Package ‘scRNAsstat’

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Type  Package
Title  A Pipeline to Process Single Cell RNAseq Data
Version  0.1.1
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Description  A pipeline that can process single or multiple Single Cell RNAseq samples primarily specializes in Clustering and Dimensionality Reduction. Meanwhile we use common cell type marker genes for T cells, B cells, Myeloid cells, Epithelial cells, and stromal cells (Fibroblast, Endothelial cells, Pericyte, Smooth muscle cells) to visualize the Seurat clusters, to facilitate labeling them by biological names. Once users named each cluster, they can evaluate the quality of them again and find the de novo marker genes also.
License  AGPL (>= 3)
Encoding  UTF-8
LazyData  true
RoxygenNote  7.1.2
Depends  R (>= 2.10)
Imports  Seurat, ggplot2, stringr, clustree, magrittr, Matrix, dplyr, patchwork
NeedsCompilation  no
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Small 'AJ064' Seurat Data After Processed

**Description**

An object of class Seurat

**Usage**

AJ064_small_last_sce

**Format**

An object of class Seurat with 627 rows and 800 columns.

Small 'AJ064' Seurat Data Set

**Description**

An object of class Seurat

**Usage**

AJ064_small_sce

**Format**

An object of class Seurat with 713 rows and 1000 columns.
basic_filter

Description
filter the genes which show expression less than 3 cells. filter the cells which percent_mito < 25 & percent_ribo > 3 & percent_hb < 10 filter the cells which nFeature_RNA > 300 & nFeature_RNA < 8000

Usage
basic_filter(sce)

Arguments
sce An object of class Seurat

Value
sce.all.filt An object of class Seurat

Examples
basic_filter(AJ064_small_sce)

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basic_find_markers Basic Find Markers

Description
To find de ‘novo’ markers by ‘FindAllMarkers’ from Seurat with default setting.

Usage
basic_find_markers(sce, group = "seurat_clusters", dir = ".")

Arguments
sce An object of class Seurat
group default:seurat_clusters, you can change it to celltype
dir path for saving results

Value
sce.markers a data.frame of markers.
Examples

```r
basic_find_markers(AJ064_small_last_sce,dir=tempdir())
```

---

### basic_markers

**Basic Markers**

**Description**
Basic Markers

**Usage**

```r
basic_markers(sce, org = "human", group = "orig.ident", dir = ".")
```

**Arguments**

- `sce`: An object of class Seurat
- `org`: human or mouse, default: human
- `group`: default:'orig.ident', you can change it to ‘seurat_clusters’ or ‘celltype’
- `dir`: the path for saving the figures by ‘DotPlot’ with known famous markers.

**Value**

a list of figures by ‘DotPlot’

**Examples**

```r
basic_markers(AJ064_small_last_sce,dir=tempdir())
```

---

### basic_qc

**Basic Quality Control**

**Description**
add ‘percent_mito’, ‘percent_ribo’, ‘percent_hb’ to the Seurat class. And draw ‘VlnPlot’ for these ‘qc’ values.

**Usage**

```r
basic_qc(sce, org = "human", group = "orig.ident", dir = ".")
```
basic_workflow

Arguments

sce An object of class Seurat
org human or mouse, default: human
group default: 'orig.ident', you can change it to 'seurat_clusters' or 'celltype'
dir the path for saving the figures by 'DotPlot' with known famous markers.

Value

list(p1, p2, p3, sce), the last one in the new 'sce'.

Examples

basic_qc(AJ064_small_sce, dir = tempdir())

basic_workflow

Basic Workflow

Description

the workflow from Seurat, including: 'NormalizeData', 'FindVariableFeatures', 'ScaleData', 'RunPCA', 'RunTSNE', 'RunUMAP', 'FindNeighbors', 'FindClusters(sce, resolution = seq(0.1,1,by=0.1))' we use 'clustree' to check the different resolution for 'FindClusters'.

Usage

basic_workflow(sce, dir = ".")

Arguments

sce An object of class Seurat
dir the path for saving the figures by 'DotPlot' with known famous markers.

Value

list(p1, p2, p3, sce), the last one in the new sce with PCA, tSNE, UMAP information.

Examples

## Not run:
basic_workflow(AJ064_small_sce, dir = tempdir())

## End(Not run)
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