

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%3E3.0.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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asymptotic_test	<i>Asymptotic test for the equality of coefficients of variation from k populations, using measurement data</i>
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Description

Test for k samples (k sample populations with unequal sized) from Feltz CJ, Miller GE (1996) An asymptotic test for the equality of coefficients of variation from k population. Stat Med 15:647–658

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

Test for k samples (k sample populations with unequal sized) from Feltz CJ, Miller GE (1996) An asymptotic test for the equality of coefficients of variation from k population. Stat Med 15:647–658

Usage

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

Arguments

k	a numeric vector the number of groups
n	a numeric vector the numer 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	<i>LRT_STAT, required by mlrt_test</i>
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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

mslr_test	<i>Modified signed-likelihood ratio test (SLRT) for equality of CVs, using measurement data</i>
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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

<http://link.springer.com/article/10.1007/s00180-013-0445-2> Krishnamoorthy, K. & Lee, M. Comput Stat (2014) 29: 215. doi:10.1007/s00180-013-0445-2

Examples

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

mslr_test(nr = 1e3, x, y)
```

mslr_test2	<i># Modified signed-likelihood ratio test (SLRT) for equality of CVs, using summary statistics when raw measurement data are not available.</i>
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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

<http://link.springer.com/article/10.1007/s00180-013-0445-2>

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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