Hands-on: Seurat Tutorial

Seurat v5 Standard Workflow

1. Data Loading & QC

```
# Read 10X data
data <- Read10X("filtered_feature_bc_matrix/")
seurat <- CreateSeuratObject(data, min.cells=3)
```

2. QC Filtering

```
# Calculate mitochondrial %
seurat[["percent.mt"]] <- PercentageFeatureSet(seurat, "^MT-")
seurat <- subset(seurat, nFeature_RNA > 200 & percent.mt < 10)
```

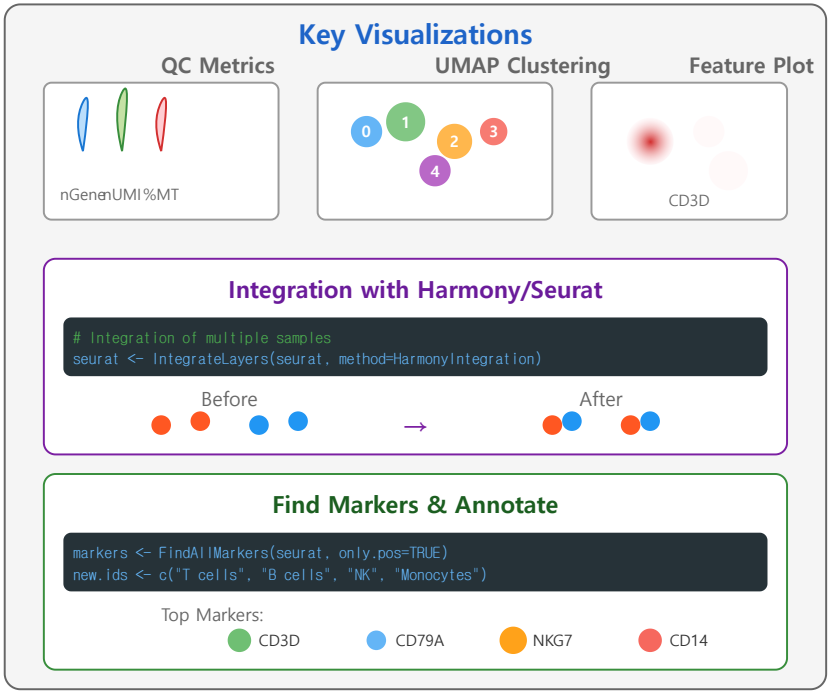
3. Normalization & Scaling

```
seurat <- NormalizeData(seurat)
seurat <- FindVariableFeatures(seurat, nfeatures=2000)
seurat <- ScaleData(seurat)
```

4. Dimension Reduction & Clustering

```
seurat <- RunPCA(seurat) %>% RunUMAP(dims=1:30)
seurat <- FindNeighbors(seurat) %>% FindClusters(res=0.5)
DimPlot(seurat, label=TRUE) + NoLegend()
```

Key Visualizations



💡 Most widely used R package for scRNA-seq analysis