

Package ‘TimeCCI’

August 30, 2024

Type Package

Title Temporal Cell-Cell Interaction Analysis in Single-Cell RNA-seq Data

Version 1.0.0

Description This package offers tools to analyze temporal correlations in cell-cell communication, specifically calculating dynamic ligand-receptor interactions over pseudotime and inferring the influence of one cell type on another's evolution, providing insights into the timing and impact of cellular interactions in biological processes.

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Imports tidy,
Seurat,
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future,
tibble

Depends R (>= 3.1.0)

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LRdf

LRdf: Ligand-Receptor Interaction Database

Description

A data frame containing ligand-receptor interactions derived from the CellChat database. This dataset includes the interaction name, ligand symbol, and receptor symbol.

Usage

```
LRdf
```

Format

A data frame with columns:

interaction_name The name of the ligand-receptor interaction.

ligand.symbol The symbol of the ligand gene.

receptor.symbol The symbol of the receptor gene.

Source

CellChatDB.human\$interaction

Examples

```
data(LRdf)
head(LRdf)
```

seu.example

seu.example: Seurat Object for mCAF and Tumor Epithelial Cells

Description

A Seurat object containing single-cell RNA-seq data and metadata for mCAF and tumor epithelial cells. This object includes the RNA assay and relevant metadata such as cell type and pseudotime annotations.

Usage

```
seu.example
```

Format

A Seurat object with RNA assay data and metadata:

RNA The RNA assay data containing gene expression values.

meta.data Metadata including cell type annotations and pseudotime values.

Examples

```
data(seu.example)
seu.example
```

TemporalCCI1

*Temporal Cell-Cell Interaction Analysis via Cell Alignment in Pseudotime***Description**

This function performs a temporal cell-cell interaction (CCI) analysis between two specified cell types over pseudotime. It leverages ligand-receptor interaction data to assess the correlation between ligand expression in one cell type and receptor expression in another across a defined pseudotime trajectory.

Usage

```
TemporalCCI1(
  seu.obj,
  CellType.name = "Cell.Type",
  Pseudotime.name = "Pseudotime",
  CCI.database = LRdf,
  source.celltype = "mCAF",
  target.celltype = "EpiT",
  window.size = 0.1,
  num.pts = 200,
  num.cores = 10,
  granger.cutoff = 0.01
)
```

Arguments

<code>seu.obj</code>	A Seurat object containing single-cell RNA-seq data and metadata.
<code>CellType.name</code>	A string specifying the name of the cell type annotation in the Seurat object metadata. Default is "Cell.Type".
<code>Pseudotime.name</code>	A string specifying the name of the pseudotime annotation in the Seurat object metadata. Default is "Pseudotime".
<code>CCI.database</code>	A data frame containing ligand-receptor interaction pairs with columns "interaction_name", "ligand.symbol", and "receptor.symbol".
<code>source.celltype</code>	A string specifying the source cell type for the ligand in the CCI analysis. Default is "mCAF".
<code>target.celltype</code>	A string specifying the target cell type for the receptor in the CCI analysis. Default is "EpiT".
<code>window.size</code>	A numeric value defining the window size for trajectory alignment. Default is 0.1.
<code>num.pts</code>	An integer specifying the number of points for trajectory interpolation. Default is 200.
<code>num.cores</code>	An integer specifying the number of CPU cores to use for parallel processing. Default is 10.
<code>granger.cutoff</code>	A numeric value for the p-value cutoff in Granger causality tests. Default is 0.01.

Details

This function is designed to analyze temporal changes in cell-cell communication by evaluating ligand-receptor pair correlations over pseudotime. It uses interpolation methods to align gene expression trajectories, enabling the comparison of expression patterns between a source and a target cell type. The function filters out ligand-receptor pairs that are not present in the RNA assay of the Seurat object. Correlation analyses are performed using both Pearson and Spearman methods, and the results are compiled into a comprehensive data frame. Parallel processing is supported to expedite computations.

Value

A list containing:

<code>res</code>	A data frame with correlation results between ligand and receptor pairs, including Pearson and Spearman correlation coefficients and p-values.
<code>source.align.matrix</code>	A data frame with the aligned and interpolated expression matrix of the source cell type.
<code>target.align.matrix</code>	A data frame with the aligned and interpolated expression matrix of the target cell type.

Author(s)

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TemporalCCI2	<i>Temporal Cell-Cell Interaction Analysis with Discrete Pseudotime Binning</i>
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Description

This function performs cell-cell interaction (CCI) analysis over discrete pseudotime intervals. It utilizes the CellChat framework to identify and analyze ligand-receptor interactions across different stages of pseudotime, and computes correlations between interaction probabilities and pseudotime stages.

Usage

```
TemporalCCI2(
  seu.obj,
  Pseudotime.name = "Pseudotime",
  CellType.name = "Cell.Type",
  discrete.numer = 20,
  CCI.database = CellChat::CellChatDB.human,
  interaction.name = "interaction_name_2"
)
```

Arguments

<code>seu.obj</code>	A Seurat object containing single-cell RNA-seq data and metadata.
<code>Pseudotime.name</code>	A string specifying the name of the pseudotime annotation in the Seurat object metadata. Default is "Pseudotime".
<code>CellType.name</code>	A string specifying the name of the cell type annotation in the Seurat object metadata. Default is "Cell.Type".
<code>discrete.numer</code>	An integer specifying the number of discrete pseudotime intervals to create. Default is 20.
<code>CCI.database</code>	A CellChat database object containing ligand-receptor interactions. Default is <code>CellChat::CellChatDB.human</code> .
<code>interaction.name</code>	A string specifying the interaction name column in the CCI database. Default is "interaction_name_2".

Details

This function first divides the pseudotime into discrete intervals and assigns each cell to an interval. It then uses the CellChat package to analyze cell-cell communication based on ligand-receptor interactions, computing the communication probabilities for each interaction across the pseudotime intervals. The function also performs correlation analyses between these probabilities and the pseudotime stages, providing insights into how interactions evolve over time.

Value

A list containing:

<code>cor.res</code>	A data frame with correlation results between interaction probabilities and pseudotime stages, including Pearson and Spearman correlation coefficients and p-values.
<code>cal.res.wide</code>	A wide-format data frame with interaction probabilities across pseudotime stages.
<code>cal.res.long</code>	A long-format data frame with interaction probabilities and corresponding pseudotime stages.
<code>cellchat</code>	The CellChat object used for the analysis, containing all intermediate results.

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