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# 整理基于R语言的单细胞数据分析--preprocessing部分

## 1.实验目的

2.1熟悉基于R的seurat标准预处理分析流程

2.2理解seurat oobject数据结构

2.3为后续细胞注释分析工作作准备

## 3.实验材料：

### 3.1数据来源：

Single-cell analysis of human glioma and immune cells identifies S100A4 as an immunotherapy target(GSE182109)

Single Cell Portal数据，人，脑胶质瘤GBM，T cells（subset）

链接: [https://singlecell.broadinstitute.org/single\\_cell/study/SCP1985/single-cell-analysis-of-human-glioma-and-immune-cells-identifies-s100a4-as-an-immunotherapy-target-gse182109](https://singlecell.broadinstitute.org/single_cell/study/SCP1985/single-cell-analysis-of-human-glioma-and-immune-cells-identifies-s100a4-as-an-immunotherapy-target-gse182109)

### 3.2 软件与平台:

R (v4.3.3) ; RStudio; Seurat (v5.0.3, <https://github.com/satijalab/seurat>) ; Seurat tutorial (<https://satijalab.org/seurat/>)

## 4. 实验步骤

简单介绍预处理流程

### 4.1 Load raw data

- 1.read10X / readhd5 / readRDS
- 2.subset my interested cell type: T cells

### 4.2 Quality control

- 1.add percent.mt
- 2.subset according to percent.mt , nFeature\_RNA and nCount\_RNA

### 4.3 Standard work flow

- 1.Normalization
- 2.FindVariableFeatures
- 3.Scale
- 4.FindNeighbours
- 5.FindClusters (we can setup resolution e.g. res=0.1, 0.8)
- 6.UMAP
- 7.Finally, we will get a clustering map

Remember: if the data comes from muti datasets, do integration(e.g. CCA-Integration, RPCA-Integration)