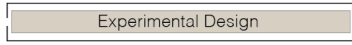


Workflow

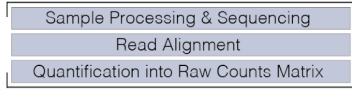
Description

Planning



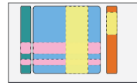
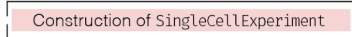
Experimental metadata is recorded for downstream annotation

Pre-processing



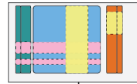
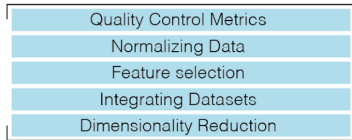
Preprocessing of raw sequencing data into primary data (counts matrix)

Import to R

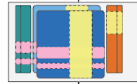


Sample metadata specified as `colData(sce)`
Reference genome specified as `rowData(sce)`
Primary data specified as `assay(sce, "counts")`

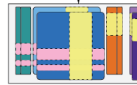
Data Processing



Quality control metrics added to `colData(sce)` and `rowData(sce)`

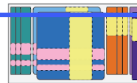
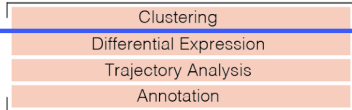


Normalized data added into `assays` slot as `assay(sce, "logcounts")`



Dimension reductions added into `reducedDims` slot as `reducedDims(sce, "PCA")` and `reducedDims(sce, "UMAP")`

Downstream statistical analysis



Cell-level results such as clusters, cell labels, trajectory-based cell order added to `colData(sce)`
Gene-level results such as differential expression and pathway annotations added to `rowData(sce)`

Accessible & Reproducible Analysis



Interactive Data Visualization & Report Generation