

Hands-on: Seurat Tutorial

Data Loading

Read 10X data, create Seurat object

QC and Filtering

Mitochondrial %, nFeature, nCount filtering

Standard Workflow

Normalize → Scale → PCA → UMAP → Cluster

Integration Example

Integrate multiple samples or conditions

Visualization

FeaturePlot, DotPlot, VlnPlot

💡 Most widely used R package for scRNA-seq analysis