

# 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

**License** Apache License (== 2.0) | file LICENSE

**LazyData** true

**Encoding** UTF-8

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

**VignetteBuilder** knitr

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/progeny>

**git\_branch** RELEASE\_3\_10

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## R topics documented:

model . . . . .	2
progeny . . . . .	2
Index	4

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model	<i>The linear model underlying PROGENy</i>
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### 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>

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progeny	<i>Calculate PROGENy pathway scores from gene expression</i>
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### 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

<code>expr</code>	A gene expression object with HGNC symbols in rows and samples in columns
<code>scale</code>	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)
```

# Index

\*Topic **datasets**

model, [2](#)

model, [2](#)

progeny, [2](#)

progeny-package (progeny), [2](#)