

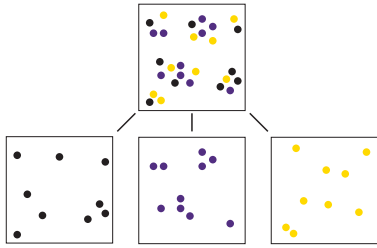
Multomics Analysis Software Workflow

1

UPLOAD DATA

MAS supports count files generated by Cell Ranger or Seurat.

```
ACTGATCGTACGCGAGTGTATCATCGCTAGCATGCATC  
GCARACTGCTCACAGTCTACAGTCGTGTCACAC  
TGCTAGCAGTCAGCATGCGAGCTCATGCTGTCAGCT  
GACAGCATGCATGCGAGCATGCTAGCATGCTAGCTAG  
GACTGATCGTACCGAGCTGATCATCGCTAGCATGCAT  
GCARACTGCTCACAGTCTACAGTCGTGTCACAC  
TGCTAGCAGTCAGCATGCGAGCTCATGCTGTCAGCT  
GACAGCATGCATGCGAGCATGCTAGCATGCTAGCTAG
```



2

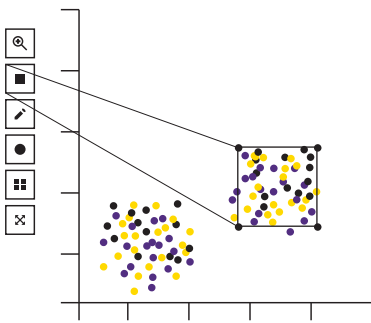
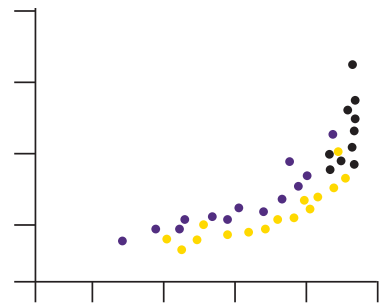
REVIEW DEMULTIPLEXING RESULTS

MAS automatically demultiplexes data by sample (when necessary) and filters cells based on UMI complexity.

3

PERFORM RNA ANALYSIS

Normalize gene expression and create thresholds for inclusion of genes in downstream analysis.



4

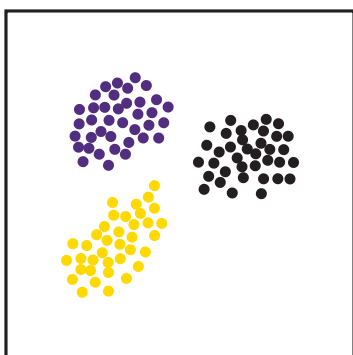
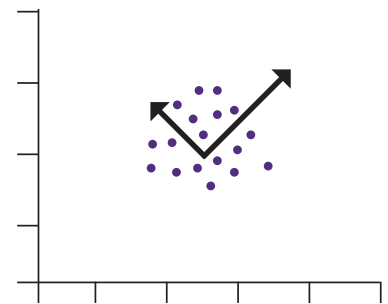
ADD GATES

Use flow cytometry-like gating strategies to clean up your data and define cell populations of interest.

5

GENERATE DIMENSIONALITY REDUCTION PLOTS

Choose from UMAP, tSNE, and TriMap plots.



6

CLUSTER CELLS TO UNDERSTAND CELLULAR HETEROGENEITY

MAS uses using community detection algorithms to cluster cells based on protein expression.

7

EXPLORE INTERACTIVE PLOTS

Perform differential expression analysis between cell clusters.

