Workflow Description Planning Experimental metadata Experimental Design is recorded for downstream annotation processing Sample Processing & Sequencing Preprocessing of raw Pre-Read Alianment sequencing data into primary data (counts matrix) Quantification into Raw Counts Matrix Sample metadata specified as colData(sce) Reference genome Construction of SingleCellExperiment specified as rowData(sce) Primary data specified as assav(sce, "counts") Quality control metrics added to colData(sce) and rowData(sce) Quality Control Metrics Processing Normalizina Data Data Normalized data Feature selection added into assays slot as assay(sce, "logcounts") Integrating Datasets Dimensionality Reduction Dimension reductions added into reducedDims slot as reducedDims(sce, "PCA") and reducedDims(sce, "UMAP") Downstre am Cell-level results such as clusters. Clustering statistical il labels, trajectory-based analys Differential Expression cell order added to colData(sce) Trajectory Analysis Gene-level results such as differential expression and pathway Annotation annotations added to rowData(sce) Accessible & Reproducible Analysis Interactive Data Interactive Data Visualization Visualization & Report Generation Report Generation