Package ‘scTensor’

May 18, 2024

Type Package

Title Detection of cell-cell interaction from single-cell RNA-seq
dataset by tensor decomposition

Version 2.14.0

Depends R (>= 4.1.0)

Imports methods, RSQLite, igraph, S4Vectors, plotly, reactome.db,
AnnotationDbi, SummarizedExperiment, SingleCellExperiment,
nnTensor (>= 1.1.5), ccTensor (>= 1.0.2), rTensor (>= 1.4.8),
abind, plotrix, heatmaply, tagcloud, rmarkdown, BiocStyle,
knitr, AnnotationHub, MeSHDbi (>= 1.29.2), grDevices, graphics,
stats, utils, outliers, Category, meshr (>= 1.99.1), GOstats,
ReactomePA, DOSE, crayon, checkmate, BiocManager, visNetwork,
schex, ggplot2

Suggests testthat, LRBaseDbi, Seurat, scTGIF, Homo.sapiens,
AnnotationHub

Description The algorithm is based on the non-negative tucker decomposition (NTD2) of nnTensor.

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biocViews DimensionReduction, SingleCell, Software, GeneExpression

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/scTensor

git_branch RELEASE_3_19

git_last_commit 5ee2a91

Repository Bioconductor 3.19

Date/Publication 2024-05-17

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scTensor-package  

Detection of cell-cell interaction from single-cell RNA-seq dataset by tensor decomposition

Description

The algorithm is based on the non-negative tucker decomposition (NTD2) of nnTensor.

Details

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Author(s)

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See Also

GermMale, labelGermMale, tsneGermMale, cellCellSetting, cellCellDecomp, cellCellReport

Examples

ls("package:scTensor")
CCSPars-class

Class "CCSPars"

Description

The parameter object to be specified against cellCellSimulate function.

Objects from the Class

Objects can be created by calls of the form new("CCSPars", ...).

Slots

nGene: The number of genes.
nCell: The number of cells.
cellInfo: The parameter to describe the CCI.
lambda: The parameter for dropout simulation.
seed: The seed for using random numbers.

Methods

newCCSPars Generator of CCSPars object.
getParam Getter function of the slot in CCSPars object.
setParam<- Setter function of the slot in CCSPars object.

See Also

newCCSPars, getParam, setParam<-

cellCellDecomp

Performing scTensor

Description

All parameters is saved to metadata slot of SingleCellExperiment object.

Usage

cellCellDecomp(sce, algorithm=c("ntd2", "ntd", "nmf", "cx", "pearson",
"spearman", "distance", "pearson.lr", "spearman.lr", "distance.lr",
"pcomb", "label.permutation", "cabello.aguilar", "halpern"), ranks=c(3,3), rank=3, thr1=log2(5), thr2=25, thr3=0.95, L1_A=0, L2_A=0, verbose=FALSE,
centering=TRUE, mergeas=c("mean", "sum"), outerfunc=c("*", "+"),
comb=c("random", "all"), num.sampling=100, num.perm=1000, assayNames = "counts", decomp=TRUE)
Arguments

sce The object generated by instantiation of SingleCellExperiment-class.
algorithm Algorithm for constructing cell-cell similarity matrix. "ntd2", "ntd", "nmf", "cx", "pearson", "spearman", "distance", "pearson.lr", "spearman.lr", "distance.lr", "pcmb" or "label.permutation" can be specified (Default: ntd2).
ranks The size of the core tensor decomposed by NTD. Each element means (Number of Ligand-Cell Pattern, Number of Receptor-Cell Pattern, Number of LR-pairs Pattern) (Default: c(3,3)).
rank The number of low dimension of NMF (Default: 3).
thr1 The threshold used by pcomb (Default: log2(5)).
thr2 The threshold used by pcomb (Default: 25).
thr3 The threshold used by cx (Default: 0.95).
L1_A The parameter to control the sparseness (Default: 0).
L2_A The parameter to control the outlier (Default: 0).
verbose The verbose parameter for nnTensor::NTD (Default: FALSE).
centering When the value is TRUE, input matrix is summarized as celltype-level vectors (Default: TRUE).
mergeas When the centering is TRUE, "sum" (celltype-level sum vector) or "mean" (celltype-level average vector) is calculated (Default: "sum").
outerfunc When the centering is TRUE, "+" (Kronecker sum) or "*" (Kronecker product) is calculated (Default: "+").
comb When the centering is FALSE, "random" (random cell-cell pairing) or "all" (all possible cell-cell pairing) is calculated (Default: "random").
um.sampling The number of random sampling used (Default: 100).
um.perm The number of the permutation in label permutation test (Default: 1000).
assayNames The unit of gene expression for using scTensor (e.g. normcounts, cpm...etc) (Default: "counts").
decomp When the value is TRUE, cell-cell interaction tensor is decomposed (Default: TRUE).

Value

The result is saved to metadata slot of SingleCellExperiment object.

Author(s)

Koki Tsuyuzaki

See Also

    SingleCellExperiment.

Examples

    showMethods("cellCellDecomp")
cellCellRanks

Rank estimation of the CCI-tensor

Description

SVD is performed in each mode.

Usage

cellCellRanks(sce, centering=TRUE, 
mergeas=c("mean", "sum"), outerfunc=c("*", "+") , comb=c("random", "all"), 
num.sampling=100, num.perm=1000, assayNames = "counts", verbose=FALSE, 
num.iter1=5, num.iter2=5, num.iter3=NULL)

Arguments

sce A object generated by instantiation of SingleCellExperiment-class.
centering When the value is TRUE, input matrix is summarized as celltype-level vectors (Default: TRUE).
mergeas When the centering is TRUE, "mean" (celltype-level mean vector) or "sum" (celltype-level sum vector) is calculated (Default: "mean").
outerfunc When the centering is TRUE, "+" (Kronecker sum) or "+" (Kronecker product) is calculated (Default: "+").
comb When the centering is FALSE, "random" (random cell-cell pairing) or "all" (all possible cell-cell pairing) is calculated (Default: "random").
um.sampling The number of random sampling used (Default: 100).
um.perm The number of the permutation in label permutation test (Default: 1000).
assayNames The unit of gene expression for using scTensor (e.g. normcounts, cpm...etc) (Default: "counts").
verbose The verbose parameter for nnTensor::NTD (Default: FALSE).
um.iter1 The number of iteration to estimate the rank of mode-1 matricised data tensor (Default: 5).
um.iter2 The number of iteration to estimate the rank of mode-2 matricised data tensor (Default: 5).
um.iter3 The number of iteration to estimate the rank of mode-3 matricised data tensor (Default: NULL).

Value

RSS: A list with three elements, in which each element means the average reconstructed error in each rank. selected: A vector with three elements, in which each element means the estimated ranks in mode-1, 2 and 3 matricization.
Author(s)
Koki Tsuyuzaki

See Also
SingleCellExperiment.

Examples
showMethods("cellCellRanks")

cellCellReport  HTML report of the result of scTensor

Description
The result is saved as HTML report which contains with multiple files.

Usage
cellCellReport(sce, reducedDimNames,  
out.dir=tempdir(), html.open=FALSE,  
title="The result of scTensor",  
author="The person who runs this script", assayNames = "counts", thr=100,  
top="full", p=0.05, upper=20,  
goenrich=TRUE, meshenrich=TRUE, reactomeenrich=TRUE, doi:enrich=TRUE, ncgenrich=TRUE, dgnenrich=TRUE, nbins=40)

Arguments
sce  A object generated by instantization of SingleCellExperiment-class.
reducedDimNames  The name of two-dimentional data saved in reducedDimNames slot of SingleCellExperiment object.
out.dir  The output directory for saving HTML report (out.dir: tempdir()).
html.open  Whether the result of HTML report is opened when the calculation is finished (Default: FALSE).
title  The title of HTML report (Default: "The result of scTensor").
author  The author of HTML report (Default: "The person who runs this script").
assayNames  The unit of gene expression for using scTensor (e.g. normcounts, cpm...etc) (Default: "counts").
thr  The threshold for selection of top percentage of core tensor elements (Default: 100 (1 to 100)).
top  top genes in each (*,*,*)-pattern which are selected and summarized in the report (Default: "full")
p The threshold of p-value of the enrichment analysis (Default: 1E-2)
upper The maximum number of HTML reports generates (Default: 20)
goenrich Whether GO-Enrichment analysis is performed (Default: TRUE)
meshenrich Whether MeSH-Enrichment analysis is performed (Default: TRUE)
reactomeenrich Whether Reactome-Enrichment analysis is performed (Default: TRUE)
doenrich Whether DO-Enrichment analysis is performed (Default: TRUE)
cngenrich Whether NCG-Enrichment analysis is performed (Default: TRUE)
dgnenrich Whether DGN-Enrichment analysis is performed (Default: TRUE)
bins The number of bins used for the two dimensional plot of schex (Default: 40)

Value
The result is saved as HTML report which contains with multiple files.

Author(s)
Koki Tsuyuzaki

See Also
   SingleCellExperiment.

Examples
if(interactive()){
  # Package Loading
  library("SingleCellExperiment")
  library("AnnotationHub")
  if(!require(LRBaseDbi)){
    BiocManager::install("LRBaseDbi")
    library(LRBaseDbi)
  }
  ah <- AnnotationHub()
  dbfile <- query(ah, c("LRBaseDb", "Homo sapiens", "v002")[[1]])
  LRBase.Hsa.eg.db <- LRBaseDbi::LRBaseDb(dbfile)

  # Data Loading
  data(GermMale)
  data(labelGermMale)
  data(tsneGermMale)

  # SingleCellExperiment Object
  sce <- SingleCellExperiment(assays=list(counts = GermMale))
  reducedDims(sce) <- SimpleList(TSNE=tsneGermMale$Y)

  # User's Original Normalization Function
  CPMED <- function(input){
    libsize <- colSums(input)
    median(libsize) * t(t(input) / libsize)
} # Normalization
normcounts(sce) <- log10(CPMED(counts(sce)) + 1)

# Registration of required information into metadata(sce)
cellCellSetting(sce, LRBase.Hsa.eg.db, names(labelGermMale))

# Rank Estimation
rks <- cellCellRanks(sce, assayNames="normcounts")

# CCI Tensor Decomposition
set.seed(1234)
cellCellDecomp(sce, ranks=rks$selected, assayNames="normcounts")

# HTML Report
options(device.ask.default = FALSE)
cellCellReport(sce, reducedDimNames="TSNE", 
out.dir=tempdir(), html.open=FALSE, 
title="The result of scTensor", 
author="The person who runs this script", 
assayNames="counts", thr=100, 
top="full", p=0.05, upper=20, 
goenrich=TRUE, meshenrich=TRUE, reactomeenrich=TRUE, 
doenrich=TRUE, ncgenrich=TRUE, dgnenrich=TRUE, nbins=40)
else{
  showMethods("cellCellReport")
}

---

cellCellSetting | Parameter setting for scTensor

Description
All parameters is saved to metadata slot of SingleCellExperiment object.

Usage
```r
cellCellSetting(sce, lrbase, label, lr.evidence="known", color=NULL)
```

Arguments

- **sce**: A object generated by instantization of SingleCellExperiment-class.
- **lrbase**: Ligand-Receptor database (LRBase.XXX.eg.db-type package).
- **label**: Cellular label information for distinguishing which cells belong to common celltypes.
- **lr.evidence**: The evidence code for L-R pair list (Default: "known"). When you specify "known", DLRP, IUPHAR, HPMR, CELLPHONEDB, SINGLECELLSIGNALR are searched, and other databases are searched, when you specify "putative". You can also specify multiple databases at once (e.g. c("SWISSPROT_STRING", "TREMBL_STRING")). cf. https://github.com/rikenbit/lrbase-workflow
cellCellSimulate

Description
All parameters is saved to metadata slot of SingleCellExperiment object.

Usage
cellCellSimulate(params = newCCSPars(), verbose = TRUE)

Arguments
params A parameter object generated by newCSPars().
verbose Whether the message is outputted or not (Default: TRUE).

Value
A list object containing simcount, LR, and celltype. simcount is the synthetic count matrix, LR is
the synthetic ligand-receptor pair list, and celltype is the vector to specity the celltype of the each
column of simcount.

Author(s)
Koki Tsuyuzaki

Examples
showMethods("cellCellSimulate")
GermMale

The matrix which is used as test data of scTensor.

Description

A matrix with 242 rows (genes) * 852 columns (cells).

Usage

data(GermMale)

Details


Only male data is extracted and then the gene symbol is converted to NCBI Gene ID by Homo.sapiens package.

For saving the package size, the number of genes are strictly reduced by the standard of highly variable genes with threshold of p-value is 1E-300.

References


See Also

labelGermMale, tsneGermMale.

Examples

data(GermMale)

getParam

Get a parameter

Description

Accessor function for getting parameter values.

Usage

getParam(object, name)

# S4 method for signature 'CCSPrams'
getParam(object, name)
labelGermMale

Arguments

- object: object to get parameter from.
- name: name of the parameter to get.

Value

The extracted parameter value

Examples

```r
params <- newCCSParams()
getParam(params, "nGene")
getParam(params, "nCell")
getParam(params, "cciInfo")
getParam(params, "lambda")
getParam(params, "seed")
```

---

labelGermMale  
*The vector contains the celltype information and color scheme of GermMale*

Description

A vector with 852 length (cells).

Usage

```r
data(labelGermMale)
```

Details


References


See Also

`GermMale, tsneGermMale`

Examples

```r
data(labelGermMale)
```
**m**

*The gene-wise mean vector of Quartz-Seq data.*

**Description**

This data is internally used in cellCellSimulate function.

**Usage**

```r
data(m)
```

**Examples**

```r
data(m)
```

---

**newCCSParsms**

*New Params*

**Description**

Create a new CCSParsms object.

**Usage**

```r
newCCSParsms()
```

**Arguments**

Nothing.

**Value**

New Params object.

**Examples**

```r
params <- newCCSParsms()
```
setParam

setParam

Set a parameter

Description

Function for setting parameter values.

Usage

setParam(object, name) <- value
## S4 method for signature 'CCSParams'
setParam(object, name, value)

Arguments

object object to set parameter in.
name name of the parameter to set.
value value to set the parameter to.

Value

Object with new parameter value.

Examples

params <- newCCSParams()

setParam(params, "nGene") <- 20000
setParam(params, "nCell") <- c(12, 43, 323)
setParam(params, "cciInfo") <- list(nPair=2000,
    CCI1=list(
        LPattern=c(1, 0, 0),
        RPattern=c(0, 1, 1),
        nGene=100,
        fc="E10"),
    CCI2=list(
        LPattern=c(0, 0, 1),
        RPattern=c(1, 1, 1),
        nGene=200,
        fc="E10"),
    CCI3=list(
        LPattern=c(1, 1, 1),
        RPattern=c(1, 0, 1),
        nGene=300,
        fc="E10")
  )
setParam(params, "lambda") <- 0.1
setParam(params, "seed") <- 111
The result of Rtsne against GermMale

Description
A List contains some parameters and the result of Rtsne function.

Usage
data(tsneGermMale)

Details
Rtsne is performed as follows.
library(Rtsne) set.seed(123) tsneGermMale <- Rtsne(dist(t(GermMale)), is_distance=TRUE, perplexity=40)

References

See Also
*labelGermMale, GermMale.*

Examples
data(tsneGermMale)

The gene-wise variance vector of Quartz-Seq data.

Description
This data is internally used in cellCellSimulate function.

Usage
data(v)

Examples
data(v)
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