

Package ‘scTensor’

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Type Package

Title Detection of cell-cell interaction from single-cell RNA-seq 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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| | |
|------------------|--|
| scTensor-package | <i>Detection of cell-cell interaction from single-cell RNA-seq dataset by tensor decomposition</i> |
|------------------|--|

Description

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

Details

The DESCRIPTION file: This package was not yet installed at build time.

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Author(s)

NA

Maintainer: NA

See Also

[GermMale](#), [labelGermMale](#), [tsneGermMale](#), [cellCellSetting](#), [cellCellDecomp](#), [cellCellReport](#)

Examples

```
ls("package:scTensor")
```

| | |
|------------------|--------------------|
| CCSPParams-class | Class "CCSPParams" |
|------------------|--------------------|

Description

The parameter object to be specified against cellCellSimulate function.

Objects from the Class

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

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

newCCSPParams Generator of CCSPParams object.

getParam Getter function of the slot in CCSPParams object.

setParam<- Setter function of the slot in CCSPParams object.

See Also

[newCCSPParams](#), [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), th
  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 | <i>Rank estimation of the CCI-tensor</i> |
|---------------|--|

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 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 | <i>HTML report of the result of scTensor</i> |
|----------------|--|

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, dgngenrich=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 | The threshold of p-value of the enrichment analysis (Default: 1E-2) |
| upper | The maximum number of HTML reports generated (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) |
| ncgenrich | Whether NCG-Enrichment analysis is performed (Default: TRUE) |
| dgnenrich | Whether DGN-Enrichment analysis is performed (Default: TRUE) |
| nbins | 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, dgenrich=TRUE, nbins=40)
}else{
  showMethods("cellCellReport")
}

```

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 distingusishing 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 |

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 = newCCSParams(), verbose = TRUE)
```

Arguments

params A parameter object generated by newCCSParams().
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 | <i>The matrix which is used as test data of scTensor.</i> |
|----------|---|

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

Li L. and Dong J. and Yan L. and Yong J. et al. (2017) Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. *Cell Stem Cell*, **20(6)**: 858-873

See Also

[labelGermMale](#), [tsneGermMale](#).

Examples

```
data(GermMale)
```

| | |
|----------|------------------------|
| getParam | <i>Get a parameter</i> |
|----------|------------------------|

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

```
params <- newCCSParams()

getParam(params, "nGene")
getParam(params, "nCell")
getParam(params, "cciInfo")
getParam(params, "lambda")
getParam(params, "seed")
```

| | |
|---------------|--|
| labelGermMale | <i>The vector contains the celltype information and color scheme of GermMale</i> |
|---------------|--|

Description

A vector with 852 length (cells).

Usage

```
data(labelGermMale)
```

Details

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

References

Li L. and Dong J. and Yan L. and Yong J. et al. (2017) Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. *Cell Stem Cell*, **20(6)**: 858-873

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)
```

`newCCSParams` *New Params*

Description

Create a new CCSParams object.

Usage

```
newCCSParams()
```

Arguments

Nothing.

Value

New Params object.

Examples

```
params <- newCCSParams()
```

| | |
|----------|------------------------|
| setParam | <i>Set a parameter</i> |
|----------|------------------------|

Description

Function for setting parameter values.

Usage

```
setParam(object, name) <- value
## S4 method for signature 'CCSPParams'
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 <- newCCSPParams()

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

```
data(tsneGermMale)
```

Details

Rtsne is performed as follows.

```
library(Rtsne) set.seed(123) tsneGermMale <- Rtsne(dist(t(GermMale)), is_distance=TRUE, perplexity=40)
```

References

Li L. and Dong J. and Yan L. and Yong J. et al. (2017) Single-Cell RNA-Seq Analysis Maps Development of Human Germline Cells and Gonadal Niche Interactions. *Cell Stem Cell*, **20(6)**: 858-873

See Also

[labelGermMale](#), [GermMale](#).

Examples

```
data(tsneGermMale)
```

`v`*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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