Package ‘progeny’

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Title Pathway RespOnsive GENes for activity inference from gene expression

Version 1.8.0

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Description This package provides a function to infer pathway activity from gene expression using PROGENy. It contains the linear model we inferred in the publication ``Perturbation-response genes reveal signaling footprints in cancer gene expression''.

URL https://github.com/saezlab/progeny

BugReports https://github.com/saezlab/progeny/issues

Depends R (>= 3.4.0)

Imports Biobase

biocViews SystemsBiology, GeneExpression, FunctionalPrediction, GeneRegulation

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LazyData true

Encoding UTF-8

Suggests airway, biomaRt, BiocFileCache, broom, DESeq2, dplyr, knitr, readr, readxl

VignetteBuilder knitr

RoxygenNote 6.0.1

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R topics documented:

`model` *The linear model underlying PROGENy*

Description

HGNC gene symbols in rows, pathways in columns. Pathway activity inference works by a matrix multiplication of gene expression with the model.

Usage

```
model
```

Format

An object of class `matrix` with 1059 rows and 11 columns.

Source

`http://biorxiv.org/content/early/2016/08/28/065672`

`progeny` *Calculate PROGENy pathway scores from gene expression*

Description

This function uses the linear model of pathway-responsive genes underlying the PROGENy method. It transforms a gene expression matrix with HGNC gene symbols in rows and sample names in columns into a pathway score matrix with samples and in rows and pathways in columns.

This function uses the linear model of pathway-responsive genes underlying the PROGENy method. It transforms a gene expression matrix with HGNC gene symbols in rows and sample names in columns into a pathway score matrix with samples and in rows and pathways in columns.

Usage

```
progeny(expr, scale = TRUE)
```

Arguments

`expr`	A gene expression object with HGNC symbols in rows and samples in columns
`scale`	Logical value indicating whether to scale the scores of each pathway to have a mean of zero and standard deviation of one

Details

The publication of the method is available at: https://www.biorxiv.org/content/early/2016/08/28/065672

The supplied expression object has to contain HGNC symbols in rows. This will, in most cases (and how we originally used it), be either normalized gene expression of a microarray experiment or log-transformed (and possible variance-stabilized) counts from an RNA-seq experiment.

The model matrix itself consists of 11 pathways and 1059 genes. Its coefficients are non-zero if the gene-pathway pair corresponds to the top 100 genes that were up-regulated upon stimulation of the pathway in a wide range of experiments. The value corresponds to the fitted z-score across experiments in our model fit. Only rows with at least one non-zero coefficient were included, as the rest is not used to infer pathway activity.

Value

A matrix with samples in columns and pathways in rows

Examples

```
# use your gene expression matrix here, this is just for illustration
gene_expression = matrix(rep(1, nrow(model)),
    dimnames=list(rownames(model), "sample"))

# calculate pathway activities
pathways = progeny(gene_expression)
```

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