Package 'cometExactTest'

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

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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

Repository CRAN

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comet_exact_test

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.



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.
is a boolean specifying to create mutation matrix of the input table or not. If
working directory.

Examples

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

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