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

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

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")
### Description

The parameter object to be specified against cellCellSimulate function.

### Objects from the Class

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

### Slots

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

### Methods

- **newCCSParams**: Generator of CCSParams object.  
- **getParam**: Getter function of the slot in CCSParams object.  
- **setParam<-**: Setter function of the slot in CCSParams object.  

### See Also

`newCCSParams`, `getParam`, `setParam<-`

---

### Description

All parameters is saved to metadata slot of SingleCellExperiment object.

### Usage

```r
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", decom=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 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").

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")
**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.
Description
The result is saved as HTML report which contains multiple files.

Usage

```r
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-dimensionnal 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 maximum 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)

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

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

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

**color**  
Color scheme for adding color against the cells (Default: NULL). If the value is not specified, automatically the color vector is generated.

**Value**  
The result is saved to metadata slot of SingleCellExperiment object.

**Author(s)**  
Koki Tsuyuzaki

**See Also**  
*SingleCellExperiment.*

**Examples**  
showMethods("cellCellSetting")

---

**cellCellSimulate**  
*Parameter Simulate for scTensor*

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

**Usage**  

`cellCellSimulate(params = newCCSPrams(), verbose = TRUE)`

**Arguments**

- `params`  
  A parameter object generated by newCCSPrams().

- `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 specify 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**

```r
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**

```r
data(GermMale)
```

---

**getParam**  

*Get a parameter*

**Description**

Accessor function for getting parameter values.

**Usage**

```r
getParam(object, name)
```

```r
## S4 method for signature 'CCSParams'
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**

`data(labelGermMale)`

**Details**


**References**


**See Also**

`GermMale, tsneGermMale`.

**Examples**

`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)

newCCSPrams

New Params

Description
Create a new CCSPrams object.

Usage
newCCSPrams()

Arguments
Nothing.

Value
New Params object.

Examples
params <- newCCSPrams()
Description

Function for setting parameter values.

Usage

```r
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

```r
params <- newCCSParams()
setParam(params, "nGene") <- 20000
setParam(params, "nCell") <- c(12, 43, 323)
setParam(params, "cciInfo") <- list(nPair=20000,
  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)
```
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