

# Package ‘cvequality’

October 12, 2022

**Type** Package

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

**Version** 0.2.0

**Maintainer** Ben Marwick <benmarwick@gmail.com>

**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](https://doi.org/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](https://doi.org/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	<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)
```

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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)
```

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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

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

---

**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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