Package: cometExactTest (via r-universe)

September 7, 2024

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.

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

Imports dplyr

NeedsCompilation yes

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

Repository https://mdml.r-universe.dev

RemoteUrl https://github.com/cran/cometExactTest

RemoteRef HEAD

RemoteSha 0426f0cca1b28658a69a78b5a83cd5c866f4f35c

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

Description

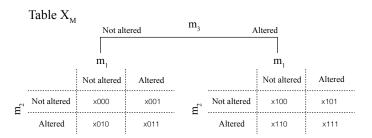This function performs the CoMEt exact test for a given 2^k contingency table.

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

		m_1		m_1	
		Not altered	Altered	Not altered	Altered
m_2	Not altered	x000	x001	x100	x101
m_2	Altered	x010	x011	x110	x111

(columns grouped: Not altered / Altered under m_3)

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
```

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