Package 'mExplorer'

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Version 1.0.0

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Description The method 'm:Explorer' associates a given list of target genes (e.g. those involved in a biological process) to gene regulators such as transcription factors. Transcription factors that bind DNA near significantly many target genes or correlate with target genes in transcriptional (microarray or RNAseq data) are selected. Selection of candidate master regulators is carried out using multinomial regression models, likelihood ratio tests and multiple testing correction. Reference: m:Explorer: multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence. Juri Reimand, Anu Aun, Jaak Vilo, Juan M Vaquerizas, Juhan Sedman and Nicholas M Luscombe. Genome Biology (2012) 13:R55 <doi:10.1186/gb-2012-13-6-r55>.

Title Identifying Master Gene Regulators from Gene Expression and DNA-Binding Data

Depends R (>= 3.0)

Imports stats, utils, nnet, parallel, qusage

Collate 'mExplorer.R'

NeedsCompilation no

RoxygenNote 6.0.1.9000

Author Juri Reimand [aut, cre]

Maintainer Juri Reimand <juri.reimand@utoronto.ca>

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Contents

mExplorer *Selection of process-specific regulators from high-throughput data using multinomial regression models.*

Description

Selection of process-specific regulators from high-throughput data using multinomial regression models.

Usage

```
mExplorer(dframe, response, interactions = F, significance = 0.05,
  n_cores = 1, multitest = "BY")
```

Arguments

dframe	Data frame of predictors. Row and column names are required for identifying samples (genes) and predictors (gene regulators), respectively.
response	Vector of factors. Names of vector need to correspond to rownames in dframe.
interactions	If enabled, pairs of predictors as interactions will be evaluated (much slower).
significance	Significance cutoff for p-values from log likelihood ratio tests.
n_cores	Number of processor cores to engage in computation. Use all available cores by default (n_cores=0).
multitest	Method to perform multiple testing correction for p-values from predictor evaluation. See p.adjust() for details.

Value

Vector of scores, with names corresponding to predictors.

Author(s)

Juri Reimand <juri.reimand@utoronto.ca>

References

m:Explorer - multinomial regression models reveal positive and negative regulators of longevity in yeast quiescence (2012, Genome Biology) by Juri Reimand, Anu Aun, Jaak Vilo, Juan M. Vaquerizas, Juhan Sedman, and Nicholas M. Luscombe

Examples

```
data(yeastCCgenes)
data(yeastTFdata)
mExplorer(yeastTFdata, yeastCCgenes)

data(mExplorer_small_test_data)
small_test_results = mExplorer(small_test_dframe, small_test_response_vec)
```

prepare_gmt_input *Creation of m:Explorer input data frame from GMT files*

Description

Creation of m:Explorer input data frame from GMT files

Usage

```
prepare_gmt_input(gmt_filename, min_genes = NA, max_genes = NA)
```

Arguments

gmt_filename	Path to GMT file to convert.
min_genes	Numeric indicating to discard pathways with less than min_genes genes. If NA, there is no lower bound on the number of genes. Default is NA.
max_genes	Numeric indicating to discard pathways with more than max_genes genes. If NA, there is no upper bound on the number of genes. Default is NA.

Value

Data frame with pathways as columns, genes as rows. Gene/pathway combinations are marked with "pw" if that gene is in the pathway, or "." if not.

Examples

```
# Create m:Explorer input data frame from GMT "small_gmt.gmt," discarding
# pathways with less than 5 genes and more than 1000 genes
gmt_file = system.file("extdata", "small_gmt.gmt", package = "mExplorer")
gmt = prepare_gmt_input(gmt_file, 5, 1000)
```

small_test_dframe *Small sample of predictor data for testing m:Explorer*

Description

Small sample of predictor data for testing m:Explorer

Usage

```
data(mExplorer_small_test_data)
```

Format

A data frame with 10 observations of 18 variables

`small_test_response_vec` *Small vector of yeast transcription factors for testing m:Explorer*

Description

Small vector of yeast transcription factors for testing m:Explorer

Usage

```
data(mExplorer_small_test_data)
```

Format

A named character vector with 4 elements

`yeastCCgenes` *Example vector of yeast transcription factors for m:Explorer*

Description

Example vector of yeast transcription factors for m:Explorer

Usage

```
data(yeastCCgenes)
```

Format

A named character vector with 186 elements

`yeastTFdata` *Example predictor data for m:Explorer*

Description

Example predictor data for m:Explorer

Usage

```
data(yeastTFdata)
```

Format

A data frame with 6253 observations of 18 variables

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