

# Package ‘GENIE3’

April 11, 2018

**Type** Package

**Title** GEne Network Inference with Ensemble of trees

**Version** 1.0.0

**Date** 2017-07-24

**Author** Van Anh Huynh-Thu, Sara Aibar, Pierre Geurts

**Maintainer** Van Anh Huynh-Thu <vahuyh@u.lg.ac.be>

**Description** This package implements the GENIE3 algorithm for inferring gene regulatory networks from expression data.

**License** GPL (>= 2)

**LazyData** TRUE

**Imports** stats, reshape2

**Suggests** knitr, rmarkdown, foreach, doRNG, doParallel, Biobase, SummarizedExperiment, testthat, methods

**NeedsCompilation** yes

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**biocViews** NetworkInference, SystemsBiology, DecisionTree, Regression, Network, GraphAndNetwork, GeneExpression

## R topics documented:

GENIE3 . . . . .	1
getLinkList . . . . .	3
<b>Index</b>	<b>4</b>

---

GENIE3

*GENIE3*

---

## Description

GENIE3 infers a gene regulatory network (in the form of a weighted adjacency matrix) from expression data, using ensembles of regression trees.

**Usage**

```
GENIE3(exprMatrix, treeMethod = "RF", K = "sqrt", nTrees = 1000,
       regulators = NULL, targets = NULL, nCores = 1, verbose = FALSE)
```

**Arguments**

exprMatrix	Expression matrix (genes x samples). Every row is a gene, every column is a sample. The expression matrix can also be provided as one of the Bioconductor classes: <ul style="list-style-type: none"> <li>• <a href="#">ExpressionSet</a>: The matrix will be obtained through <code>exprs(exprMatrix)</code></li> <li>• <a href="#">RangedSummarizedExperiment</a>: The matrix will be obtained through <code>assay(exprMatrix)</code>, which will extract the first assay (usually the counts)</li> </ul>
treeMethod	Tree-based method used. Must be either "RF" for Random Forests (default) or "ET" for Extra-Trees.
K	Number of candidate regulators randomly selected at each tree node (for the determination of the best split). Must be either "sqrt" for the square root of the total number of candidate regulators (default), "all" for the total number of candidate regulators, or a strictly positive integer.
nTrees	Number of trees in an ensemble for each target gene. Default: 1000.
regulators	Subset of genes used as candidate regulators. Must be either a vector of indices, e.g. <code>c(1, 5, 6, 7)</code> , or a vector of gene names, e.g. <code>c("at_12377", "at_10912")</code> . The default value NULL means that all the genes are used as candidate regulators.
targets	Subset of genes to which potential regulators will be calculated. Must be either a vector of indices, e.g. <code>c(1, 5, 6, 7)</code> , or a vector of gene names, e.g. <code>c("at_12377", "at_10912")</code> . If NULL (default), regulators will be calculated for all genes in the input matrix.
nCores	Number of cores to use for parallel computing. Default: 1.
verbose	If set to TRUE, a feedback on the progress of the calculations is given. Default: FALSE.

**Value**

Weighted adjacency matrix of inferred network. Element  $w_{ij}$  (row  $i$ , column  $j$ ) gives the importance of the link from regulatory gene  $i$  to target gene  $j$ .

**Examples**

```
## Generate fake expression matrix
exprMatrix <- matrix(sample(1:10, 100, replace=TRUE), nrow=20)
rownames(exprMatrix) <- paste("Gene", 1:20, sep="")
colnames(exprMatrix) <- paste("Sample", 1:5, sep="")

## Run GENIE3
set.seed(123) # For reproducibility of results
weightMatrix <- GENIE3(exprMatrix, regulators=paste("Gene", 1:5, sep=""))

## Get ranking of edges
linkList <- getLinkList(weightMatrix)
head(linkList)
```

---

getLinkList	<i>getLinkList</i>
-------------	--------------------

---

### Description

getLinkList Converts the weight matrix, as returned by [GENIE3](#), to a sorted list of regulatory links (most likely links first).

### Usage

```
getLinkList(weightMatrix, reportMax = NULL, threshold = 0)
```

### Arguments

weightMatrix	Weighted adjacency matrix as returned by <a href="#">GENIE3</a> .
reportMax	Maximum number of links to report. The default value NULL means that all the links are reported.
threshold	Only links with a weight above the threshold are reported. Default: threshold = 0, i.e. all the links are reported.

### Value

List of regulatory links in a data frame. Each line of the data frame corresponds to a link. The first column is the regulatory gene, the second column is the target gene, and the third column is the weight of the link.

### See Also

[GENIE3](#)

### Examples

```
## Generate fake expression matrix
exprMat <- matrix(sample(1:10, 100, replace=TRUE), nrow=20)
rownames(exprMat) <- paste("Gene", 1:20, sep="")
colnames(exprMat) <- paste("Sample", 1:5, sep="")

## Run GENIE3
weightMat <- GENIE3(exprMat, regulators=paste("Gene", 1:5, sep=""))

## Get ranking of edges
linkList <- getLinkList(weightMat)
head(linkList)
```

# Index

ExpressionSet, [2](#)

GENIE3, [1](#), [3](#)

getLinkList, [3](#)

RangedSummarizedExperiment, [2](#)