Package 'scTenifoldKnk'

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Type Package

Title In-Silico Knockout Experiments from Single-Cell Gene Regulatory Networks

Version 1.0.1

Description A workflow based on 'scTenifoldNet' to perform in-silico knockout experiments using single-cell RNA sequencing (scRNA-seq) data from wild-type (WT) control samples as input. First, the package constructs a single-cell gene regulatory network (scGRN) and knocks out a target gene from the adjacency matrix of the WT scGRN by setting the gene's outdegree edges to zero. Then, it compares the knocked out scGRN with the WT scGRN to identify differentially regulated genes, called virtual-knockout perturbed genes, which are used to assess the impact of the gene knockout and reveal the gene's function in the analyzed cells.

URL https://github.com/cailab-tamu/scTenifoldKnk

BugReports https://github.com/cailab-tamu/scTenifoldKnk/issues

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

biocViews

Imports pbapply, RSpectra, Matrix, methods, stats, utils, MASS, scTenifoldNet

Suggests testthat (>= 2.1.0)

NeedsCompilation no

Author Daniel Osorio [aut, cre] (<https://orcid.org/0000-0003-4424-8422>),
Yan Zhong [aut, ctb],
Guanxun Li [aut, ctb],
Qian Xu [aut, ctb],
Andrew Hillhouse [aut, ctb],
Jingshu Chen [aut, ctb],
Laurie Davidson [aut, ctb],
Yanan Tian [aut, ctb],

Robert Chapkin [aut, ctb],
Jianhua Huang [aut, ctb],
James Cai [aut, ctb, ths] (<https://orcid.org/0000-0002-8081-6725>)

Maintainer Daniel Osorio <dcosorioh@tamu.edu>

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R topics documented:

`scTenifoldKnk` *scTenifoldKNK*

Description

Predict gene perturbations

Usage

```
scTenifoldKnk(
  countMatrix,
  gKO = NULL,
  qc_mtThreshold = 0.1,
  qc_minLSize = 1000,
  nc_lambda = 0,
  nc_nNet = 10,
  nc_nCells = 500,
  nc_nComp = 3,
  nc_scaleScores = TRUE,
  nc_symmetric = FALSE,
  nc_q = 0.9,
  td_K = 3,
  td_maxIter = 1000,
  td_maxError = 1e-05,
  td_nDecimal = 3,
  ma_nDim = 2
)
```

Arguments

`countMatrix`	countMatrix
`gKO`	gKO

qc_mtThreshold	A decimal value between 0 and 1. Defines the maximum ratio of mitochondrial reads (mithocondrial reads / library size) present in a cell to be included in the analysis. It's computed using the symbol genes starting with 'MT-' non-case sensitive.
qc_minLSize	An integer value. Defines the minimum library size required for a cell to be included in the analysis.
nc_lambda	A continuous value between 0 and 1. Defines the multiplicative value (1-lambda) to be applied over the weaker edge connecting two genes to maximize the adjacency matrix directionality.
nc_nNet	An integer value. The number of networks based on principal components regression to generate.
nc_nCells	An integer value. The number of cells to subsample each time to generate a network.
nc_nComp	An integer value. The number of principal components in PCA to generate the networks. Should be greater than 2 and lower than the total number of genes.
nc_scaleScores	A boolean value (TRUE/FALSE), if TRUE, the weights will be normalized such that the maximum absolute value is 1.
nc_symmetric	A boolean value (TRUE/FALSE), if TRUE, the weights matrix returned will be symmetric.
nc_q	A decimal value between 0 and 1. Defines the cut-off threshold of top q% relationships to be returned.
td_K	An integer value. Defines the number of rank-one tensors used to approximate the data using CANDECOMP/PARAFAC (CP) Tensor Decomposition.
td_maxIter	An integer value. Defines the maximum number of iterations if error stay above td_maxError.
td_maxError	A decimal value between 0 and 1. Defines the relative Frobenius norm error tolerance.
td_nDecimal	An integer value indicating the number of decimal places to be used.
ma_nDim	An integer value. Defines the number of dimensions of the low-dimensional feature space to be returned from the non-linear manifold alignment.

Author(s)

Daniel Osorio <dcosorioh@tamu.edu>

Examples

```
# Loading single-cell data
scRNAseq <- system.file("single-cell/example.csv",package="scTenifoldKnk")
scRNAseq <- read.csv(scRNAseq, row.names = 1)

# Running scTenifoldKnk
scTenifoldKnk(countMatrix = scRNAseq, gKO = 'G100', qc_minLSize = 0)
```

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