

Package ‘scTGIF’

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Type Package

Title Cell type annotation for unannotated single-cell RNA-Seq data

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Suggests testthat

Description scTGIF connects the cells and the related gene functions without cell type label.

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| | |
|----------------|--|
| scTGIF-package | <i>Cell type annotation for unannotated single-cell RNA-Seq data</i> |
|----------------|--|

Description

scTGIF connects the cells and the related gene functions without cell type label.

Details

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

Index: This package was not yet installed at build time.

[calcTGIF](#) function calculates what kind of cellular patterns and functional patterns are contained in single-cell RNA-seq data and [reportTGIF](#) function generates report of analytic result. The algorithm is based on joint NMF, which is implemented in nnTensor package.

Author(s)

NA

Maintainer: NA

References

Dominic Grun, Anna Lyubimova, Lennart Kester, Kay Wiebrands, Onur Basak, Nobuo Sasaki, Hans Clevers, Alexander van Oudenaarden (2015) Single-cell messenger RNA sequencing reveals rare intestinal cell types. *Nature*, **525**: 251-255

| | |
|----------|---|
| calcTGIF | <i>Function for connecting cellular patterns and functional patterns using jNMF</i> |
|----------|---|

Description

[calcTGIF](#) function calculates what kind of cellular patterns and functional patterns are contained in single-cell RNA-seq data and [reportTGIF](#) function generates report of analytic result.

Usage

```
calcTGIF(sce, ndim, verbose=FALSE, droplet=TRUE)
```

Arguments

| | |
|---------|--|
| sce | A object generated by instantiation of SingleCellExperiment-class. |
| ndim | The number of low-dimension of joint NMF algorithm. |
| verbose | The verbose parameter for nnTensor::jNMF (Default: FALSE). |
| droplet | Whether Droplet-based single-cell RNA-Seq or not (Default: TRUE). |

Value

The result is saved to metadata slot of SingleCellExperiment object.

Author(s)

NA

Examples

```
showMethods("calcTGIF")
```

| | |
|-----------------|--|
| cellMarkerToGmt | <i>A function to convert the CellMarker data to GMT files.</i> |
|-----------------|--|

Description

The GMT (Gene Matrix Transposed file format : *.gmt) file is formatted by the Broad Institute (https://software.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data_formats#GMT:_Gene_Matrix_Transposed_files)
The data can be downloaded from the website of CellMarker (<http://biocc.hrbmu.edu.cn/CellMarker>).

Usage

```
cellMarkerToGmt(infile, outfile,
  uniq.column=c("tissueType", "cellName"),
  geneid.type=c("geneID", "geneSymbol"))
```

Arguments

| | |
|-------------|--|
| infile | The input file downloaded from CellMarker website |
| outfile | The output GMT file converted from the CellMarker data |
| uniq.column | The duplicated terms in the specified column are aggregated as a row of GMT file (Default: geneID) |
| geneid.type | Output gene identifier. (Default: geneID) |

Value

output A GMT file is generated.

Author(s)

NA

Examples

```

library("GSEABase")

tmp <- tempdir()
infile1 = paste0(tmp, "/Human_cell_markers.txt")
outfile1_1 = paste0(tmp, "/Human_cell_markers_1.gmt")
outfile1_2 = paste0(tmp, "/Human_cell_markers_2.gmt")
outfile1_3 = paste0(tmp, "/Human_cell_markers_3.gmt")
outfile1_4 = paste0(tmp, "/Human_cell_markers_4.gmt")

sink(infile1)
cat("speciesType\ttissueType\tUberonOntologyID\tcancerType\tcellType\tcellName\tCellOntologyID\tcellMarker\tgt
cat("Human\tKidney\tUBERON_0002113\tNormal\tNormal cell\tProximal tubular cell\tNA\tIntestinal Alkaline Phospha
cat("Human\tLiver\tUBERON_0002107\tNormal\tNormal cell\tIto cell (hepatic stellate cell)\tCL_0000632\tSynaptoph
cat("Human\tEndometrium\tUBERON_0001295\tNormal\tNormal cell\tTrophoblast cell\tCL_0000351\tCEACAM1\tCEACAM1\t
cat("Human\tGerm\tUBERON_0000923\tNormal\tNormal cell\tPrimordial germ cell\tCL_0000670\tVASA\tDDX4\t54514\tDD
cat("Human\tCorneal epithelium\tUBERON_0001772\tNormal\tNormal cell\tEpithelial cell\tCL_0000066\tKLF6\tKLF6\t
cat("Human\tPlacenta\tUBERON_0001987\tNormal\tNormal cell\tCytotrophoblast\tCL_0000351\tFGF10\tFGF10\t2255\tF
cat("Human\tPeriosteum\tUBERON_0002515\tNormal\tNormal cell\tPeriosteum-derived progenitor cell\tNA\tCD166, CD
cat("Human\tAmniotic membrane\tUBERON_0009742\tNormal\tNormal cell\tAmnion epithelial cell\tCL_0002536\tNANOG,
cat("Human\tPrimitive streak\tUBERON_0004341\tNormal\tNormal cell\tPrimitive streak cell\tNA\tLHX1, MIXL1\tLHX1
sink()

cellMarkerToGmt(infile1, outfile1_1, uniq.column=c("tissueType"),
  geneid.type=c("geneID"))
cellMarkerToGmt(infile1, outfile1_2, uniq.column=c("tissueType"),
  geneid.type=c("geneSymbol"))
cellMarkerToGmt(infile1, outfile1_3, uniq.column=c("cellName"),
  geneid.type=c("geneID"))
cellMarkerToGmt(infile1, outfile1_4, uniq.column=c("cellName"),
  geneid.type=c("geneSymbol"))

gmt1_1 <- getGmt(outfile1_1)
gmt1_2 <- getGmt(outfile1_2)
gmt1_3 <- getGmt(outfile1_3)
gmt1_4 <- getGmt(outfile1_4)

```

 convertRowID

A function to change the row names of a matrix.

Description

To avoid to specify the duplicated row names against matrix, multiple aggregation rules are implemented.

Usage

```
convertRowID(input, rowID, LtoR,
             aggr.rule=c("sum", "mean", "large.mean", "large.var", "large.cv2"))
```

Arguments

| | |
|-----------|---|
| input | A matrix filled with number (n * m). |
| rowID | A vector to specify the row names of input (length: n). |
| LtoR | A corresponding table to covert the row names of input as different type of IDs. (Left: current row names -> Right: new row names) |
| aggr.rule | The aggregation rule to change the row names of input and collapse/select the values, if the row names changed by LtoR are duplicated. sum: Collapses multiple row vectors by summation. mean: Collapses multiple row vectors by mean. large.mean: Select a vector having the largest mean in the duplicated vectors. large.var: Select a vector having the largest variance in the duplicated vectors. large.cv2: Select a vector having the largest CV2 in the duplicated vectors. |

Value

| | |
|--------|--|
| output | A matrix, in which the row names are changed, according to the aggregation rule user specified. |
| ctable | The corresponding table explaining the relationship between previous row names and changed row names of input. |

Author(s)

NA

Examples

```
input <- matrix(1:20, nrow=4, ncol=5)
rowID <- c("A", "B", "C", "D")
LtoR <- rbind(
  c("A", "3"),
  c("B", "2"),
  c("C", "4"),
  c("D", "7"))
(input2 <- convertRowID(input, rowID, LtoR, "sum"))
(input3 <- convertRowID(input, rowID, LtoR, "mean"))
(input4 <- convertRowID(input, rowID, LtoR, "large.mean"))
(input5 <- convertRowID(input, rowID, LtoR, "large.var"))
(input6 <- convertRowID(input, rowID, LtoR, "large.cv2"))
```

DistalLungEpithelium *Gene expression matrix of DistalLungEpithelium dataset containing five cluster.*

Description

A data frame with 3397 rows (genes) with following 80 columns (cells).

The data is downloaded as supplementary information of the distal lung epithelium paper (<https://www.nature.com/articles/nature13005>)

Low-expressed genes are filtered.

All Gene ID is converted to Human Entrez Gene ID for applying the data to scTGIF.

Usage

```
data("DistalLungEpithelium")
```

Source

<http://www.nature.com/nbt/journal/v33/n2/full/nbt.3102.html>

References

Treutlein, B. et al. (2014) Reconstructing lineage hierarchies of the distal lung epithelium using single-cell RNA-seq. *Nature* **509**, 371-375

Examples

```
data("DistalLungEpithelium")
```

label.DistalLungEpithelium
Cellular label of DistalLungEpithelium dataset containing five cluster.

Description

A vector containing 80 elements (cells).

Usage

```
data("label.DistalLungEpithelium")
```

References

Treutlein, B. et al. (2014) Reconstructing lineage hierarchies of the distal lung epithelium using single-cell RNA-seq. *Nature* **509**, 371-375

Examples

```
data("label.DistalLungEpithelium")
```

```
pca.DistalLungEpithelium
```

The result of PCA of the DistalLungEpithelium dataset.

Description

A matrix having 80 (cells) * 2 (PCs) elements.

Usage

```
data("pca.DistalLungEpithelium")
```

References

Treutlein, B. et al. (2014) Reconstructing lineage hierarchies of the distal lung epithelium using single-cell RNA-seq. *Nature* **509**, 371-375

Examples

```
data("pca.DistalLungEpithelium")
```

```
reportTGIF
```

Function for reporting the result of [calcTGIF](#) function

Description

[calcTGIF](#) function calculates what kind of cellular patterns and functional patterns are contained in single-cell RNA-seq data and [reportTGIF](#) function generates report of analytic result.

Usage

```
reportTGIF(sce, out.dir=tempdir(), html.open=FALSE,
           title="The result of scTGIF",
           author="The person who runs this script",
           assayNames="counts")
```

Arguments

| | |
|------------|--|
| sce | A object generated by instantiation of SingleCellExperiment-class. |
| out.dir | Output directory user want to save the report (Default: tempdir()). |
| html.open | Whether html is opened when reportTGIF is finished (Default: FALSE) |
| title | Title of report (Default: "The result of scTGIF") |
| author | The name of user name (Default: "The person who runs this script") |
| assayNames | The unit of gene expression for using scTGIF (e.g. normcounts, cpm...etc) (Default: "counts"). |

Value

Some file is generated to output directory user specified.

Author(s)

NA

Examples

```

if(interactive()){
  # Package loading
  library("SingleCellExperiment")
  library("GSEABase")
  library("msigbr")

  # Test data
  data("DistalLungEpithelium")
  data("pca.DistalLungEpithelium")
  data("label.DistalLungEpithelium")

  # Test data
  par(ask=FALSE)
  plot(pca.DistalLungEpithelium, col=label.DistalLungEpithelium, pch=16,
       main="Distal lung epithelium dataset", xlab="PCA1",
       ylab="PCA2", bty="n")
  text(0.1, 0.05, "AT1", col="#FF7F00", cex=2)
  text(0.07, -0.15, "AT2", col="#E41A1C", cex=2)
  text(0.13, -0.04, "BP", col="#A65628", cex=2)
  text(0.125, -0.15, "Clara", col="#377EB8", cex=2)
  text(0.09, -0.2, "Ciliated", col="#4DAF4A", cex=2)

  # Load the gmt file from MSigDB
  # Only "Entrez Gene ID" can be used in scTGIF
  # e.g. gmt <- GSEABase::getGmt(
  #   "/PATH/YOU/SAVED/THE/GMTFILES/h.all.v6.0.entrez.gmt")
  # Here we use msigbr to retrieve mouse gene sets

  # Mouse gene set (NCBI Gene ID)
  m_df <- msigbr(species = "Mus musculus", category = "H"),
  c("gs_name", "entrez_gene")]

  # Convert to GeneSetCollection
  hallmark = unique(m_df$gs_name)
  gsc <- lapply(hallmark, function(h){
    target = which(m_df$gs_name == h)
    geneIds = unique(as.character(m_df$entrez_gene[target]))
    GeneSet(setName=h, geneIds)
  })
  gmt <- GeneSetCollection(gsc)

  # SingleCellExperiment-class
  sce <- SingleCellExperiment(

```



```

    assays = list(counts = DistalLungEpithelium))
  reducedDims(sce) <- SimpleList(PCA=pca.DistalLungEpithelium)

  # 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)
  settingTGIF(sce, gmt, reducedDimNames="PCA",
    assayNames="normcounts")

  # Functional Annotation based on jNMF
  calcTGIF(sce, ndim=7)

  # HTML Reprt
  reportTGIF(sce,
    html.open=TRUE,
    title="scTGIF Report for DistalLungEpithelium dataset",
    author="Koki Tsuyuzaki")
}

```

 settingTGIF

Parameter setting for scTGIF

Description

All parameters is saved to metadata slot of SingleCellExperiment object.

Usage

```
settingTGIF(sce, gmt, reducedDimNames, assayNames="counts", nbins=40)
```

Arguments

| | |
|-----------------|--|
| sce | A object generated by instantiation of SingleCellExperiment-class. |
| gmt | Object generated from GSEABase::getGmt function. GMT file can be downloaded from MSigDB web (site http://software.broadinstitute.org/gsea/login.jsp#msigdb). Please confirm that the gmt file contains Human Entrez Gene ID, not gene symbol. Also confirm that the DataMatrix has Human Entrez Gene ID. |
| reducedDimNames | The names of reducedDim(sce) that user want use in scTGIF. |
| assayNames | The unit of gene expression for using scTGIF (e.g. normcounts, cpm...etc) (Default: "counts"). |
| nbins | The number of bins of schex (Default: 40). |

Value

The result is saved to metadata slot of SingleCellExperiment object.

Author(s)

NA

Examples

```
showMethods("settingTGIF")
```

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