Package ‘scTensor’

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dataset by tensor decomposition

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

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Author Koki Tsuyuzaki [aut, cre],
Kozo Nishida [aut]

Maintainer Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>
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<td>Detection of cell-cell interaction from single-cell RNA-seq dataset by tensor decomposition</td>
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Description

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

Details

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Author(s)

Koki Tsuyuzaki [aut, cre], Kozo Nishida [aut]

Maintainer: Koki Tsuyuzaki <k.t.the-answer@hotmail.co.jp>

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<-

---

**cellCellDecomp**

Performing scTensor

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", 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 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")
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.
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 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-dimensional 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
upper
goenrich
meshenrich
reactomeenrich
doenrich
ncgenrich
dgnenrich
nbins

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)
})
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

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<td>sce</td>
<td>A object generated by instantiation 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 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**

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

---

### cellCellSimulate

**Parameter Simulate for scTensor**

**Description**

All parameters is saved to metadata slot of SingleCellExperiment object.

**Usage**

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

**Arguments**

- `params` A parameter object generated by `newCCSParms()`.
- `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 each column of simcount.

**Author(s)**

Koki Tsuyuzaki

**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


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 'CCSParams'
getParam(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

```r
data(m)
```

### Examples

```r
data(m)
```

### newCCSPrams

*New Params*

### Description

Create a new CCSPrams object.

### Usage

```r
newCCSPrams()
```

### Arguments

Nothing.

### Value

New Params object.

### Examples

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

**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=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)
```
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