Package ‘cvequality’

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Type Package

Title Tests for the Equality of Coefficients of Variation from Multiple Groups

Version 0.2.0

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Description Contains functions for testing for significant differences between multiple coefficients of variation. Includes Feltz and Miller's (1996) <DOI:10.1002/(SICI)1097-0258(19960330)15:6%3C647::AID-SIM184%3E0.CO;2-P> asymptotic test and Krishnamoorthy and Lee's (2014) <DOI:10.1007/s00180-013-0445-2> modified signed-likelihood ratio test. See the vignette for more, including full details of citations.

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests knitr, ggplot2, rmarkdown, testthat, dplyr, tidyr, ggbeeswarm, covr

VignetteBuilder knitr

URL https://github.com/benmarwick/cvequality

BugReports https://github.com/benmarwick/cvequality/issues

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NeedsCompilation no

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Repository CRAN

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Asymptotic test for the equality of coefficients of variation from k populations, using measurement data

Description


Usage

asymptotic_test(x, y, seed)

Arguments

x a numeric vector containing individual measurement values
y a vector of any type containing a grouping variable
seed optional, an integer that is the starting point used in the generation of a sequence of random numbers. Include a seed if you want reproducible output.

Value

a list with the test statistic and p-value

Examples

```r
y <- unlist(lapply(letters[1:5], function(i) rep(i, 20)))
x <- rnorm(100)

asymptotic_test(x, y)
```
asymptotic_test2

Asymptotic test for the equality of coefficients of variation from k populations, using summary statistics when raw measurement data are not available.

Description


Usage

asymptotic_test2(k, n, s, x, seed)

Arguments

k

a numeric vector the number of groups

n

a numeric vector the number of measurements in each group

s

a numeric vector the standard deviation of each group

x

a numeric vector the mean of each group

seed

optional, an integer that is the starting point used in the generation of a sequence of random numbers. Include a seed if you want reproducible output.

Value

a list with the test statistic and p-value

Examples

# Summary stats from Feltz and Miller 1996

miller <- data.frame(test = c('ELISA', 'WEHI', \"Viral inhibition\"),
                      Mean = c(6.8, 8.5, 6.0),
                      CV = c(0.090, 0.462, 0.340),
                      N = c(5, 5, 5))

# compute SD from mean and cv
miller$SD <- with(miller, CV * Mean)

asymptotic_test2(k = nrow(miller), n = miller$N, s = miller$SD, x = miller$Mean)
**LRT_STAT**  
*LRT_STAT, required by mlr_test*

**Description**  
LRT_STAT, required by mlr_test

**Usage**  
LRT_STAT(n, x, s, seed)

**Arguments**
- **n**  
  ... as above
- **x**  
  ...
- **s**  
  ...
- **seed**  
  optional, an integer that is the starting point used in the generation of a sequence of random numbers. Include a seed if you want reproducible output.

**Value**  
xx

**mslr_test**  
*Modified signed-likelihood ratio test (SLRT) for equality of CVs, using measurement data*

**Description**  
Modified signed-likelihood ratio test (SLRT) for equality of CVs, using measurement data

**Usage**  
mslr_test(nr = 1000, x, y, seed)

**Arguments**
- **nr**  
  numeric vector length one, number of simulation runs, default is 1e3
- **x**  
  a numeric vector containing individual measurement values
- **y**  
  a vector of any type containing a grouping variable
- **seed**  
  optional, an integer that is the starting point used in the generation of a sequence of random numbers. Include a seed if you want reproducible output.
**mslr_test2**

**Value**

a list with the test statistic and p-value

**References**


**Examples**

```r
x <- rnorm(100)
y <- unlist(lapply(letters[1:5], function(i) rep(i, 20)))
mslr_test(nr = 1e3, x, y)
```

**Description**

# Modified signed-likelihood ratio test (SLRT) for equality of CVs, using summary statistics when raw measurement data are not available.

**Usage**

`mslr_test2(nr, n, x, s, seed)`

**Arguments**

- `nr` numeric vector length one, number of simulation runs
- `n` a numeric vector, the number of observations in each group
- `x` a numeric vector, the mean of each group
- `s` a numeric vector, the standard deviation of each group
- `seed` optional, an integer that is the starting point used in the generation of a sequence of random numbers. Include a seed if you want reproducible output.

**Value**

a list with the test statistic and p-value

**References**

Examples

# Summary stats from Feltz and Miller 1996

miller <- data.frame(test = c('ELISA', 'WEHI', 'Viral inhibition'),
                     Mean = c(6.8, 8.5, 6.0),
                     CV = c(0.090, 0.462, 0.340),
                     N = c(5, 5, 5))

# compute SD from mean and cv
miller$SD <- with(miller, CV * Mean)

mslr_test2(nr = 1e3, n = miller$N, s = miller$SD, x = miller$Mean)
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