Package 'CoRe'

May 4, 2020

Type Package

Title CoRe R package

Version 0.1.0

Author Emre Karakoc, Clare Pacini and Francesco Iorio

Maintainer Francesco Iorio <francesco.iorio@sanger.ac.uk>

Description
The CoRe package implements algorithms for the identification of core-fitness and common-essential genes from joint analyses of multiple CRISPR-cas9 (or RNAi) viability screens

License GNU GPLv3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Imports mixdist

R topics documented:

CoRe.generateNullModel

Null model of number of fitness genes across numbers of cell lines and their cumulative sums

---

Description

This function randomly perturbs the binary dependency matrix to generate a null distribution of profiles of fitness genes across fixed number of cell lines, and corresponding null distribution of cumulative sums.

1

Usage

```
CoRe.generateNullModel(depMat,
                        ntrials=1000,
                        display=TRUE)
```

Arguments

depMat   Binary dependency matrix, rows are genes and columns are samples. 1 in po-
                sition *[i,j]* indicates that inactivation of the *i*-th gene exerts a significant loss of
                fitness in the *j*-th sample, 0 otherwise.

ntrials   Integer, default = 1000. How many times to randomly perturb dependency ma-
                trix to generate the null distributions.

display   Boolean, default is TRUE. Should bar plots of the dependency profiles be plotted

Details

For a number of trials specified in (`ntrials`) the inputted binary dependency matrix is randomised,
keeping its column marginal sums. The profiles of fitness genes across fixed number of cell lines,
and corresponding cumulative sums, are returned for each random perturbation.

Value

A list with the following two named vectors:

nullProf   Matrix of number of fitness genes for fixed number of cell lines from. Each rows
                of matrix corresponds to a randomisation trial.

nullCumSum   Matrix of profile of cumulative number of fitness genes in fixed number of cell
                lines. Each row of matrix is one randomisation trial.

Author(s)

C. Pacini, E. Karakoc & F. Iorio

Examples

```
data(exampleDepMat)
pprofile <- CoRe.generateNullModel(depMat = exampleDepMat)
```

CoRe.panessprofile   *Profile of number of fitness genes across fixed numbers of cell lines*
                            and its cumulative sums

Description

This function calculates the numbers (and cumulative numbers) of genes whose inactivation exerts
a fitness effect in *n* cell lines, varying *n* from 1 to the number of cell lines in the dataset in input.

Usage

```
CoRe.panessprofile(depMat,
                    display=TRUE,
                    main_suffix='fitness genes in at least 1 cell line',
                    xlab='n. dependent cell lines')
```

Arguments

depMat	A binary dependency matrix, i.e. a binary matrix with genes on rows and samples on columns. A 1 in position *[i,j]* indicates that inactivation of the *i*-th gene exerts a significant loss of fitness in the *j*-th sample, 0 otherwise.
display	Boolean, default is TRUE. Should bar plots of the dependency profiles be plotted
main_suffix	If display=TRUE, title suffix to give to plot showing number of genes depleted across fixed number of cell lines, default is 'genes depleted in at least 1 cell line'
xlab	If display=TRUE, label to be given to the x-axis of the plots, default is 'n. cell lines'

Value

A list with the following two named vectors:

panessprof	Number of genes that are depleted for a number of cell lines
CUMsums	Cumulative number of genes depleted in at least x cell lines

Author(s)

C. Pacini, E. Karakoc & F. Iorio

Examples

```
data(exampleDepMat)
pprofile <- CoRe.panessprofile(depMat = exampleDepMat)
pprofile
```

CoRe.randomisedepMat   *Column-wise matrix randomisation*

Description

This function takes in input a matrix and shuffles its entries column wisely. If the matrix is binary then then matrix resulting from this shuffling will have the same column marginal totals of the inpputted one.

Usage

```
CoRe.randomisedepMat(depMat)
```

Arguments

depMat	A numeric matrix

Value

The matrix given in input with entries shuffled column wisely.

Author(s)

C. Pacini, E. Karakoc & F. Iorio

Examples

```
data(exampleDepMat)
rnd_exampleDepMat<-CoRe.randomisedepMat(exampleDepMat)
```

Index