Package 'EZsinglecell2'

January 5, 2022

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

Imports EnsDb.Hsapiens.v86,Seurat,Signac,dplyr,ggplot2

License `use_mit_license()`, `use_gpl3_license()` or friends to pick a
license

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

R topics documented:

---

docluster_GEM *Wrap Seurat RNA clustering*

Description

This function allows you to perform standard sc-RNA clustering

Usage

```
docluster_GEM(mtx = bmmc.data$`Gene Expression`, exp = "DN1_BMMC1")
```

Arguments

`mtx`	sparse Matrix of class "dgCMatrix", each row is a gene, each column is a cell,
`exp`	The name of this sample/experiment

Examples

```
bmmc.data=Read10X(data.dir = "/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/Se
docluster_GEM(mtx=bmmc.data$`Gene Expression`,exp="DN1_BMMC1")
```

MultiWrapper	*Wrap Seurat Multiomics clustering*

Description

This function allows you to perform standard sc-multiome clustering

Usage

```
MultiWrapper(

    path = "/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAn
)
```

Arguments

path   this should be the path to the cell-ranger results XX/outs

Examples

```
bmmc.data=Read10X(data.dir = "/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/Se
docluster_GEM(mtx=bmmc.data$`Gene Expression`,exp="DN1_BMMC1")
```

Index