Package ‘scTensor’

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

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scTensor-package

R topics documented:

- scTensor-package ....................................................... 2
- CCSParams-class ...................................................... 3
- cellCellDecomp ......................................................... 3
- cellCellRanks .......................................................... 5
- cellCellReport .......................................................... 6
- cellCellSetting ......................................................... 8
- cellCellSimulate ....................................................... 9
- GermMale ............................................................... 10
-getParam ............................................................... 10
- labelGermMale .......................................................... 11
- m .......................................................... 12
- newCCSParams ............................................................ 12
- setParam ............................................................... 13
- tsneGermMale ............................................................ 14
- v .......................................................... 14

Index 15

| 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")
CCParams-class

Class "CCParams"

Description

The parameter object to be specified against cellCellSimulate function.

Objects from the Class

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

Slots

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

Methods

newCCParams Generator of CCParams object.
getParam Getter function of the slot in CCParams object.
setParam<- Setter function of the slot in CCParams object.

See Also

newCCParams, 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", "pcmb", "label.permutation", "cabelllo.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", "pcomb" 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 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").

num.sampling
The number of random sampling used (Default: 100).

num.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

```r
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 product) or "+" (Kronecker sum) or 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").
- **num.sampling**: The number of random sampling used (Default: 100).
- **num.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).
- **num.iter1**: The number of iteration to estimate the rank of mode-1 matricised data tensor (Default: 5).
- **num.iter2**: The number of iteration to estimate the rank of mode-2 matricised data tensor (Default: 5).
- **num.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.
cellCellReport

Description

The result is saved as HTML report which contains 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, 
   doenrich=TRUE, ncgenrich=TRUE, dgnenrich=TRUE, nbins=40)

Arguments

sce A object generated by instantiation 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")
The threshold of p-value of the enrichment analysis (Default: 1E-2)
The maxium number of HTML reports generates (Default: 20)
Whether GO-Enrichment analysis is performed (Default: TRUE)
Whether MeSH-Enrichment analysis is performed (Default: TRUE)
Whether Reactome-Enrichment analysis is performed (Default: TRUE)
Whether DO-Enrichment analysis is performed (Default: TRUE)
Whether NCG-Enrichment analysis is performed (Default: TRUE)
Whether DGN-Enrichment analysis is performed (Default: TRUE)
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

```r
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)
}
```
cellCellSetting

Parameter setting for scTensor

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

Usage
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 distinguising 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

```r
cellCellSimulate(params = newCCSPars(), verbose = TRUE)
```

#### Arguments

- `params`: A parameter object generated by `newCCSPars()`.
- `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

#### See Also

`SingleCellExperiment`

#### Examples

```r
showMethods("cellCellSetting")
```

---

### cellCellSimulate

**Parameter Simulate for scTensor**

#### Description

All parameters is saved to metadata slot of SingleCellExperiment object.

#### Usage

```r
cellCellSimulate(params = newCCSPars(), verbose = TRUE)
```

#### Arguments

- `params`: A parameter object generated by `newCCSPars()`.
- `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

#### See Also

`SingleCellExperiment`

#### Examples

```r
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
The data matrix is downloaded from GEO Series GSE86146 (https://www.ncbi.nlm.nih.gov/geo/download/?acc=GSE86146). 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
gParam(object, name)

## S4 method for signature 'CCSParams'
gParam(object, name)
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

The Cluster label is downloaded from original paper page of Cell Stem Cell (https://www.sciencedirect.com/science/article/pii/S1934590917300784)

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
data(m)

Examples
data(m)

newCCSParms

New Params

Description
Create a new CCSParms object.

Usage
newCCSParms()

Arguments
Nothing.

Value
New Params object.

Examples
params <- newCCSParms()
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
**tsneGermMale**  
*The result of Rtsne against GermMale*

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

### Usage
```r
data(tsneGermMale)
```

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

### References

### See Also
`labelGermMale`, `GermMale`.

### Examples
```r
data(tsneGermMale)
```

---

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

### Description
This data is internally used in cellCellSimulate function.

### Usage
```r
data(v)
```

### Examples
```r
data(v)
```
Index

* classes
  CCSParams-class, 3

* datasets
  GermMale, 10
  labelGermMale, 11
  m, 12
  tsneGermMale, 14
  v, 14

* methods
  cellCellDecomp, 3
  cellCellRanks, 5
  cellCellReport, 6
  cellCellSetting, 8
  cellCellSimulate, 9

* package
  scTensor-package, 2
  CCSParams-class, 3
  cellCellDecomp, 2, 3
  cellCellDecomp,SingleCellExperiment-method
    (cellCellDecomp), 3
  cellCellRanks, 5
  cellCellRanks,SingleCellExperiment-method
    (cellCellRanks), 5
  cellCellReport, 2, 6
  cellCellReport,SingleCellExperiment-method
    (cellCellReport), 6
  cellCellSetting, 2, 8
  cellCellSetting,SingleCellExperiment-method
    (cellCellSetting), 8
  cellCellSimulate, 9
  cellCellSimulate,SingleCellExperiment-method
    (cellCellSimulate), 9

  GermMale, 2, 10, 11, 14
  getParam, 3, 10
  getParam,CCSParams-method (getParam), 10

  labelGermMale, 2, 10, 11, 14

  m, 12

  newCCSParams, 3, 12

  scTensor (scTensor-package), 2
  scTensor-package, 2
  setParam, 13
  setParam,CCSParams,ANY-method
    (setParam), 13
  tsneGermMale, 2, 10, 11, 14

  v, 14