Package 'scPipeline'

March 7, 2025

Title A Wrapper for 'Seurat' and Related R Packages for End-to-End Single Cell Analysis

Version 0.2.0.0

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Description Reports markers list, differentially expressed genes, associated pathways, cell-type annotations, does batch correction and other related single cell analyses all wrapped within 'Seurat'.

Imports Seurat, batchelor, dplyr, ReactomeGSA, celldex, SingleR, SummarizedExperiment, biomaRt, magrittr, rlang

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Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

Suggests knitr, rmarkdown

NeedsCompilation no

Repository CRAN

Date/Publication 2025-03-07 11:40:06 UTC

Contents

AnnotateCellsWithSingleR

Annotate cells in a Seurat object using SingleR with Celldex

Description

This function annotates the cells in a Seurat object using the SingleR package with reference data obtained from the Celldex package.

Usage

```
AnnotateCellsWithSingleR(seurat_object, reference_data = NULL, assay = "RNA")
```

Arguments

seurat_object	A Seurat object to be annotated.
reference_data	A reference dataset to use for annotation (e.g., HumanPrimaryCellAtlasData from Celldex). If NULL, HumanPrimaryCellAtlasData is used by default.
assay	The assay in the Seurat object to use for annotation. Default is "RNA".

Value

The Seurat object with cell annotations added to the metadata.

ConvertGeneIdentifiers

Convert Gene Identifiers in a Seurat Object

Description

This function takes a Seurat object with gene identifiers as row names (e.g., RefSeq, Ensembl, Entrez) and converts those identifiers to gene symbols (or Ensembl Gene IDs) using the biomaRt package. The function can handle various types of gene identifiers and returns a Seurat object with updated row names.

Usage

```
ConvertGeneIdentifiers(
  seurat_object,
  id_type = "refseq",
  to_id_type = "symbol"
)
```

Arguments

seurat_object	A Seurat object. The row names of the Seurat object's data or assay slot should represent gene identifiers (e.g., RefSeq, Ensembl, or Entrez IDs).
id_type	A string specifying the type of the input gene identifiers. Options are: "refseq", "ensembl", "entrez". Default is "refseq".
to_id_type	A string specifying the type of output gene identifiers. Options are: "symbol", "ensembl". Default is "symbol".

Value

A Seurat object with updated gene names (row names) based on the specified conversion.

Examples

```
# Read 10X counts data from matrix.mtx, barcodes.tsv and genes.tsv
library(Seurat)
counts <- Read10X(data.dir = "../inst/extdata", gene.column = 1)

# Create Seurat object without batch correction
seurat_obj <- SeuratPreprocess(counts)
seurat_obj <- SeuratLowDim(seurat_obj)
# Convert RefSeq IDs to gene symbols
seurat_obj_converted <- ConvertGeneIdentifiers(
  seurat_obj,
  id_type = "refseq",
  to_id_type = "symbol"
)
```

ReactomeData *Reactome Data Analysis for Seurat Object*

Description

This function performs pathway analysis using ReactomeGSA on a Seurat object with cluster information.

Usage

```
ReactomeData(lowdim_seurat_object)
```

Arguments

lowdim_seurat_object	Seurat object that has clusters information

Value

A list containing: - GSVA result (`gsva_result`) - Pathway expression data (`pathway_expression`) - Max difference between pathway expression values (`max_difference`)

Examples

```
library(Seurat)
# Read 10X counts data from matrix.mtx, barcodes.tsv and genes.tsv
counts <- Read10X(data.dir = "../inst/extdata", gene.column = 1)

# Create Seurat object without batch correction
seurat_obj <- SeuratPreprocess(counts)
seurat_obj <- SeuratLowDim(seurat_obj)
# Reactome Analysis
seurat_reactome <- ReactomeData(seurat_obj)
```

SeuratLowDim *Create a Low dimensional Seurat object from scaled seurat object*

Description

This function converts the transformed data to low-dimensional data for downstream analysis.

Usage

```
SeuratLowDim(scaled_seurat_object, ...)
```

Arguments

`scaled_seurat_object`	A scaled Seurat object.
`...`	Additional arguments to be passed for downstream analyses.

Value

A Seurat object.

Examples

```
library(Seurat)
# Read 10X counts data from matrix.mtx, barcodes.tsv and genes.tsv
counts <- Read10X(data.dir = "../inst/extdata", gene.column = 1)

# Create Seurat object without batch correction
seurat_obj <- SeuratPreprocess(counts)
seurat_obj <- SeuratLowDim(seurat_obj)
```

SeuratMarkers *A thresholded markers list for better calculation of DE genes*

Description

This function calculates differentially expressed genes using Seurat::FindAllMarkers.

Usage

```
SeuratMarkers(lowdim_seurat_object)
```

Arguments

lowdim_seurat_object	Seurat object with cluster information

Value

A list containing two marker lists: - Full markers list - Thresholded markers list with `min.pct = 0.1`

Examples

```
library(Seurat)
# Read 10X counts data from matrix.mtx, barcodes.tsv and genes.tsv
counts <- Read10X(data.dir = "../inst/extdata", gene.column = 1)

# Create Seurat object without batch correction
seurat_obj <- SeuratPreprocess(counts)
seurat_obj <- SeuratLowDim(seurat_obj)
# Create Markers list
seurat_markers <- SeuratMarkers(seurat_obj)
```

SeuratPreprocess *Preprocess count data and create a Seurat object*

Description

This function preprocesses count data, optionally applying batch correction using batchelor::fastMNN, and creates a Seurat object.

Usage

```
SeuratPreprocess(
  counts_data,
  meta.data = NULL,
  batch_column = NULL,
  use_fastMNN = FALSE,
  ...
)
```

Arguments

counts_data	A matrix or data frame of count data.
meta.data	A data frame containing metadata to include in the Seurat object. Default is NULL.
batch_column	A vector or factor specifying batch assignments for each cell. Default is NULL.
use_fastMNN	Logical. Whether to apply batch correction using fastMNN. Default is FALSE.
...	Additional arguments to be passed to Seurat::CreateSeuratObject.

Value

A Seurat object.

Examples

```
library(Seurat)
# Read 10X counts data from matrix.mtx, barcodes.tsv and genes.tsv
counts <- Read10X(data.dir = "../inst/extdata", gene.column = 1)

# Create Seurat object without batch correction
seurat_obj <- SeuratPreprocess(counts)
```

TransferAnnotations *Transfer annotations to Seurat clusters*

Description

This function assigns cluster-level annotations in a Seurat object based on the majority annotation of cells within each cluster.

Usage

```
TransferAnnotations(seurat_object, annotation_col, cluster_col, output_col)
```

Arguments

`seurat_object`	Seurat object containing cluster and annotation information.
`annotation_col`	The name of the metadata column with annotations (character string).
`cluster_col`	The name of the metadata column with cluster information (character string).
`output_col`	The name of the output column to store cluster annotations (character string).

Value

The Seurat object with an additional column in its metadata, specified by `output_col`.

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