SEURATEXT

An R Package extension for single cell sequencing analysis based on Seurat V3.0 Pipeline Objects



An output folder from the 10X Genomics single sequencing pipeline



Preprocessing Using
Seurat Pipeline



Dimensionality
Reduction and Cluster
Identification UMAP





Cluster-Based Cell Type
Assignment based on
reference marker list





In Silico Cell Cytometry based on 2 selected cell type markers. Quadrant-Based Cell Reclustering





Reclustered sub-population for downstream analysis





Wrapper functions for convenient conserved markers and differentially expressed genes Analysis





Interactive ShinyApp Session for manual inspection of various features



Utility Functions for crossplatform analysis between CellPhoneDB and Seurat with customized visualization





CytoScape for Visualization of interaction network between cell types





Customized tutorial on immune cell trajectory analysis by applying Seurat Object into Monocle 2 and Monocle 3 pipeline