# Package: scTGIF (via r-universe)

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**Type** Package

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

**Version** 1.27.0

**Depends** R (>= 3.6.0)

**Imports** GSEABase, Biobase, SingleCellExperiment, BiocStyle, plotly, tagcloud, rmarkdown, Rcpp, grDevices, graphics, utils, knitr, S4Vectors, SummarizedExperiment, RColorBrewer, nnTensor, methods, scales, msigdbr, schex, tibble, ggplot2, igraph

**Suggests** testthat

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

**License** Artistic-2.0

**biocViews** DimensionReduction, QualityControl, SingleCell, Software, GeneExpression

**VignetteBuilder** knitr

**Config/pak/sysreqs** libabsl-dev cmake libfontconfig1-dev libfreetype6-dev libgdal-dev gdal-bin libgeos-dev libglpk-dev make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev libnode-dev zlib1g-dev

**Repository** https://bioc.r-universe.dev

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`scTGIF-package` *Cell type annotation for unannotated single-cell RNA-Seq data*

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## 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)

Koki Tsuyuzaki [aut, cre]

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## 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` *Function for connecting cellular patterns and functional patterns using jNMF*

---

## 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 instantization 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)

Koki Tsuyuzaki [aut, cre]

### Examples

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

---

## cellMarkerToGmt *A function to convert the CellMarker data to GMT files.*

---

### 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_fi
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 aggrgated as a row of GMT file (Default: geneID) |
| geneid.type | Output gene identifier. (Default: geneID) |

### Value

| | |
|---|---|
| output | A GMT file is generated. |

## Author(s)

Koki Tsuyuzaki [aut, cre]

## 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\tg
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.<br>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)

Koki Tsuyuzaki [aut, cre]

## 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/na

Low-expressed genes are filted.

*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 instantization 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)

Koki Tsuyuzaki [aut, cre]

## Examples

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

    # 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, "Cilliated", 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 msigdbr to retrieve mouse gene sets

    # Mouse gene set (NCBI Gene ID)
    m_df <- msigdbr(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` *Paramter 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 instantization 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)

Koki Tsuyuzaki [aut, cre]

## Examples

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

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