

Package ‘NewCCI’

September 11, 2024

Type Package

Title Identify Novel Cell-Cell Interactions

Version 1.0.0

Description This function allows users to input their hypothesized ligand candidates and apply statistical methods for receptor filtering in target cells, further revealing novel cell-cell interactions based on the CellChat algorithm.

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Imports Seurat,
CellChat,
dplyr,
TimeCCI,
presto

Depends R (>= 3.1.0)

Contents

FindNewCCI	1
Index	4

FindNewCCI	<i>Identifying New Cell-Cell Interactions Using Latent Ligands</i>
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Description

This function performs a detailed analysis of cell-cell interactions (CCI) in single-cell RNA sequencing data using latent ligand-receptor pairs. The function integrates cell type information and differentially expressed genes to identify potential cell-cell interactions. It uses the CellChat database and the wilcoxauc method from Presto for differential expression analysis.

Usage

```
FindNewCCI(
  seu.obj,
  latent.ligands,
  source.celltype,
  target.celltype,
  celltype.colname = "Cell.Type",
  logFC.cutoff = 0.2,
  pct.dff.cutoff = 0.1,
  padj.cutoff = 0.05,
  CCI.database = TimeCCI::LRdf,
  species = "human"
)
```

Arguments

<code>seu.obj</code>	A Seurat object containing the single-cell RNA-seq data.
<code>latent.ligands</code>	A vector of latent ligand gene symbols that are hypothesized to be involved in cell-cell communication.
<code>source.celltype</code>	The source cell type from which ligand signals are hypothesized to originate.
<code>target.celltype</code>	The target cell type that receives signals via receptors.
<code>celltype.colname</code>	The name of the column in <code>seu.obj@meta.data</code> that contains the cell type annotations. Default is 'Cell.Type'.
<code>logFC.cutoff</code>	Numeric value specifying the log fold change threshold for filtering differentially expressed genes. Default is 0.2.
<code>pct.dff.cutoff</code>	Numeric value for the percent difference cutoff between in-group and out-group cells. Default is 0.1.
<code>padj.cutoff</code>	Numeric value specifying the adjusted p-value threshold for filtering significant interactions. Default is 0.05.
<code>CCI.database</code>	The CellChat database to use for CCI analysis. Default is <code>TimeCCI::LRdf</code> .
<code>species</code>	The species for the analysis. Default is "human".

Details

This function operates as follows:

1. Differential expression analysis is performed on the target cell type using the Wilcoxon rank-sum test via the `presto::wilcoxauc()` function.
2. Genes are filtered based on log fold change, percentage difference, and adjusted p-value cutoffs.
3. Receptor genes are identified from the latent ligand-receptor pairs and filtered from the differentially expressed genes.
4. A custom ligand-receptor interaction database is created using the provided latent ligands and the receptors identified from differentially expressed genes.
5. The function creates a CellChat object from the Seurat object's expression data and metadata.

6. The custom ligand-receptor database is applied, and the CellChat pipeline is executed to identify overexpressed genes and interactions, compute communication probabilities, and aggregate interaction networks.

The function returns a CellChat object that can be further used for visualizing and interpreting cell-cell communication.

Value

A CellChat object containing identified cell-cell interactions between the specified source and target cell types based on the given ligand-receptor pairs.

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Index

FindNewCCI, [1](#)