

# Package ‘scRNAstat’

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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 (Fiboblast, 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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**Repository** CRAN

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## R topics documented:

AJ064_small_last_sce . . . . .	2
AJ064_small_sce . . . . .	2
basic_filter . . . . .	3
basic_find_markers . . . . .	3

basic_markers . . . . .	4
basic_qc . . . . .	4
basic_workflow . . . . .	5

<b>Index</b>	<b>6</b>
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AJ064\_small\_last\_sce    *Small 'AJ064' Seurat Data After Processed*

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### Description

An object of class Seurat

### Usage

AJ064\_small\_last\_sce

### Format

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

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AJ064\_small\_sce    *Small 'AJ064' Seurat Data Set*

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### Description

An object of class Seurat

### Usage

AJ064\_small\_sce

### Format

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

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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)
```

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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())
```

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```
basic_qc
```

```
Basic Quality Control
```

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**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())
```

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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)
```

# Index

## \* datasets

AJ064\_small\_last\_sce, [2](#)

AJ064\_small\_sce, [2](#)

AJ064\_small\_last\_sce, [2](#)

AJ064\_small\_sce, [2](#)

basic\_filter, [3](#)

basic\_find\_markers, [3](#)

basic\_markers, [4](#)

basic\_qc, [4](#)

basic\_workflow, [5](#)