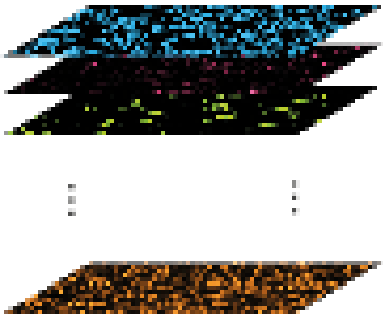


# SIMPLI: Single-cell Identification from Multiplexed Images

## NextFlow (workflow management)

**Process 1A: Extraction**  
Singularity (Python)



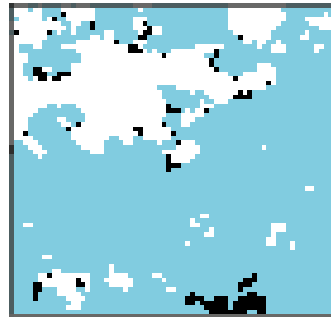
Step 1

- Extracted tiff files

**Process 2A: Normalization**  
Singularity (R)

**Process 2B: Preprocessing**  
Singularity (CellProfiler)

**Process 2C: Pixel analysis**  
Singularity (R)



Step 2

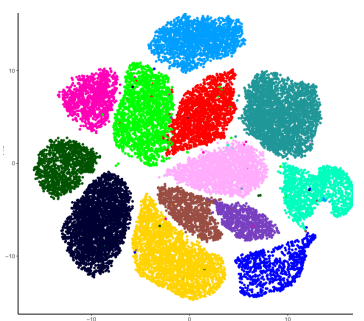
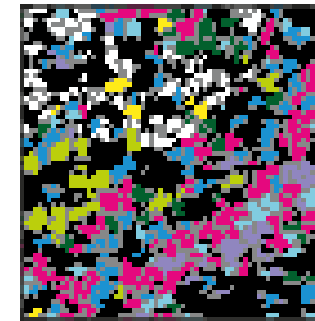
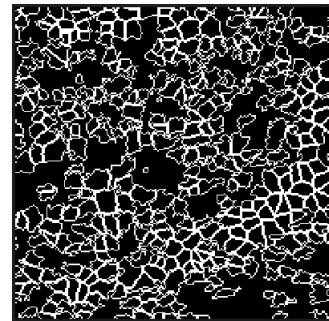
- Preprocessed tiff files
- Pixel area measurements

**Process 3A: Cell segmentation**  
Singularity (CellProfiler)

**Process 3B: Cell identification**  
Singularity (R)

**Process 3C: Cell clustering**  
Singularity (R)

**Process 3D: Single cell analysis**  
Singularity (R)



Step 3

- Single-cell data
- Single-cell population and sub-populations
- Marker expression heatmaps
- Tissue visualizations