

Data Preprocessing

Cell Filtering

Remove low-quality cells and empty droplets

Gene Filtering

Exclude genes detected in too few cells

Normalization Methods

Account for sequencing depth and composition

Imputation Strategies

Handle dropout events (use with caution)

Batch Effects

Technical variation from sample processing



💡 Quality control is critical for downstream analysis



QC Metrics: nGene: 200-6000 nUMI: 500-50000 %mito < 10% %ribo: varies Doublets: <5%