

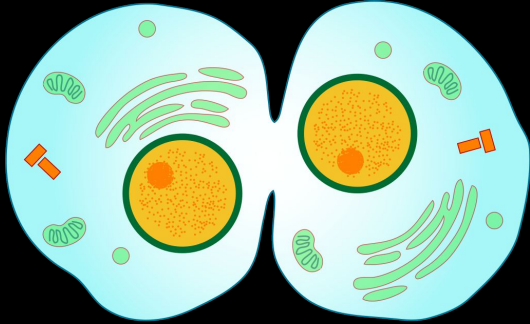
Cell Segmentation and Tracking

S. Shailja

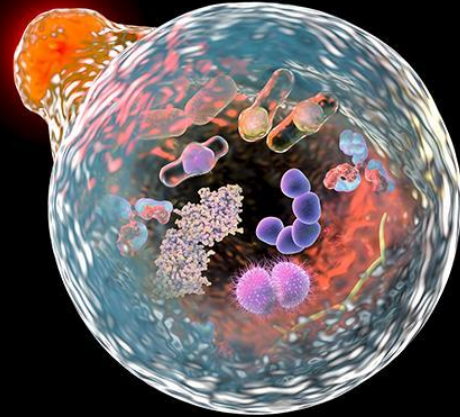
Jiaying (Tom) Jiang

Motivation

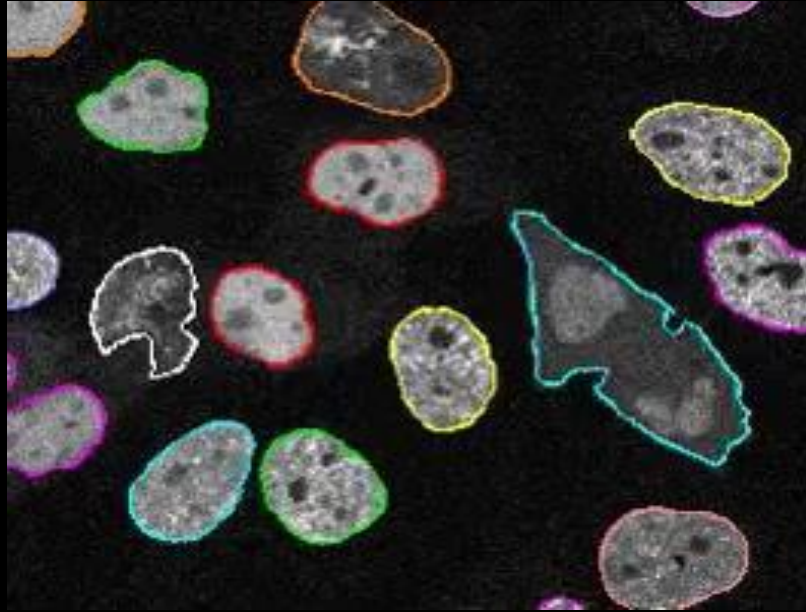
- Biological Process



- Disease Progress

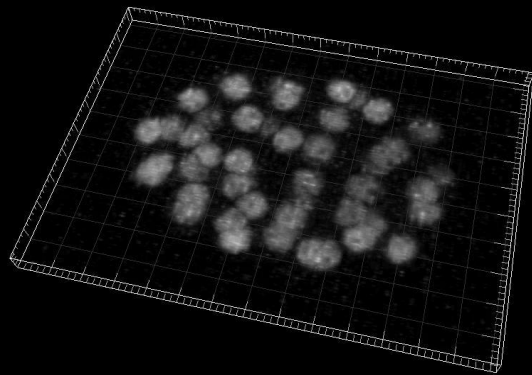


Problem Statement



Dataset

- *C.elegans* developing embryo
Waterston Lab, University of Washington
- Voxel size: $0.09 \times 0.09 \times 1.0 \mu\text{m}$
- Time step (min): 1 (1.5)

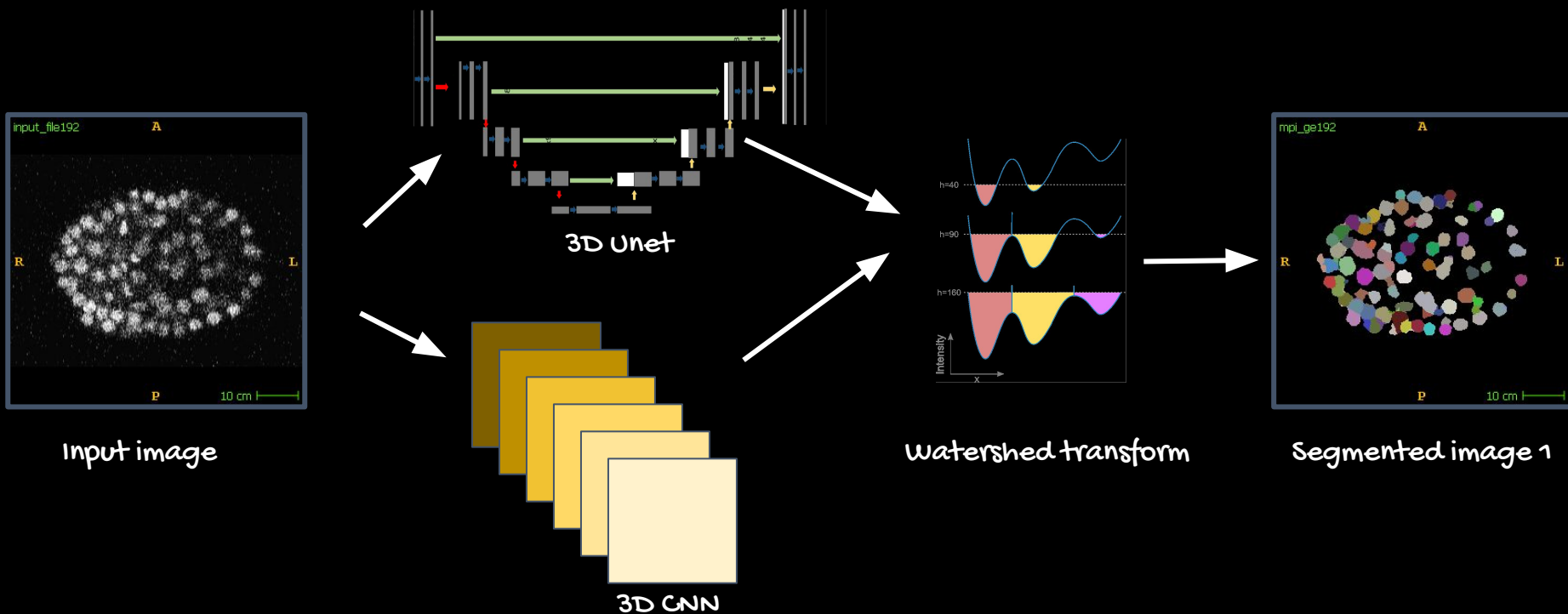


100 μm
0000.01:57.000

time

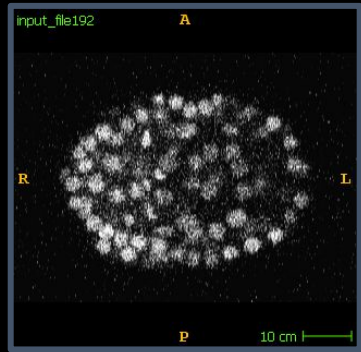
Segmentation: Algorithm

Level 1: Initial segmentation (proposed by MPI-GE (benchmark))

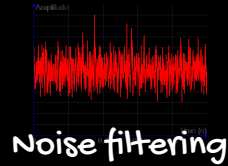


Segmentation: Algorithm

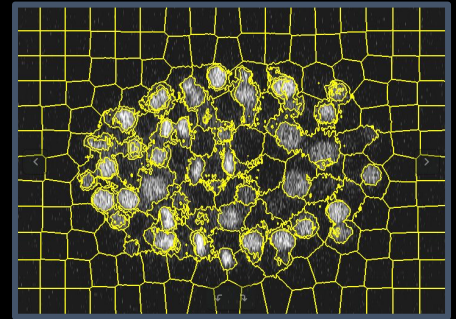
Level 2: Superpixel segmentation



Input image



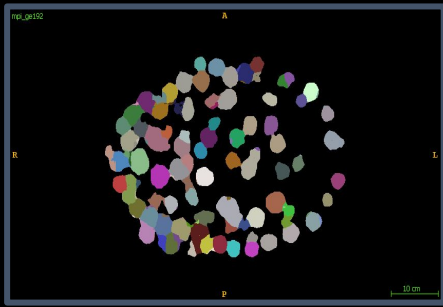
Superpixel segmentation



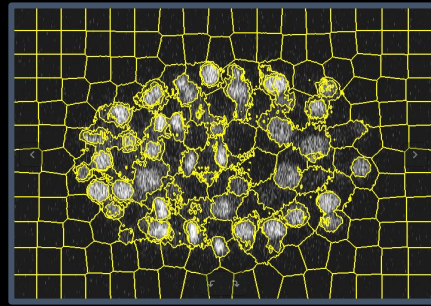
Segmented image 2

Segmentation: Algorithm

Level 3: Boundary Correction



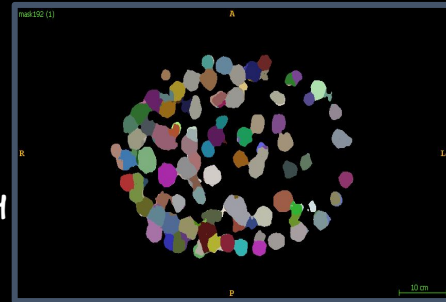
Segmented image 1



Segmented image 2



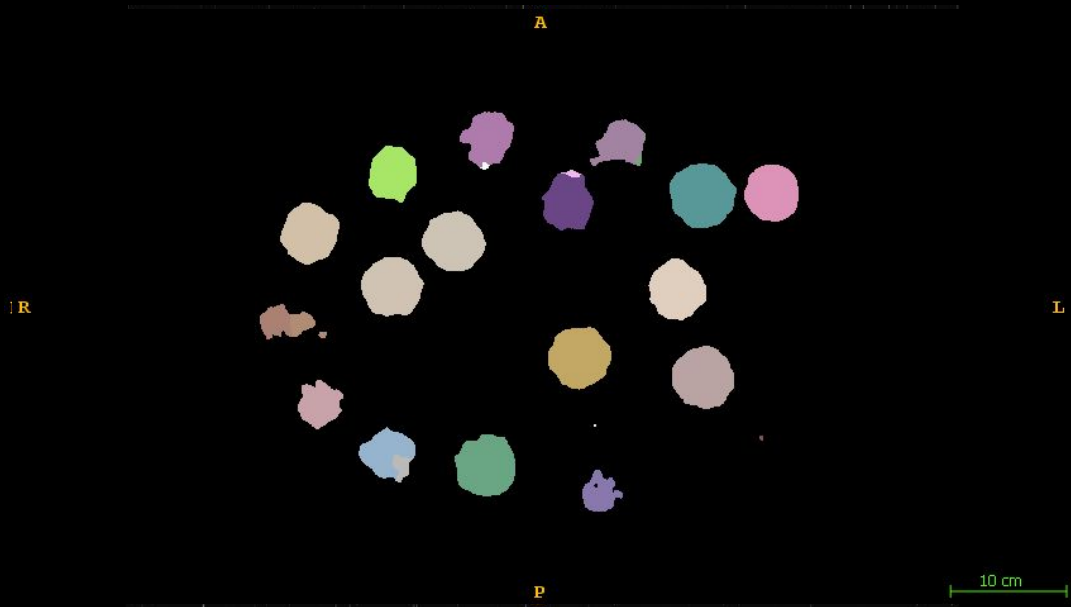
Majority voting on boundary
of segmented nuclei



output image

Segmentation: Comparison

Input Data



Benchmark Segmentation

Segmentation: Comparison

Input Data

A

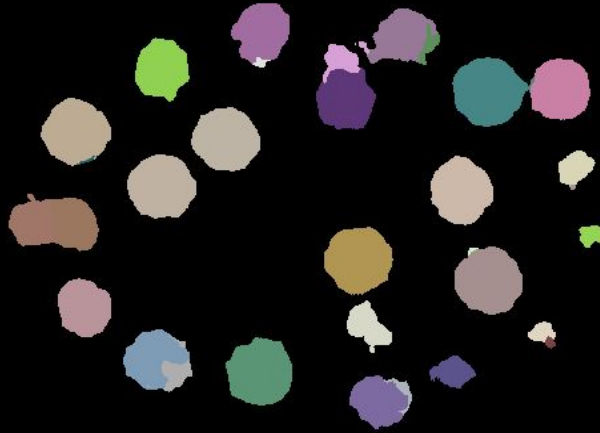
R

L

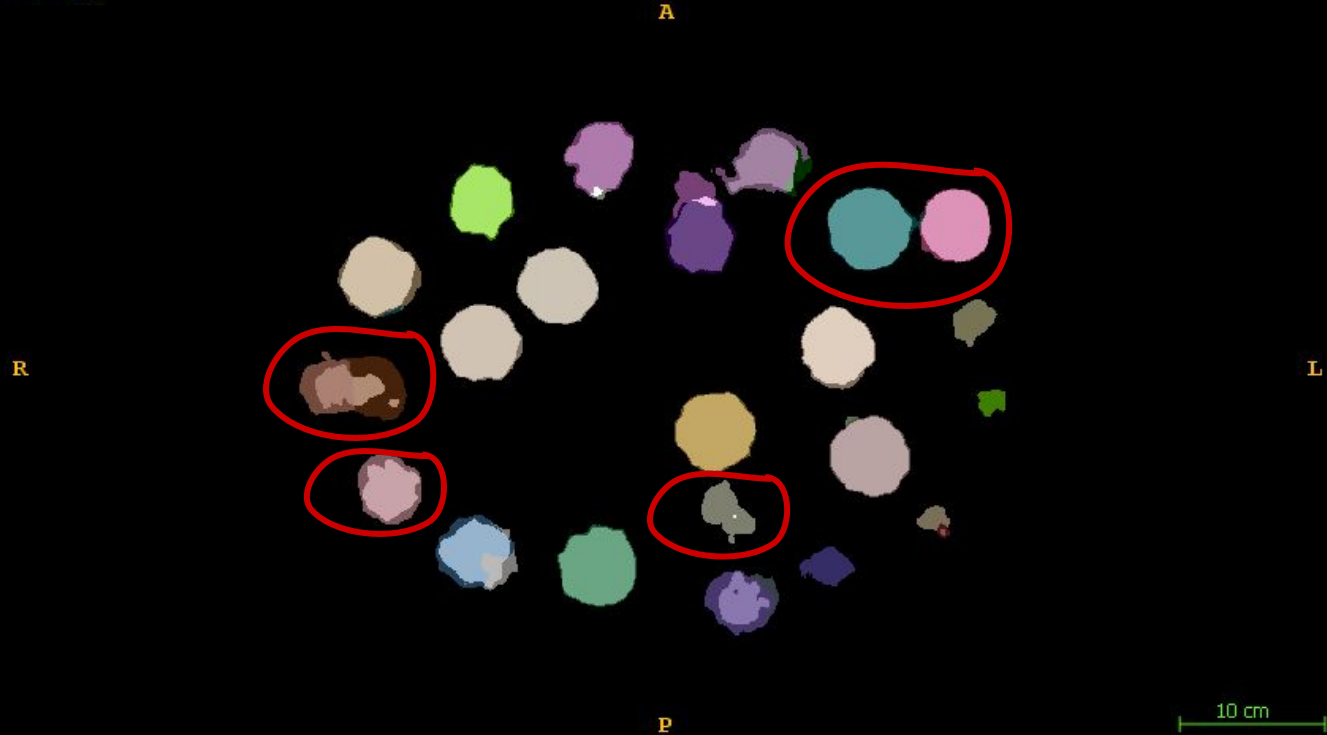
P

10 cm

our Algorithm



Segmentation: Comparison



Segmentation: Results

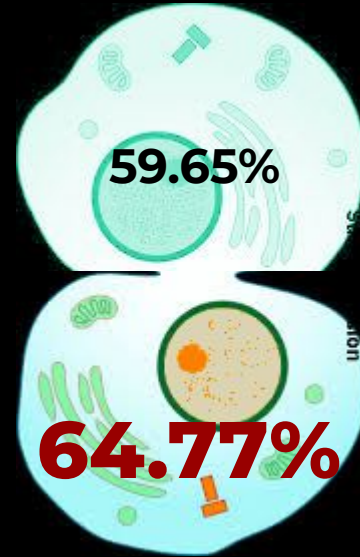
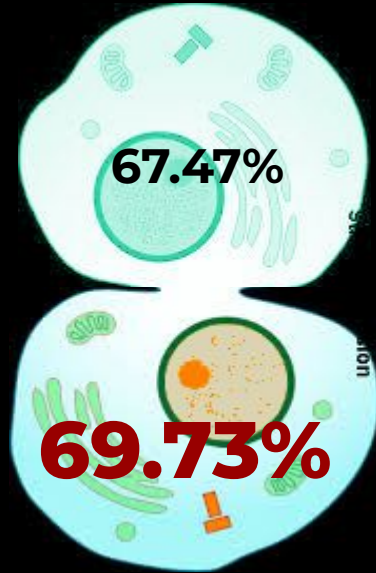
Validation

Dataset 01

Dataset 02

Benchmark

Proposed algorithm



Take-home message

Addition of the proposed boundary correction pipeline improves the segmentation accuracy.

UC SANTA BARBARA



Prof. B.S. Manjunath



Jiaxiang (Tom) Jiang

CELL TRACKING CHALLENGE TEAM

Martin Maška

Carlos Ortiz De Solorzano Aurusa



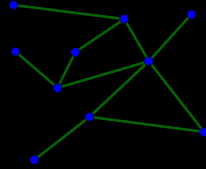
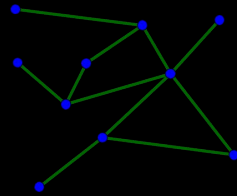
Tracking: Algorithm



Two consecutive segmented images



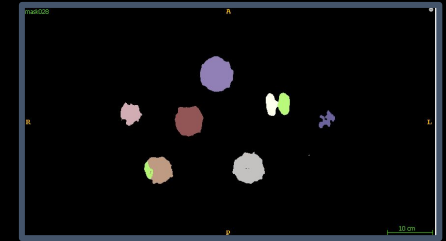
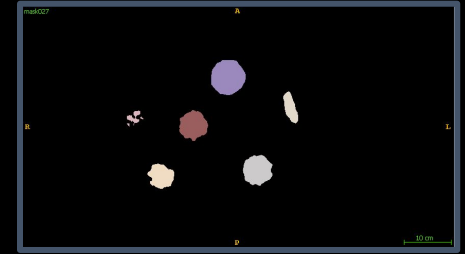
Graph construction



Undirected graphs



Node matching



Final labels

Tracking: Results (to do ..)

Validation

Dataset 01

Dataset 02

Proposed algorithm



67.47%

59.65%

Benchmark



69.73%

69.73%

