Package ‘countdata’

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Type Package

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bb.test

The beta-binomial test

Description

Performs the beta-binomial test for count data.

Usage

bb.test(x, tx, group, alternative = c("two.sided", "less", "greater"),
        n.threads = -1, verbose = TRUE)

Arguments

x        A vector or matrix of counts. When x a matrix, the test is performed row by row.
tx       A vector or matrix of the total sample counts. When tx is a matrix, the number of rows must be equal to the number of rows of x.
group    A vector of group indicators.
alternative A character string specifying the alternative hypothesis: "two.sided" (default), "greater" or "less".
n.threads The number of threads to be used. When n.threads is 0, the maximal number of CPU cores is used. When n.threads is -1 (default), one CPU core less than the maximum is used, and so on.
verbose  A logical value. If TRUE (default), status information is printed.

Details

This test is designed for independent samples, two or more groups.

Value

A list with a single component is returned

p.value The p-value of the test.

Author(s)

Thang V. Pham

References

Examples

```r
x <- c(1, 5, 10, 9, 11, 2, 8)

tx <- c(19609, 19053, 19235, 19374, 18868, 19018, 18844, 19271)

group <- c(rep("cancer", 3), rep("normal", 5))

bb.test(x, tx, group)
# p.value = 0.01568598
```

---

**fold.change**  
*Fold change calculation*

**Description**
Calculates the fold changes between two numerical matrices row by row.

**Usage**

```r
fold.change(d1, d2, BIG = 1e4)
```

**Arguments**

- `d1`  
The first data matrix.
- `d2`  
The second data matrix.
- `BIG`  
A number representing a big value of the result, i.e. black-and-white regulation.

**Details**
The two matrices `d1` and `d2` must have the same number of rows. A positive value means up-regulation where the average of `d2` is higher than that of `d1`. Conversely, a negative value means down-regulation where the average of `d1` is higher than that of `d2`. If one group contains all zeros, a positive or negative BIG value is returned.

**Value**
A vector of fold changes is returned.

**Author(s)**
Thang V. Pham

**References**
https://CRAN.R-project.org/package=countdata
Examples

```r
x <- rbind(c(1.5, 1.2, 10.2),
           c(9.1, 2.2, 8.1))
fold.change(x, 2 * x)
  # returns a column vector of 2
fold.change(x, 0.5 * x)
  # returns a column vector of -2
```

---

**ibb.test**  
*The inverted beta-binomial test*

**Description**

Performs the inverted beta-binomial test for paired count data.

**Usage**

```r
ibb.test(x, tx, group, alternative = c("two.sided", "less", "greater"),
         n.threads = -1, BIG = 1e4, verbose = TRUE)
```

**Arguments**

- **x**: A vector or matrix of counts. When `x` is a matrix, the test is performed row by row.
- **tx**: A vector or matrix of the total sample counts. When `tx` is a matrix, the number of rows must be equal to the number of rows of `x`.
- **group**: A vector of group indicators. There should be two groups of equal size. The samples are matched by the order of appearance in each group.
- **alternative**: A character string specifying the alternative hypothesis: "two.sided" (default), "greater" or "less".
- **n.threads**: The number of threads to be used. When `n.threads` is 0, the maximal number of CPU cores is used. When `n.threads` is -1 (default), one CPU core less than the maximum is used, and so on.
- **BIG**: A number representing a big value of the result, i.e. black-and-white regulation.
- **verbose**: A logical value. If `TRUE` (default), status information is printed.

**Details**

This test is designed for paired samples, for example data acquired before and after treatment.
Value

A list of values is returned

- p.value: The p-value of the test.
- fc: An estimation of the common fold change for all sample pairs. A positive value means up-regulation, i.e. the second group is higher, and a negative value down-regulation. A black-and-white regulation is denoted by the BIG value.

Author(s)

Thang V. Pham

References


Examples

```r
x <- c(33, 32, 86, 51, 52, 149)

tx <- c(7742608, 15581382, 20933491, 7126839, 13842297, 14760103)

group <- c(rep("cancer", 3), rep("normal", 3))

ibb.test(x, tx, group)
# p.value = 0.004103636
# fc = 2.137632
```

normalize

Global normalization of count data

**Description**

Normalize a numerical matrix by scaling each column so that the scaled column sums are equal.

**Usage**

```r
normalize(d)
```

**Arguments**

- `d`: A numerical matrix.

**Details**

The average of column sums is computed. A scaling factor is calculated for each column so that the scaled column sum is equal to the computed average value.
Value

A matrix of the same size as \( d \) is returned. The column sums of this matrix are equal.

Author(s)

Thang V. Pham

References


Examples

d <- rbind(c(2.5, 11.2, 7.2),
c(9.1, 2.2, 7.1))

colSums(d)
# 11.6 13.4 14.3

colSums(normalize(d))
# 13.1 13.1 13.1
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