

Package ‘cometExactTest’

January 29, 2018

Version 0.1.5

Date 2018-01-29

Title Exact Test from the Combinations of Mutually Exclusive Alterations (CoMEt) Algorithm

Author Max Leiserson [aut, cre],
Hsin-Ta Wu [aut],
Fabio Vandin [ctb],
Vivian Hsiao [ctb],
Benjamin Raphael [ctb]

Maintainer Max Leiserson <mdml@cs.umd.edu>

Depends R (>= 3.4.0)

Description An algorithm for identifying combinations of mutually exclusive alterations in cancer genomes. CoMEt represents the mutations in a set M of k genes with a 2^k dimensional contingency table, and then computes the tail probability of observing $T(M)$ exclusive alterations using an exact statistical test.

License MIT + file LICENSE

URL <http://compbio.cs.brown.edu/projects/comet>,
<https://www.r-project.org>

Imports dplyr

NeedsCompilation yes

Repository CRAN

Date/Publication 2018-01-29 19:30:12 UTC

R topics documented:

comet_exact_test 2

Index 3

comet_exact_test *CoMEt exact test for 2^k contingency tables*

Description

This function performs the CoMEt exact test for a given 2^k contingency table.

Usage

```
comet_exact_test(tbl, pvalthresh=1.1, mutmatplot=T)
```

Arguments

tbl is a vector of 2^k non-negative integers (where k is the number of dimensions in your contingency table). We represent each cell of the contingency table as a binary string, and the order of values in the table follows the Least Significant Bit for the binary representation of a given cell. The binary representation for the 2x2 contingency table X for a pair of genes is x00, x01, x10, x11, where x00 is the cell where neither gene is mutated, x01 is the cell where the first gene is mutated and the second is not, etc. Take the following 2x2x2 contingency table as an additional example, where the ordering of the vector is x000, x001, x010, x011, x100, x101, x110, x111.

Table X_M

		Not altered		m ₃	Altered		
		m ₁			m ₁		
		Not altered	Altered		Not altered	Altered	
m ₂	Not altered	x000	x001	m ₂	Not altered	x100	x101
	Altered	x010	x011		Altered	x110	x111

pvalthresh is a float specifying the threshold at which the cometexacttest will halt execution if the P-value being computed is ever more than the threshold.

mutmatplot is a boolean specifying to create mutation matrix of the input table or not. If mutmatplot==T, a file "cometExactTest_plot.pdf" will be created under your working directory.

Examples

```
comet_exact_test(c(33, 10, 10, 1, 10, 0, 0, 1)) # 2^3 test => 0.02303503
```

Index

comet_exact_test, [2](#)