

# Package ‘mExplorer’

May 8, 2026

**Version** 1.0.0

**License** GPL (>= 2)

**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

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**Repository** CRAN

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mExplorer	<i>Selection of process-specific regulators from high-throughput data using multinomial regression models.</i>
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**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)**

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**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)
```

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prepare\_gmt\_input      *Creation of m:Explorer input data frame from GMT files*

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**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)
```

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small\_test\_dframe      *Small sample of predictor data for testing m:Explorer*

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**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*

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**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

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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

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yeastTFdata

*Example predictor data for m:Explorer*

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**Description**

Example predictor data for m:Explorer

**Usage**

```
data(yeastTFdata)
```

**Format**

A data frame with 6253 observations of 18 variables

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