

Package: scPipeline (via r-universe)

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

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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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`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	<i>A thresholded markers list for better calculation of DE genes</i>
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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	<i>Preprocess count data and create a Seurat object</i>
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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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