Package ‘countdata’

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Type Package

Title The Beta-Binomial Test for Count Data

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Description The beta-binomial test is used for significance analysis of independent samples by Pham et al. (2010) <doi:10.1093/bioinformatics/btp677>. The inverted beta-binomial test is used for paired sample testing, e.g. pre-treatment and post-treatment data, by Pham and Jimenez (2012) <doi:10.1093/bioinformatics/bts394>.

Depends R (>= 2.10)

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Encoding UTF-8

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

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Contents

`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

Pham TV, Piersma SR, Warmoes M, Jimenez CR (2010) On the beta binomial model for analysis of spectral count data in label-free tandem mass spectrometry-based proteomics. *Bioinformatics*, 26(3):363-369.

Examples

```
x <- c(1, 5, 1, 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

```
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 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

Pham TV (2021). countdata: The Beta-Binomial Test for Count Data. R package version 1.1. https://CRAN.R-project.org/package=countdata

Examples

```
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

```
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

Pham TV, Jimenez CR (2012) An accurate paired sample test for count data. *Bioinformatics*, 28(18):i596-i602.

Examples

```
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

```
normalize(d)
```

Arguments

`d`	A numerical matrix.

Details

The average of column sums is computed. A scaling factor is calculated for each colunm 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

Pham TV (2021). countdata: The Beta-Binomial Test for Count Data. R package version 1.1. https://CRAN.R-project.org/package=countdata

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
```

Index