

Sequencing

Raw sequence reads

Count matrix

Pre-processing

ScFlow
Integration / QC / Clustering brain

Filtering of microglia

Processing

Integration

Processing
Normalization, PCA

unsupervised approaches

Sub-clustering of microglia

Cluster marker identification

Differential expression analysis

Functional enrichment

supervised approach

Alignment to mouse dataset
PCA space

Classification using trained models

Downstream analyses

Comparison of microglia subtypes