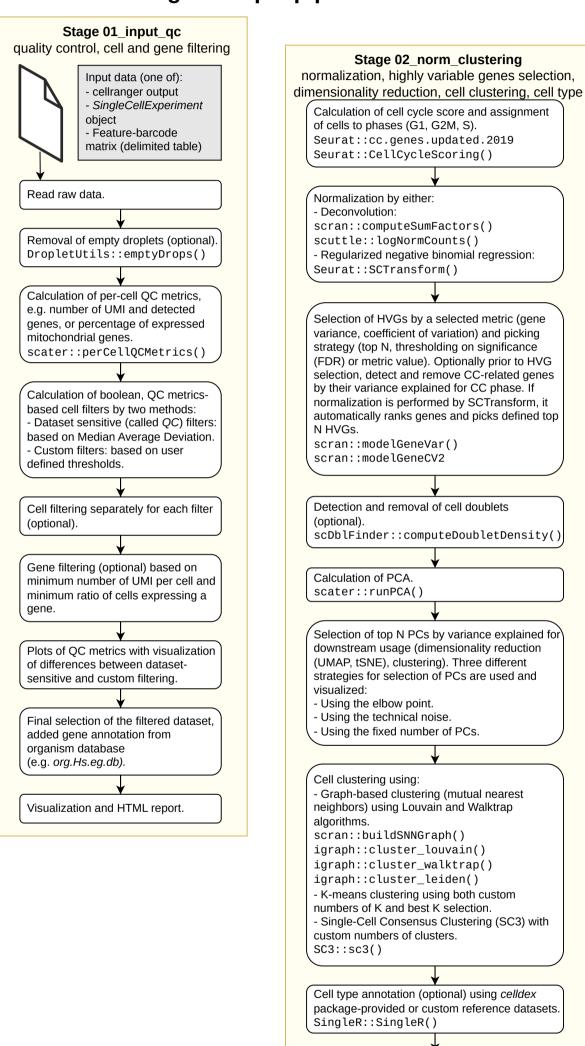
Supplementary Figure 1: High-level overview of scdrake pipelines and methods

Note: the pipeline implementation does not consist of linear workflow as depicted here - some parts are branched and can be automatically computed concurrently.

Abbreviations SCE = SingleCellExperiment object CC = cell cycle HVG = highly variable gene PC = principal component dimred = DIMensionality REDuction

Single-sample pipeline



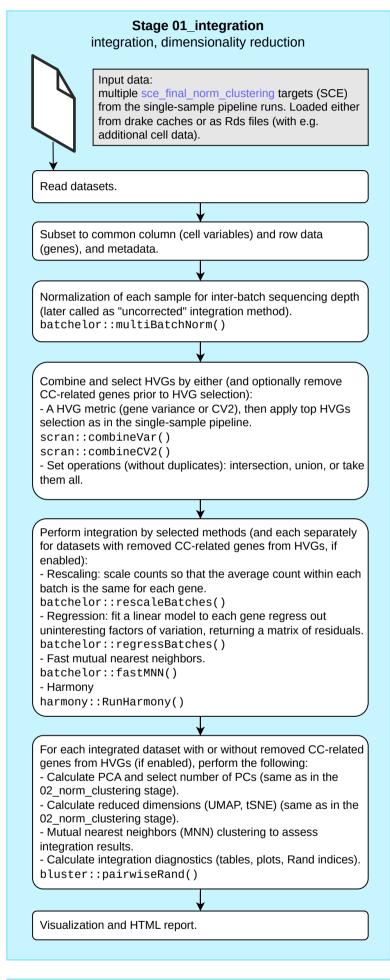
Dimensionality reduction by UMAP and tSNE.

scater::runUMAP()

scater::runTSNE()

Visualization and HTML report.

Integration pipeline Stage 01 integration



Stage 02_int_clustering cell clustering, cell type annotation, visualization Select the final integrated dataset. This is upon the user preference, i.e. the integration method and whether CC-related genes were removed from HVGs (if enabled previously). Perform the same procedures as in the 02_norm_clustering Cell clustering. Cell type annotation. Visualization and HTML report.

Common pipelines

stages common to both single-sample and integration pipelines

