# 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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**Repository** CRAN

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## `asymptotic_test` *Asymptotic test for the equality of coefficients of variation from k populations, using measurement data*

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

---

### 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` *LRT_STAT, required by mlrt_test*

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

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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 lenght 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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