Package 'SAVERg'

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Type Package

Title A supplementary package to package SAVER

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Description Carry out cell clustering analysis and pseudotime trajectory analysis to assess the imputation accuracy of SAVER.

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Depends R (>= 3.0.1)

Imports SAVER, TSCAN, igraph, Rtsne, mclust, scales

Suggests knitr

VignetteBuilder knitr

R topics documented:

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cell_clustering   *Cell clustering analysis*

Description

Cell clustering analysis

Usage

```
cell_clustering(count_data, percent = 0.1, ncores = 4,
  perplexity = 30, need.imputation = FALSE, imputed.data = TRUE)
```

Arguments

count_data	The count expression matrix. The rows correspond to genes and the columns correspond to cells. Can be sparse.
percent	Genes that are expressed in less than 100*percent% of the cells are filtered out. Default is 0.1.
ncores	Number of cores to use. Default is 4.
perplexity	Perplexity parameter of function Rtsne.
need.imputation	
	Whether the input matrix needs imputation. Default is FALSE.
imputed.data	Whether the input matrix has been imputed. Default is TRUE.

Value

The t-SNE visualization and aRI value of the dataset.

Author(s)

Yiqiu Tan

Examples

```
data('ipsc_saver')
cell_clustering(ipsc_saver)
```

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preprocessing	*Normalization*

Description

Performs preprocessing and log-normalization on the raw count dataset.

Usage

```
preprocessing(x, percent)

log_normalization(x)
```

Arguments

x	The expression matrix that needs preprocessing or log-normalization.
percent	Genes that are expressed in less than 100*percent% of the cells are filtered out.

Value

The preprocessed and log-normalized expression matrix.

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trajectory_analysis *Pseudotime trajectory analysis*

Description

Carries out cell trajectory analysis to assess the imputation accuracy of SAVER.

Usage

```
trajectory_analysis(count_data, cellLabels, percent = 0.1, ncores = 4,
  need.imputation = FALSE, imputed.data = TRUE)
```

Arguments

count_data	The count expression matrix. The rows correspond to genes and the columns correspond to cells. Can be sparse.
cellLabels	The cell labels of the dataset, which is the gold standard of the trajectory analysis.
percent	Genes that are expressed in less than 100*percent% of the cells are filtered out. Default is 0.1.
ncores	Number of cores to use. Default is 4.
need.imputation	
	Whether the input matrix needs imputation. Default is FALSE.
imputed.data	Whether the input matrix has been imputed. Default is TRUE.

Value

Two metrics: Pseudo-temporal Ordering Score (POS) and Kendall's rank correlation score, which are used to assess the accuracy of the inferred cell trajectory and the plot of the cell trajectory.

Author(s)

Yiqiu Tang

Examples

```
data('deng_saver')
deng_cellLabels <- factor(colnames(deng_saver),
                          levels=c('zygote', 'early 2-cell',
                                   'mid 2-cell', 'late 2-cell',
                                   '4-cell', '8-cell', '16-cell', 'early blastocyst',
                                   'mid blastocyst', 'late blastocyst'))
trajectory_analysis(deng_saver, deng_cellLabels)
```

Index