Package ‘cvequality’

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Type Package

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

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Maintainer Ben Marwick <benmarwick@gmail.com>


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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

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

VignetteBuilder knitr

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

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

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Author Ben Marwick [aut, cre], Kalimuthu Krishnamoorthy [aut]

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asymptotic_test

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asymptotic_test  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

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 nume 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 mlrt_test**

**Description**

LRT_STAT, required by mlrt_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

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**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.
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

```r
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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