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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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**

**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**

```r
basic_filter(sce)
```

**Arguments**

- `sce` An object of class Seurat

**Value**

- `sce.all.filt` An object of class Seurat

**Examples**

```r
basic_filter(AJ064_small_sce)
```

---

**basic_find_markers**

**Basic Find Markers**

**Description**

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

**Usage**

```r
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 = ".")
```
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**

```r
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**

```r
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**

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