

Package ‘scRNAstat’

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Type Package

Title A Pipeline to Process Single Cell RNAseq Data

Version 0.1.1.1

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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

Suggests DBI

NeedsCompilation no

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AJ064_small_last_sce *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.

AJ064_small_sce *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	<i>basic_filter</i>
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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)
```

basic_find_markers	<i>Basic Find Markers</i>
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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

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

basic_markers

Basic Markers

Description

Basic Markers

Usage

```
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

```
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

```
basic_qc(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

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

Examples

```
basic_qc(AJ064_small_sce,dir= tempdir())
```

basic_workflow	<i>Basic Workflow</i>
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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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