Hands-on: Integration Workflow

1 Data Loading
RNA DNA IMG

2 Preprocessing
Normalize QC Filter

3 Integration Methods
MOFA CCA SNF

4 Visualization
UMAP Heatmap

5 Biological Interpretation
Enrichment Pathways

Step 1 ~5 min
Step 2 ~15 min
Step 3 ~30 min
Step 4 ~10 min
Step 5 ~20 min

↻ QC Feedback Loop

Total: ~80 minutes
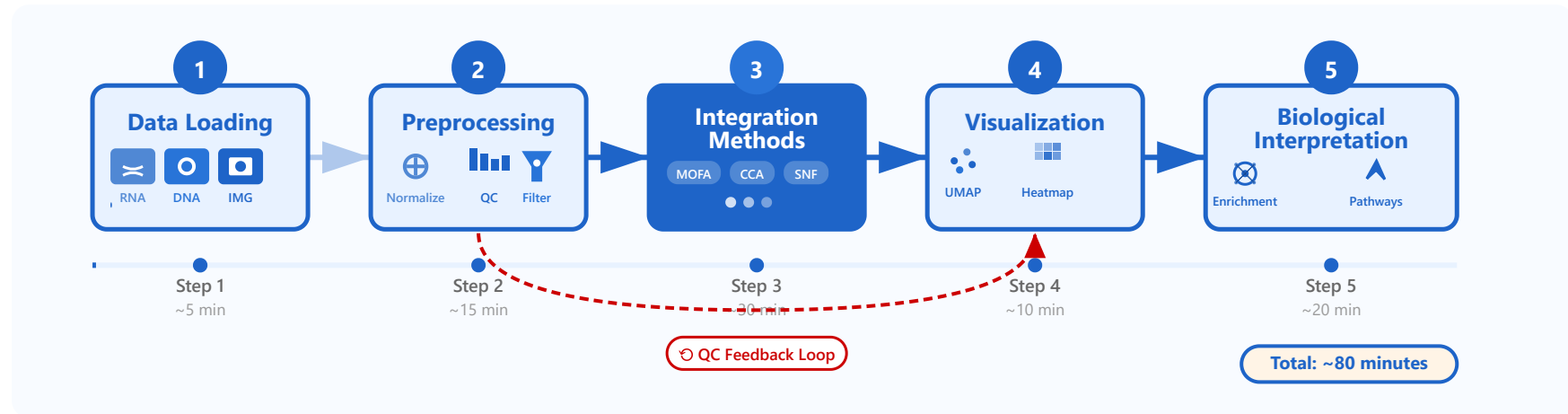
Data Loading
Reading multi-modal datasets

Preprocessing
Normalization and quality control

Integration Methods
Applying different integration approaches

Visualization
UMAP, t-SNE, heatmaps

Biological Interpretation
Functional enrichment analysis