Package 'scTenifoldKnk'

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Type Package

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

Version 1.0.3

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

RoxygenNote 7.3.3

Imports pbapply, Matrix, methods, stats, utils, MASS, scTenifoldNet, cli, enrichR, igraph, reshape2

Suggests testthat (>= 2.1.0)

NeedsCompilation no

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`plotKO` *Plot KO network*

Description

Generate and plot a KO-centered subnetwork from the output of 'scTenifoldKnk'. The function selects genes with significant differential regulation, extracts their interactions from the reconstructed WT network, filters edges by weight quantile, and displays the network. When 'annotate = TRUE' the function queries enrichment databases and overlays category pies on nodes and a legend of significant terms.

Usage

```
plotKO(
  X,
  gKO,
  q = 0.99,
  annotate = TRUE,
  nCategories = 20,
  fdrThreshold = 0.05
)
```

Arguments

`X`	List. Output from 'scTenifoldKnk' function.
`gKO`	Character. Gene symbol of simulated knockout gene.
`q`	Numeric. Edge-weight quantile used to threshold weak edges (default 0.99).
`annotate`	Logical. If TRUE, perform enrichment annotation and display pies on nodes (default TRUE).
`nCategories`	Integer. Maximum number of enrichment categories to show in the legend when annotation is requested (default 20).
`fdrThreshold`	Numeric. Adjusted p-value cutoff (FDR) for reporting enriched terms (default 0.05).

Details

Plot a KO-centered subnetwork and (optionally) annotate with enrichment

Value

Invisibly returns NULL. The primary purpose is plotting the network as a side effect.

Examples

```
## Not run:
res <- scTenifoldKnk(countMatrix, gKO = "G100")
plotKO(res, gKO = "G100")

## End(Not run)
```

`scTenifoldKnk` *scTenifoldKNK*

Description

Predict gene perturbations

Usage

```
scTenifoldKnk(
  countMatrix,
  qc = TRUE,
  gKO = NULL,
  qc_mtThreshold = 0.1,
  qc_minLSize = 1000,
  qc_minCells = 25,
  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,
  nCores = parallel::detectCores()
)
```

Arguments

countMatrix	countMatrix
qc	A boolean value (TRUE/FALSE), if TRUE, a quality control is applied over the data.
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.
qc_minCells	An integer value. Defines the minimum number of cells a gene should be expressed in to be included in the analysis. By default, it's set to 25.
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.
nCores	An integer value. Defines the number of cores to be used.

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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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