
```

`the_1x2_table_CIs` *The 1x2 Table CIs*

Description

The 1x2 Table CIs

Usage

```
the_1x2_table_CIs(X, n, alpha = 0.05)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs

Value

NULL. This function should be called for its printed output

Examples

```
# The number of 1st order male births (Singh et al. 2010)
the_1x2_table_CIs(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
the_1x2_table_CIs(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
the_1x2_table_CIs(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
the_1x2_table_CIs(X = 33, n = 45)
# Ligarden et al. (2010)
the_1x2_table_CIs(X = 13, n = 16)
```

`the_1x2_table_tests` *The 1x2 Table tests*

Description

The 1x2 Table tests

Usage

```
the_1x2_table_tests(X, n, pi0)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability

Value

NULL. This function should be called for its printed output

Examples

```
# Example: The number of 1st order male births (Singh et al. 2010)
the_1x2_table_tests(X = 250, n = 533, pi0 = 0.513)
# Example: The number of 2nd order male births (Singh et al. 2010)
the_1x2_table_tests(X = 204, n = 412, pi0 = 0.513)
# Example: The number of 3rd order male births (Singh et al. 2010)
the_1x2_table_tests(X = 103, n = 167, pi0 = 0.513)
# Example: The number of 4th order male births (Singh et al. 2010)
the_1x2_table_tests(X = 33, n = 45, pi0 = 0.513)
# Example: Ligarden et al. (2010)
the_1x2_table_tests(X = 13, n = 16, pi0 = 0.5)
```

`the_1xc_table_CIs` *The 1xc table CIs*

Description

The 1xc table CIs

Usage

```
the_1xc_table_CIs(n, alpha = 0.05)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`alpha`	the nominal level, e.g. 0.05 for 95# CIs

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
the_1xc_table_CIs(n = c(276, 380, 118))
```

`the_1xc_table_tests` *The 1xc table tests*

Description

The 1xc table tests

Usage

```
the_1xc_table_tests(n, pi0, chacko.test = FALSE)
```

Arguments

`n`	the observed counts (a 1xc vector, where c is the number of categories)
`pi0`	given probabilities (a 1xc vector)
`chacko.test`	if TRUE, only performs the Chacko test

Value

NULL. This function should be called for its printed output

Examples

```
# Genotype counts for SNP rs 6498169 in RA patients
the_1xc_table_tests(n = c(276, 380, 118), pi0 = c(0.402, 0.479, 0.119))
# subset of 10 patients
the_1xc_table_tests(n = c(6, 1, 3), pi0 = c(0.402, 0.479, 0.119))
# Example for the Chacko test: Hypothetical experiment
the_1xc_table_tests(n = c(1, 4, 3, 11, 9), pi0 = c(0.402, 0.479, 0.119), TRUE)
```

`the_2x2_table_CIs_difference`

The 2x2 table CIs difference

Description

Wrapper for `_CI_2x2` functions on Chapter 4.

Usage

```
the_2x2_table_CIs_difference(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string of "-". This function should be called for its printed output

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
the_2x2_table_CIs_difference(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
the_2x2_table_CIs_difference(n)
```

`the_2x2_table_CIs_OR` *The 2x2 table CIs odds ratio*

Description

Wrapper for `_CI_OR_2x2` functions on Chapter 4.

Usage

```
the_2x2_table_CIs_OR(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string of "-". This function should be called for its printed output

Examples

```
# Example: A lady tasting a cup of tea
n <- rbind(c(3, 1), c(1, 3))
the_2x2_table_CIs_OR(n)

# Example: Perondi et al. (2004)
n <- rbind(c(7, 27), c(1, 33))
the_2x2_table_CIs_OR(n)

# Example: Lampasona et al. (2013)
n <- rbind(c(9, 4), c(4, 10))
the_2x2_table_CIs_OR(n)

# Example: Ritland et al. (2007)
n <- rbind(c(0, 16), c(15, 57))
the_2x2_table_CIs_OR(n)
```

`the_2x2_table_CIs_ratio` *The 2x2 table CIs ratio*

Description

Wrapper for `_CI_2x2` functions on Chapter 4.

Usage

```
the_2x2_table_CIs_ratio(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string of "-". This function should be called for its printed output

See Also

the_2x2_table_CIs_difference the_2x2_table_CIs_OR the_2x2_table_tests

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
the_2x2_table_CIs_ratio(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
the_2x2_table_CIs_ratio(n)
```

`the_2x2_table_tests` *The 2x2 table tests*

Description

Wrapper for `_test_2x2` functions on Chapter 4.

Usage

```
the_2x2_table_tests(n, gamma = 1e-04)
```

Arguments

`n`	frequency matrix
`gamma`	parameter for the Berger and Boos procedure

Value

The value of gamma. This function should be called for its printed output.

Examples

```
# Example: A lady tasting a cup of tea
n <- rbind(c(3, 1), c(1, 3))
the_2x2_table_tests(n)

# Example: Perondi et al. (2004)
n <- rbind(c(7, 27), c(1, 33))
the_2x2_table_tests(n)

# Example: Lampasona et al. (2013)
n <- rbind(c(9, 4), c(4, 10))
the_2x2_table_tests(n)

# Example: Ritland et al. (2007)
n <- rbind(c(0, 16), c(15, 57))
the_2x2_table_tests(n)
```

`the_2xc_table` *The 2xc table*

Description

The 2xc table

Usage

```
the_2xc_table(n, alpha = 0.05, direction = "increasing")
```

Arguments

`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`direction`	the direction of the success probabilities

Value

A string of "-". This function should be called for its printed output.

Examples

```
## Not run:
# The Adolescent Placement Study (Fontanella et al., 2008)
n <- rbind(c(8, 28, 72, 126), c(46, 73, 69, 86))
the_2xc_table(n)

# Postoperative nausea (Lydersen et al., 2012a)
n <- rbind(c(14, 10, 3, 2), c(11, 7, 8, 4))
```

```
dir <- "decreasing"
the_2xc_table(n, direction = dir)

## End(Not run)
```

---

the_paired_2x2_table_CIs_difference

The Paired 2x2 table CIs difference

Description

The Paired 2x2 table CIs difference

Usage

```
the_paired_2x2_table_CIs_difference(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string of "-". This function should be called for its printed output.

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
the_paired_2x2_table_CIs_difference(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
the_paired_2x2_table_CIs_difference(n)
```

`the_paired_2x2_table_CIs_OR`
The Paired 2x2 table CIs OR

Description

The Paired 2x2 table CIs OR

Usage

```
the_paired_2x2_table_CIs_OR(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string of "-". This function should be called for its printed output.

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
the_paired_2x2_table_CIs_OR(n)
```

`the_paired_2x2_table_CIs_ratio`
The Paired 2x2 table CIs ratio

Description

The Paired 2x2 table CIs ratio

Usage

```
the_paired_2x2_table_CIs_ratio(n, alpha = 0.05)
```

Arguments

`n`	frequency matrix
`alpha`	type I error

Value

A string containing the last line of the printed text. This function should be called for its printed output.

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
the_paired_2x2_table_CIs_ratio(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
the_paired_2x2_table_CIs_ratio(n)
```

`the_paired_2x2_table_tests`

The Paired 2x2 table tests

Description

The Paired 2x2 table tests

Usage

```
the_paired_2x2_table_tests(n, gamma = 1e-04)
```

Arguments

`n`	frequency matrix
`gamma`	parameter for the Berger and Boos procedure

Value

The value of gamma. This function should be called for its printed output.

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
the_paired_2x2_table_tests(n)

## Not run:
# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
```

```
the_paired_2x2_table_tests(n)

#' # Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
the_paired_2x2_table_tests(n)

## End(Not run)
```

`the_paired_cxc_table_nominal`

The Paired CxC table - nominal

Description

The Paired CxC table - nominal

Usage

```
the_paired_cxc_table_nominal(n, alpha = 0.05)
```

Arguments

`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs

Value

A string containing the last line of the printed text. This function should be called for its printed output.

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(c(596, 18, 6, 5), c(0, 2, 0, 0), c(0, 0, 42, 0), c(11, 0, 0, 0))
the_paired_cxc_table_nominal(n)
```

`the_paired_cxc_table_ordinal`

The Paired CxC table - ordinal

Description

The Paired CxC table - ordinal

Usage

```
the_paired_cxc_table_ordinal(n, a, alpha = 0.05)
```

Arguments

`n`	the total number of observations
`a`	scores assigned to the outcome categories
`alpha`	the nominal level, e.g. 0.05 for 95% CIs

Value

A string containing the last line of the printed text. This function should be called for its printed output.

Examples

```
# Pretherapy susceptability of pathogens (Peterson et al., 2007)
n <- rbind(
  c(1, 0, 1, 0, 0),
  c(0, 2, 8, 4, 4),
  c(1, 1, 31, 14, 11),
  c(1, 0, 15, 9, 12),
  c(0, 0, 2, 1, 3)
)
a <- c(8, 3.5, 0, -3.5, -8)
the_paired_cxc_table_ordinal(n, a)
```

`the_rx2_table` *The rx2 table*

Description

The rx2 table

Usage

```
the_rx2_table(n, alpha = 0.05, direction = "increasing", skip_exact = FALSE)
```

Arguments

`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`direction`	the direction of the success probabilities
`skip_exact`	If `FALSE`, skips the exact conditional and mid-P tests for unspecific ordering (often saves calculation time) ("increasing" or "decreasing")

Value

A string of "-". This function should be called for its printed output.

Examples

```
## Not run:

# Alcohol consumption and malformations (Mills and Graubard, 1987)
n.0 <- rbind(c(48, 17066), c(38, 14464), c(5, 788), c(1, 126), c(1, 37))
a.0 <- c(1, 2, 3, 4, 5)
the_rx2_table(n.0, a.0, "increasing")


# Elevated troponin T levels in stroke patients (Indredavik et al., 2008)
n.1 <- rbind(c(8, 53), c(10, 48), c(11, 100), c(22, 102), c(6, 129))
a.1 <- c(7, 22, 37, 48, 55)
the_rx2_table(n.1, a.1, "decreasing")

## End(Not run)
```

`the_rxc_table` *The rxc table*

Description

The rxc table

Usage

```
the_rxc_table(n, alpha = 0.05, nboot = 10000)
```

Arguments

`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`nboot`	number of boostrap samples. If 0, skips tests that use bootstrapping

Value

NULL. This function should be called for its printed output.

Examples

```
## Not run:
# Unordered tables

## Treatment for ear infection (van Balen et al., 2003)
n <- matrix(c(40, 25, 54, 7, 63, 10), byrow = TRUE, ncol = 2)
the_rxc_table(n)

## Psychiatric diagnoses vs PA (Mangerud et al., 2004)
n <- matrix(
```

```
  c(62, 21, 97, 48, 10, 12, 30, 7, 132, 78, 34, 17),
  byrow = TRUE, ncol = 2
)
the_rxc_table(n)

# Singly ordered tables
## Psychiatric diag. vs BMI (Mangerud et al., 2004)
n <- matrix(
  c(3, 55, 23, 8, 102, 36, 6, 14, 1, 5, 21, 12, 19, 130, 64, 7, 26, 18),
  byrow = TRUE, ncol = 3
)
the_rxc_table(n)

## Low birth weight vs psychiatric morbitidy (Lund et al., 2012)
n <- matrix(c(22, 4, 12, 24, 9, 10, 51, 7, 6), byrow = TRUE, ncol = 3)
the_rxc_table(n)

# Doubly ordered tables
# Colorectal cancer (Jullumstroe et al., 2009)
n <- rbind(
  c(2, 4, 29, 19), c(7, 6, 116, 51), c(19, 27, 201, 76), c(18, 22, 133, 54)
)
the_rxc_table(n)

# Breast Tumor (Bofin et al., 2004)
n <- matrix(
  c(15, 35, 6, 9, 6, 2, 4, 2, 11, 11, 0, 0, 1, 10, 21),
  byrow = TRUE, ncol = 5
)
the_rxc_table(n)

# Self-rated health (Breidablik et al., 2008)
n <- matrix(
  c(2, 3, 3, 3, 2, 58, 98, 14, 8, 162, 949, 252, 4, 48, 373, 369),
  byrow = TRUE, ncol = 4
)
the_rxc_table(n)

## End(Not run)
```

`Transformed_Blaker_exact_CI_paired_2x2` *The Transformed Blaker exact confidence interval for the conditional odds ratio*

Description

The Transformed Blaker exact confidence interval for the conditional odds ratio

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Transformed_Blaker_exact_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Transformed_Blaker_exact_CI_paired_2x2(n)
```

`Transformed_Clopper_Pearson_exact_CI_paired_2x2` *The Transformed Clopper-Pearson exact confidence interval for the conditional odds ratio*

Description

The Transformed Clopper-Pearson exact confidence interval for the conditional odds ratio

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Transformed_Clopper_Pearson_exact_CI_paired_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Transformed_Clopper_Pearson_exact_CI_paired_2x2(n)
```

`Transformed_Clopper_Pearson_midP_CI_paired_2x2` *The Transformed Clopper-Pearson mid-P confidence interval for the conditional odds ratio*

Description

The Transformed Clopper-Pearson mid-P confidence interval for the conditional odds ratio

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Transformed_Clopper_Pearson_midP_CI_paired_2x2(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Transformed_Clopper_Pearson_midP_CI_paired_2x2(n)
```

`Transformed_Wilson_score_CI_paired_2x2` *The Transformed Wilson score confidence interval for the conditional odds ratio*

Description

The Transformed Wilson score confidence interval for the conditional odds ratio

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Transformed_Wilson_score_CI_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Transformed_Wilson_score_CI_paired_2x2(n)
```

`Trend_estimate_CI_tests_rx2` *Trend estimate for linear and logit models*

Description

Trend estimate for linear and logit models

- The Wald test and CI
- Likelihood ratio test
- The Pearson goodness-of-fit test
- Likelihood ratio (deviance) goodness-of-fit test

Described in Chapter 5 "The Ordered rx2 Table"

Usage

```
Trend_estimate_CI_tests_rx2(
  n,
  a,
  linkfunction = "logit",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed counts (an rx2 matrix)
`a`	scores assigned to the rows
`linkfunction`	Link function for the binomial distribution see `?family` for more details
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A list containing several test statistics (see description above).

Examples

```
# Alcohol consumption and malformations (Mills and Graubard, 1987)
n <- matrix(
  c(48, 17066, 38, 14464, 5, 788, 1, 126, 1, 37),
  ncol = 2,
  byrow = TRUE
)
n <- rbind(c(48, 17066), c(38, 14464), c(5, 788), c(1, 126), c(1, 37)) # same as before
a <- c(1, 2, 3, 4, 5)
Trend_estimate_CI_tests_rx2(n, a)

# levated troponin T levels in stroke patients (Indredavik et al., 2008)
n <- rbind(c(8, 53), c(10, 48), c(11, 100), c(22, 102), c(6, 129))
a <- c(1, 2, 3, 4, 5)
Trend_estimate_CI_tests_rx2(n, a)
```

`Uncorrected_asymptotic_score_CI_2x2` *The uncorrected asymptotic score confidence interval for the odds ratio*

Description

The uncorrected asymptotic score confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Uncorrected_asymptotic_score_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Uncorrected_asymptotic_score_CI_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Uncorrected_asymptotic_score_CI_2x2(n)
```

`Wald_CI_1x2` *The Wald confidence interval for the binomial probability*

Description

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Wald_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (`FALSE` = no, `TRUE` = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
Wald_CI_1x2(X = 250, n = 533) # The number of 1st order male births (Singh et al. 2010)
Wald_CI_1x2(X = 204, n = 412) # The number of 2nd order male births (Singh et al. 2010)
Wald_CI_1x2(X = 103, n = 167) # The number of 3rd order male births (Singh et al. 2010)
Wald_CI_1x2(X = 33, n = 45) # The number of 4th order male births (Singh et al. 2010)
Wald_CI_1x2(X = 13, n = 16) # Ligarden et al. (2010)
```

`Wald_CI_2x2` *The Wald confidence interval for the difference between probabilities*

Description

The Wald confidence interval for the difference between probabilities

Described in Chapter 4 "The 2x2 Table"

Usage

```
Wald_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004):
Wald_CI_2x2(n = matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE))
# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
Wald_CI_2x2(n = matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE))
```

`Wald_CI_AgrestiMin_paired_2x2`
The Wald confidence interval for the difference between paired probabilities

---

Description

The Wald confidence interval for the difference between paired probabilities

with the pseudo-frequency adjustment suggested by Agresti and Min (2005)

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_AgrestiMin_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Wald_CI_AgrestiMin_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Wald_CI_AgrestiMin_paired_2x2(n)
```

`Wald_CI_BonettPrice_paired_2x2` *The Wald confidence interval for the difference between paired probabilities*

Description

The Wald confidence interval for the difference between paired probabilities

with the pseudo-frequency adjustment suggested by Bonett and Price(2012)

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_BonettPrice_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Wald_CI_BonettPrice_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Wald_CI_BonettPrice_paired_2x2(n)
```

`Wald_CI_CC_1x2` *The Wald CI with CC for the binomial probability*

Description

The Wald confidence interval with continuity correction for the binomial probability. Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Wald_CI_CC_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95# CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Wald_CI_CC_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Wald_CI_CC_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Wald_CI_CC_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Wald_CI_CC_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Wald_CI_CC_1x2(X = 13, n = 16)
```

`Wald_CI_CC_2x2` *The Wald confidence interval for the difference between probabilities*

Description

The Wald confidence interval for the difference between probabilities with Yates's continuity correction. Described in Chapter 4 "The 2x2 Table"

Usage

```
Wald_CI_CC_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A data frame containing lower, upper and point estimates of the statistic

Examples

```
# An RCT of high vs standard dose of epinephrine (Perondi et al., 2004)
n <- matrix(c(7, 27, 1, 33), nrow = 2, byrow = TRUE)
Wald_CI_CC_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007)
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Wald_CI_CC_2x2(n)
```

`Wald_CI_diff_CC_paired_2x2` *The Wald confidence interval for the difference between paired probabilities*

Description

The Wald confidence interval for the difference between paired probabilities

with continuity correction

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_diff_CC_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Wald_CI_diff_CC_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Wald_CI_diff_CC_paired_2x2(n)
```

`Wald_CI_diff_paired_2x2` *The Wald confidence interval for the difference between paired probabilities*

Description

The Wald confidence interval for the difference between paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_diff_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Wald_CI_diff_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
```

```
n <- rbind(c(59, 6), c(16, 80))
Wald_CI_diff_paired_2x2(n)
```

Wald_CI_OR_Laplace_paired_2x2 *The Wald confidence interval for the conditional odds ratio with Laplace adjustment*

Description

The Wald confidence interval for the conditional odds ratio with Laplace adjustment

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_OR_Laplace_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Wald_CI_OR_Laplace_paired_2x2(n)
```

`Wald_CI_OR_paired_2x2` *The Wald confidence interval for the conditional odds ratio*

Description

The Wald confidence interval for the conditional odds ratio

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_OR_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Floppy eyelid syndrome vs obstructive sleep apnea (Ezra et al., 2010)
n <- rbind(c(7, 25), c(2, 68))
Wald_CI_OR_paired_2x2(n)
```

`Wald_CI_ratio_paired_2x2` *The Wald confidence interval for the ratio of paired probabilities*

Description

The Wald confidence interval for the ratio of paired probabilities

Described in Chapter 8 "The Paired 2x2 Table"

Usage

```
Wald_CI_ratio_paired_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing lower, upper and point estimates of the statistic

Examples

```
# Airway hyper-responsiveness before and after stem cell transplantation
# (Bentur et al., 2009)
n <- rbind(c(1, 1), c(7, 12))
Wald_CI_ratio_paired_2x2(n)

# Complete response before and after consolidation therapy
# (Cavo et al., 2012)
n <- rbind(c(59, 6), c(16, 80))
Wald_CI_ratio_paired_2x2(n)
```

`Wald_test_1x2` *The Wald test for the binomial probability (pi)*

Description

The Wald test for the binomial probability (pi)

H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided)

Usage

```
Wald_test_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing the two-sided p-value and the Wald test statistic

Examples

```
# The number of 1st order male births (adapted from Singh et al. 2010)
Wald_test_1x2(X = 250, n = 533, pi0 = 0.1)
# The number of 2nd order male births (adapted from Singh et al. 2010)
Wald_test_1x2(X = 204, n = 412, pi0 = 0.1)
# The number of 3rd order male births (adapted from Singh et al. 2010)
Wald_test_1x2(X = 103, n = 167, pi0 = 0.1)
# The number of 4th order male births (adapted from Singh et al. 2010)
Wald_test_1x2(X = 33, n = 45, pi0 = 0.1)
# Ligarden et al. (2010)
Wald_test_1x2(X = 13, n = 16, pi0 = 0.1)
```

`Wald_test_and_CI_common_diff_stratified_2x2`
The Wald test and CI for a common difference between probabilities

Description

The Wald test and CI for a common difference between probabilities

based on either the Mantel-Haenszel or inverse variance estimate

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Wald_test_and_CI_common_diff_stratified_2x2(
  n,
  estimatetype = "MH",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`estimatetype`	Mantel-Haenszel or inverse variance estimate ('MH' or 'IV')
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the Wald test statistic, and the lower, upper and point estimates for delta

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Wald_test_and_CI_common_diff_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Wald_test_and_CI_common_diff_stratified_2x2(n)
```

`Wald_test_and_CI_common_ratio_stratified_2x2`

The Wald test and CI for a common ratio of probabilities

Description

The Wald test and CI for a common ratio of probabilities

based on either the Mantel-Haenszel or inverse variance estimate

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Wald_test_and_CI_common_ratio_stratified_2x2(
  n,
  estimatetype = "MH",
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`estimatetype`	Mantel-Haenszel or inverse variance estimate ('MH' or 'IV')
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the Wald test statistic, and the lower, upper and point estimates for phi

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Wald_test_and_CI_common_ratio_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Wald_test_and_CI_common_ratio_stratified_2x2(n)
```

`Wald_test_and_CI_marginal_mean_ranks_paired_cxc`

The Wald test and confidence interval for the difference between marginal mean ranks / ridits

---

Description

The Wald test and confidence interval for the difference between marginal mean ranks / ridits

Described in Chapter 9 "The Paired cxc Table"

Usage

```
Wald_test_and_CI_marginal_mean_ranks_paired_cxc(
  n,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a cxc matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the test statistic estimates

Examples

```
# A comparison between serial and retrospective measurements
# (Fischer et al., 1999)
n <- rbind(
  c(1, 0, 1, 0, 0),
  c(0, 2, 8, 4, 4),
  c(1, 1, 31, 14, 11),
  c(1, 0, 15, 9, 12),
  c(0, 0, 2, 1, 3)
)
Wald_test_and_CI_marginal_mean_ranks_paired_cxc(n)
```

`Wald_test_and_CI_marginal_mean_scores_paired_cxc` *The Wald test and confidence interval for the difference between marginal mean scores*

Description

The Wald test and confidence interval for the difference between marginal mean scores

Described in Chapter 9 "The Paired cxc Table"

Usage

```
Wald_test_and_CI_marginal_mean_scores_paired_cxc(
  n,
  a,
  alpha = 0.05,
  printresults = TRUE
)
```

Arguments

`n`	the observed table (a cxc matrix)
`a`	scores assigned to the outcome categories
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the Wald test and the Wald CI statistics

Examples

```
# A comparison between serial and retrospective measurements
# (Fischer et al., 1999)
n <- rbind(
  c(1, 0, 1, 0, 0),
  c(0, 2, 8, 4, 4),
  c(1, 1, 31, 14, 11),
  c(1, 0, 15, 9, 12),
  c(0, 0, 2, 1, 3)
)
a <- c(8, 3.5, 0, -3.5, -8)
Wald_test_and_CI_marginal_mean_scores_paired_cxc(n, a)
```

`Wald_test_CC_1x2` *The Wald test with continuity correction for the binomial probability (pi)*

Description

The Wald test with continuity correction for the binomial probability (pi)

H_0: pi = pi0 vs H_A: pi ~= pi0 (two-sided)

Usage

```
Wald_test_CC_1x2(X, n, pi0, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`pi0`	a given probability
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing the two-sided p-value and the Wald test statistic

Examples

```
# The number of 1st order male births (adapted from Singh et al. 2010)
Wald_test_CC_1x2(X = 250, n = 533, pi0 = 0.1)
# The number of 2nd order male births (adapted from Singh et al. 2010)
Wald_test_CC_1x2(X = 204, n = 412, pi0 = 0.1)
# The number of 3rd order male births (adapted from Singh et al. 2010)
Wald_test_CC_1x2(X = 103, n = 167, pi0 = 0.1)
# The number of 4th order male births (adapted from Singh et al. 2010)
Wald_test_CC_1x2(X = 33, n = 45, pi0 = 0.1)
# Ligarden et al. (2010)
Wald_test_CC_1x2(X = 13, n = 16, pi0 = 0.1)
```

`Wilson_score_CI_1x2` *The Wilson score confidence interval*

Description

The Wilson score confidence interval

Usage

```
Wilson_score_CI_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (F = no, T = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Reference Wilson EB (1927) Probable inference, the law of succession, and statistical inference. Journal of the American Statistical Association 22209-212

Examples

```
# birth order 1, Singh et al. (2010)
Wilson_score_CI_1x2(X = 250, n = 533)
# birth order 2, Singh et al. (2010)
Wilson_score_CI_1x2(X = 204, n = 412)
# birth order 3, Singh et al. (2010)
Wilson_score_CI_1x2(X = 103, n = 167)
# birth order 4, Singh et al. (2010)
Wilson_score_CI_1x2(X = 33, n = 45)
# Ligarden (2010)
Wilson_score_CI_1x2(X = 13, n = 16)
```

`Wilson_score_CI_CC_1x2` *The Wilson score confidence interval with continuity correction for the binomial probability*

Description

Described in Chapter 2 "The 1x2 Table and the Binomial Distribution"

Usage

```
Wilson_score_CI_CC_1x2(X, n, alpha = 0.05, printresults = TRUE)
```

Arguments

`X`	the number of successes
`n`	the total number of observations
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (0 = no, 1 = yes)

Value

A vector containing lower, upper and point estimates of the statistic

References

Reference Wilson EB (1927) Probable inference, the law of succession, and statistical inference. Journal of the American Statistical Association; 22209-212

Examples

```
# The number of 1st order male births (Singh et al. 2010)
Wilson_score_CI_CC_1x2(X = 250, n = 533)
# The number of 2nd order male births (Singh et al. 2010)
Wilson_score_CI_CC_1x2(X = 204, n = 412)
# The number of 3rd order male births (Singh et al. 2010)
Wilson_score_CI_CC_1x2(X = 103, n = 167)
# The number of 4th order male births (Singh et al. 2010)
Wilson_score_CI_CC_1x2(X = 33, n = 45)
# Ligarden et al. (2010)
Wilson_score_CI_CC_1x2(X = 13, n = 16)
```

`Woolf_logit_CI_2x2` *The Woolf logit confidence interval for the odds ratio*

Description

The Woolf logit confidence interval for the odds ratio

Described in Chapter 4 "The 2x2 Table"

Usage

```
Woolf_logit_CI_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2 matrix)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A vector containing lower, upper and point estimates of the statistic

Examples

```
# A case-control study of GADA exposure on IPEX syndrome (Lampasona et al., 2013):
n <- matrix(c(9, 4, 4, 10), nrow = 2, byrow = TRUE)
Woolf_logit_CI_2x2(n)

# The association between CHRNA4 genotype and XFS (Ritland et al., 2007):
n <- matrix(c(0, 16, 15, 57), nrow = 2, byrow = TRUE)
Woolf_logit_CI_2x2(n)
```

`Woolf_test_and_CI_stratified_2x2`
The Woolf test and CI for a common odds ratio

Description

The Woolf test and CI for a common odds ratio

(A Wald-type test and CI based on the inverse variance estimate)

Described in Chapter 10 "Stratified 2x2 Tables and Meta-Analysis"

Usage

```
Woolf_test_and_CI_stratified_2x2(n, alpha = 0.05, printresults = TRUE)
```

Arguments

`n`	the observed table (a 2x2xk matrix, where k is the number of strata)
`alpha`	the nominal level, e.g. 0.05 for 95% CIs
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A list containing the two-sided p-value, the Wald test statistic, and the lower, upper and point estimate thetahatIV

Examples

```
# Smoking and lung cancer (Doll and Hill, 1950)
n <- array(dim = c(2, 2, 2))
n[, , 1] <- matrix(c(647, 622, 2, 27), 2, byrow = TRUE)
n[, , 2] <- matrix(c(41, 28, 19, 32), 2, byrow = TRUE)
Woolf_test_and_CI_stratified_2x2(n)

# Prophylactice use of Lidocaine in myocardial infarction (Hine et al., 1989)
n <- array(0, dim = c(2, 2, 6))
n[, , 1] <- rbind(c(2, 37), c(1, 42))
n[, , 2] <- rbind(c(4, 40), c(4, 40))
n[, , 3] <- rbind(c(6, 101), c(4, 106))
n[, , 4] <- rbind(c(7, 96), c(5, 95))
n[, , 5] <- rbind(c(7, 103), c(3, 103))
n[, , 6] <- rbind(c(11, 143), c(4, 142))
Woolf_test_and_CI_stratified_2x2(n)
```

`Z_unpooled_test_2x2` *The Z-unpooled test for association in 2x2 tables*

Description

The Z-unpooled test for association in 2x2 tables

Described in Chapter 4 "The 2x2 Table"

Usage

```
Z_unpooled_test_2x2(n, printresults = TRUE)
```

Arguments

`n`	the observed counts (a 2x2 matrix)
`printresults`	display results (FALSE = no, TRUE = yes)

Value

A vector containing the two-sided p-value and the unpooled Z statistic

Examples

```
# Example: A lady tasting a cup of tea
n <- rbind(c(3, 1), c(1, 3))
Z_unpooled_test_2x2(n)

# Example: Perondi et al. (2004)
n <- rbind(c(7, 27), c(1, 33))
Z_unpooled_test_2x2(n)

# Example: Lampasona et al. (2013)
n <- rbind(c(9, 4), c(4, 10))
Z_unpooled_test_2x2(n)

# Example: Ritland et al. (2007)
n <- rbind(c(0, 16), c(15, 57))
Z_unpooled_test_2x2(n)
```

Index