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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**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**

```r
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, 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").
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

```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) 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

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,
doenrich=TRUE, ncgenrich=TRUE, dgenrich=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 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

sce A object generated by instantiation 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

   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 = 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 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**

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**

`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)
```

---

**newCCSParsms**  

*New Params*

---

**Description**

Create a new CCSParsms object.

**Usage**

```r
newCCSParsms()
```

**Arguments**

Nothing.

**Value**

New Params object.

**Examples**

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

*Set a parameter*

---

**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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