

# 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%