

Metrics for Comparing 3D Neuron Segmentations in Expansion Microscopy Connectomics

By Albert Gerovitch

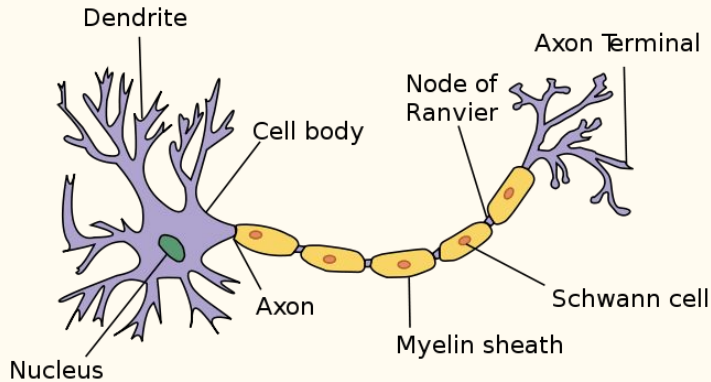
Mentors: Adam Marblestone, Daniel Goodwin (Boyden Lab)

Background Information

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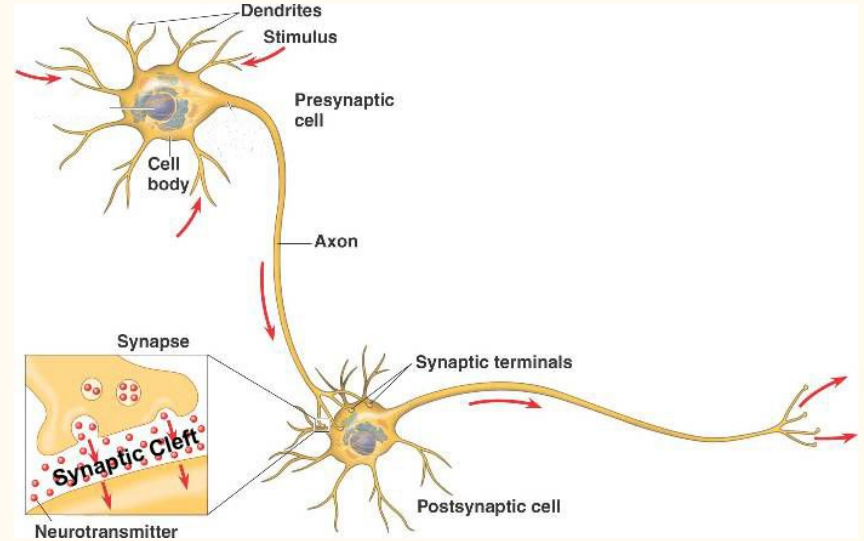
Neurons

- Functional unit (cell) of the nervous system
 - Convey information in the brain
 - Electrical and chemical signals
- Provide foundation for brain function
 - Understanding the brain



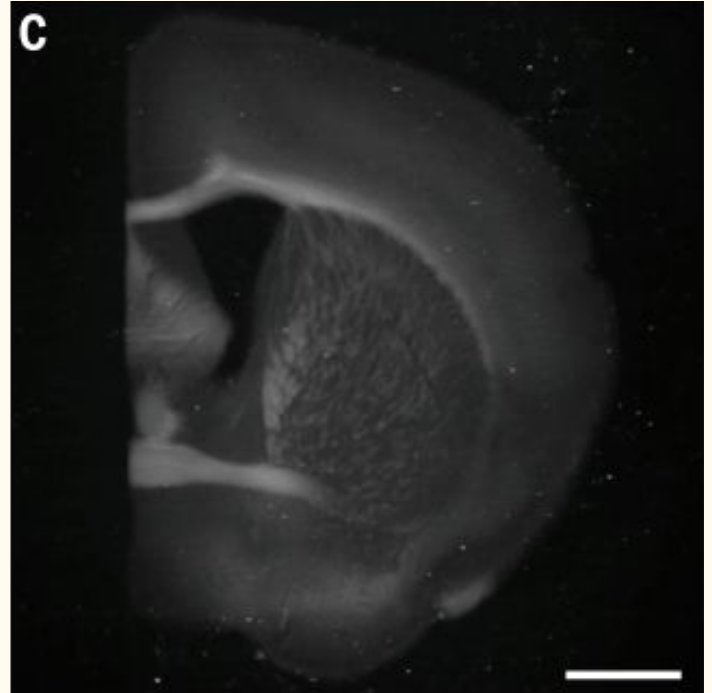
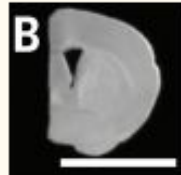
Synapses

- Connections between neurons
 - Signals transferred
- Knowing shape of neuron would help track signals
- Looking at individual neurons for now
 - Multi-cell connected networks later



Expansion Microscopy Connectomics

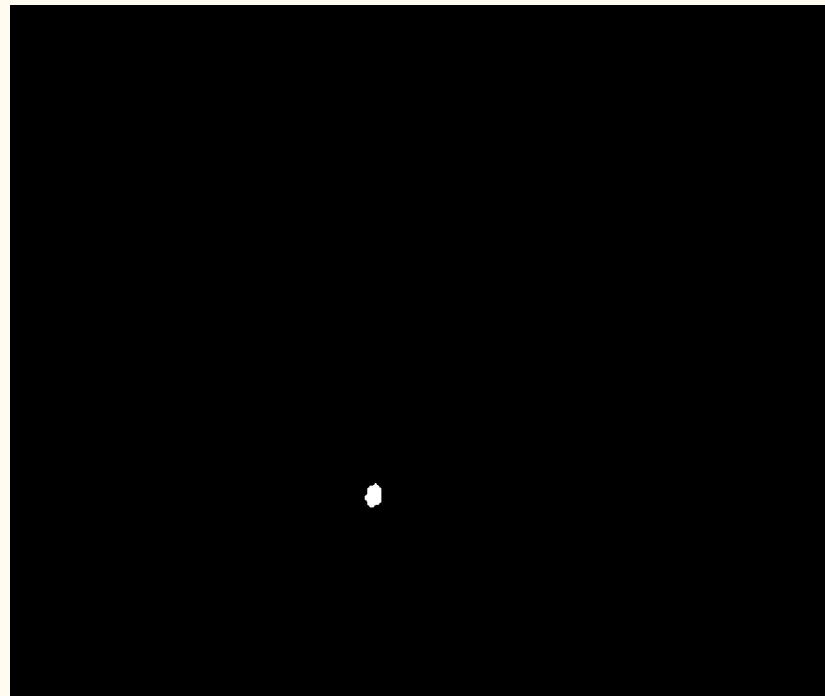
- Study of comprehensive maps of connections in the nervous system
- Traditional light microscopy up to 300nm
- Expansion microscopy works by physically expanding tissue
 - Allows large 3D images at high resolutions
 - Color
 - 5x can see down to 60nm



(Chen, Tillberg, Boyden 2014)

Segmentation

- Finding and isolating shape of individual neuron(s)
- Laborious for humans, computers would accelerate process
- Difficulties with misleading background “noise,” isolating individual neuron



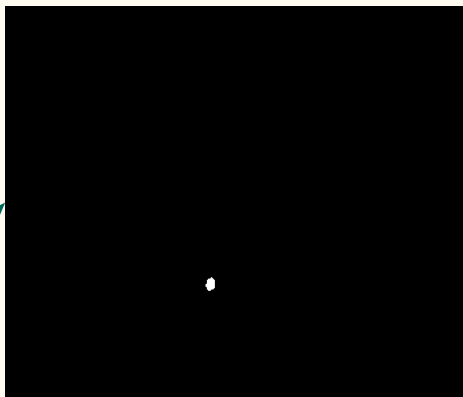
Goal

- Implement metrics to evaluate the performance of a computer algorithm at segmenting neurons in 3D
- Ultimately find the best segmentation algorithm

1. Raw Data

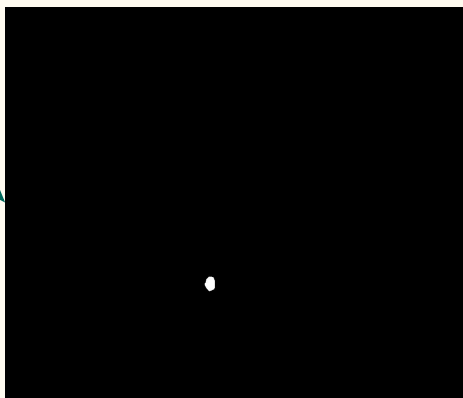


2. Segmentations



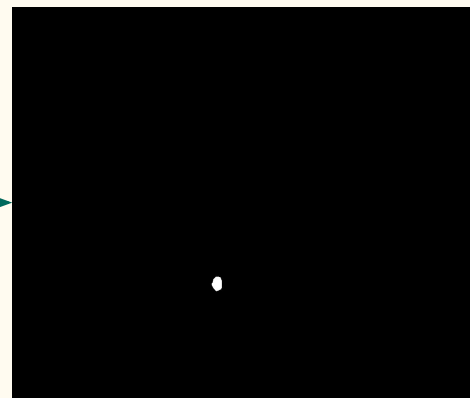
Algorithm #1

Algorithm #2



3. Adjusted

MATLAB
imclose,
imfill



Obtaining Segmentations

Metrics of Segmentation Performance

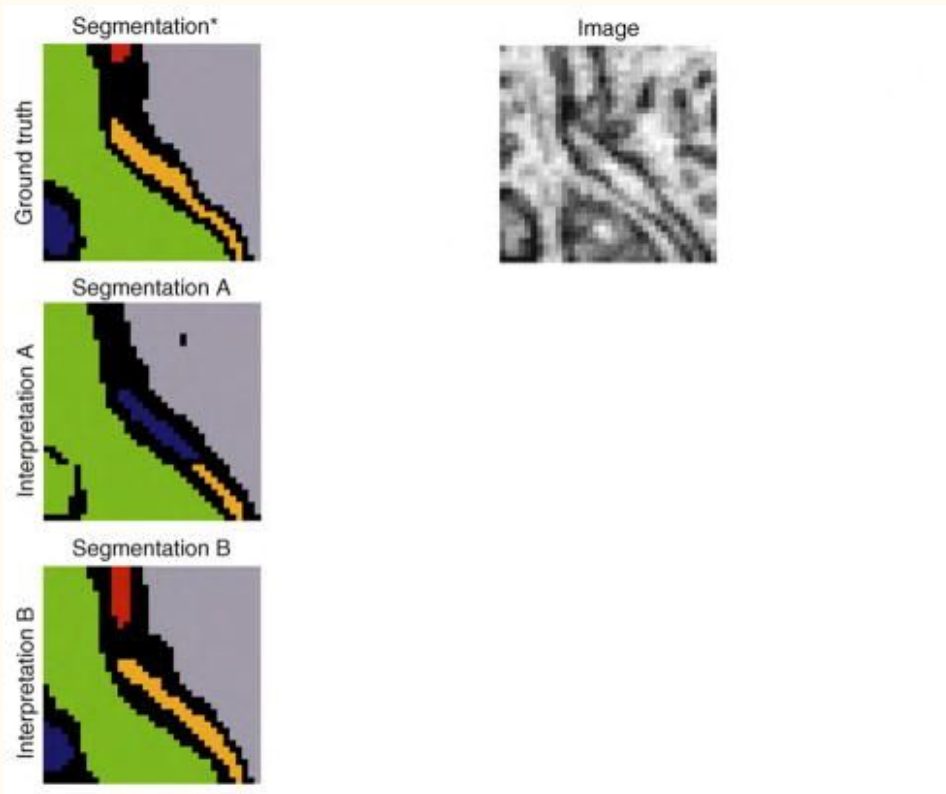


Metrics of Segmentation Performance

- Compare segmentation from computer vs. human (“ground truth”)
- Error types: deletion, split (incorrect boundary), merger (incorrect gap)
- Ideal metric: tolerate minor differences, strongly penalize splits/mergers (topological disagreements)

Evaluation metrics:

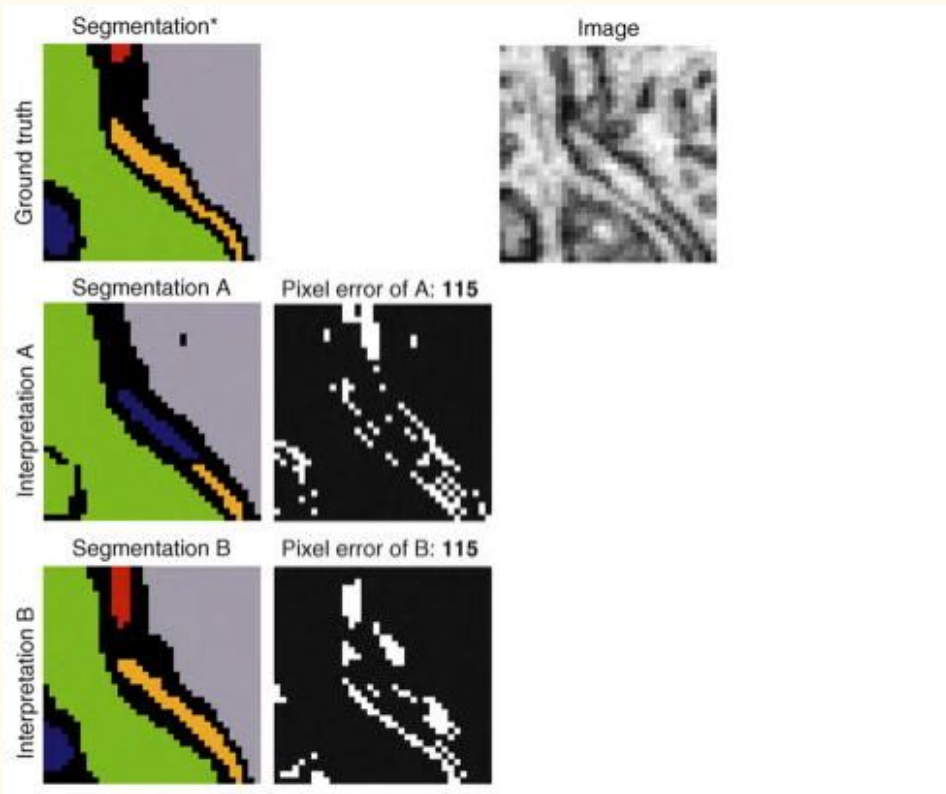
- *Pixel error* - count number of pixels where computer disagrees with human
 - Misleading, fails to notice intuitive disagreements
- *Rand error* - fraction of pixels pairs that belong to same region in one segmentation but not other
- *Warping error* - count of topologically-relevant boundary labeling errors



- Human interpretation
- Contains deletion, split, and merger
- Contains no serious errors

(Jam, Seung, Turaga)

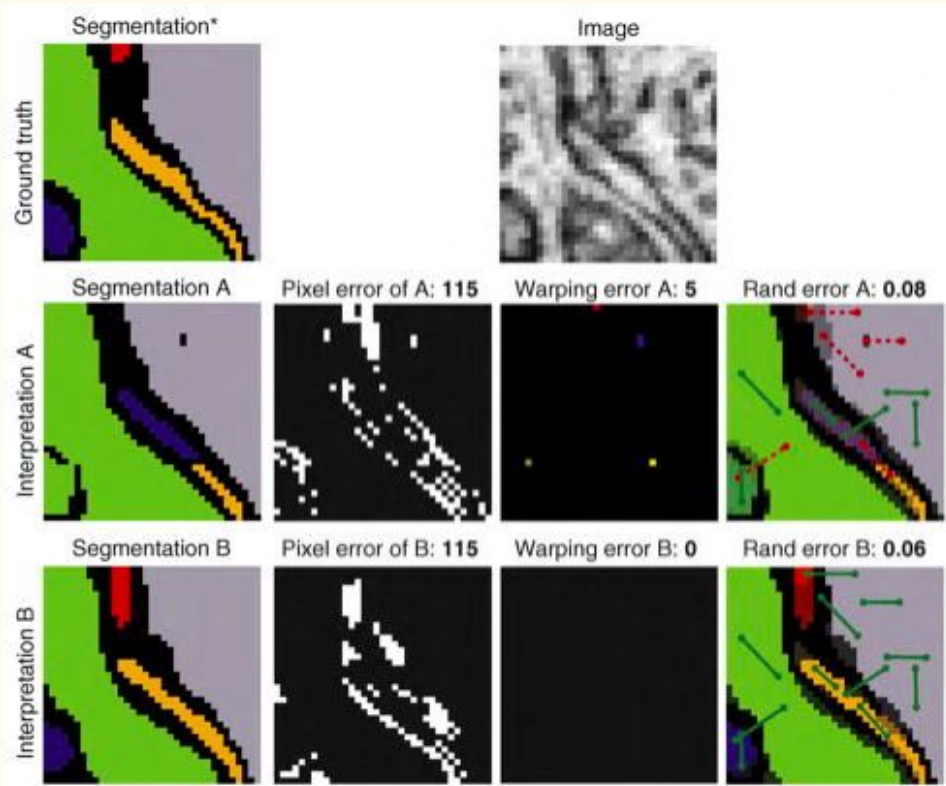
Visual comparison of evaluation metrics



- Human interpretation
- Contains deletion, split, and merger
- *Pixel error* misleading
- Contains no serious errors

(Jam, Seung, Turaga)

Visual comparison of evaluation metrics



- Human interpretation
- Contains deletion, split, and merger
- *Pixel error* misleading
- Contains no serious errors
- *Warping error* and *Rand error* much better representation

(Jam, Seung, Turaga)

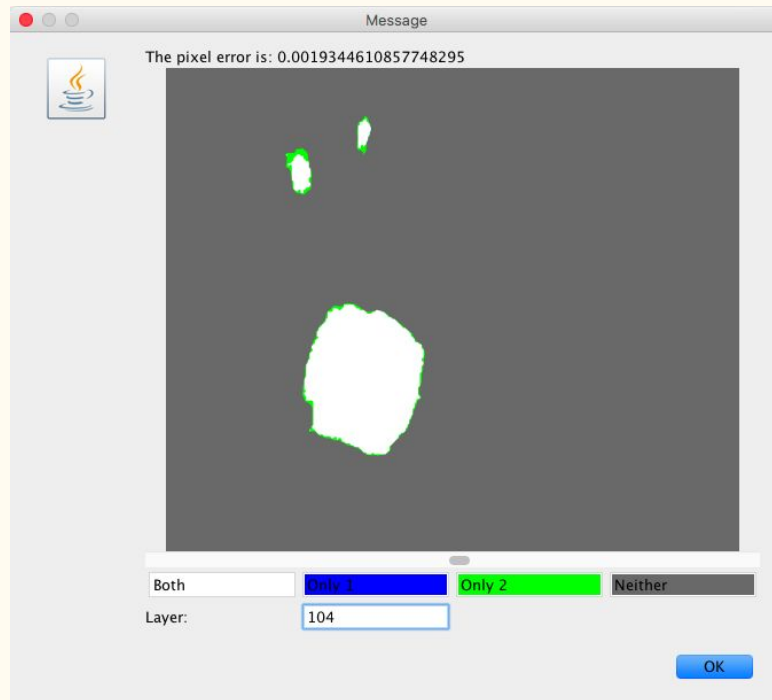
Visual comparison of evaluation metrics

Developing an Application



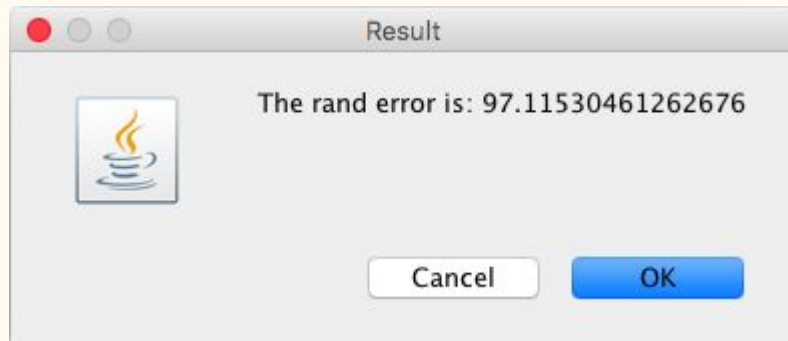
Working with Pixel Error

- *Pixel error* - count number of pixels where computer disagrees with human
- Wrote program in Java
- Able to:
 - Give score as decimal
 - Visualize error
 - See where segmentations differ
 - Provide feedback for developers of algorithms
 - Export result as TIFF



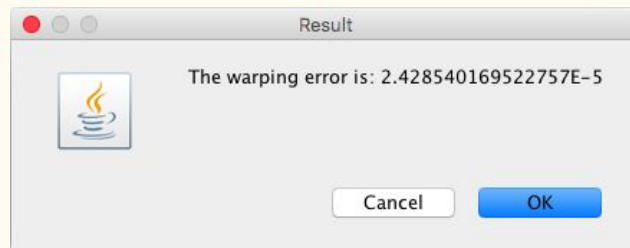
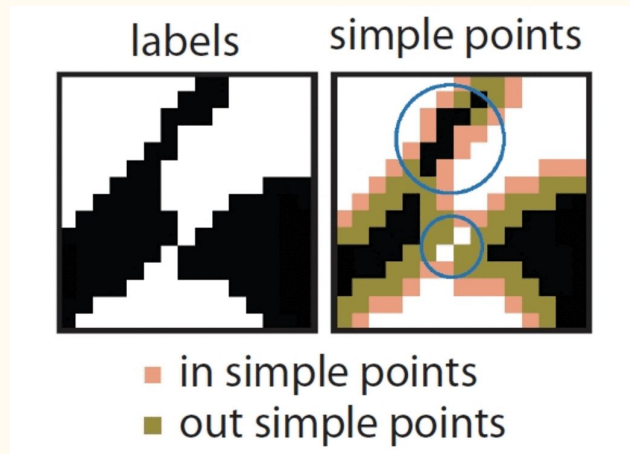
Working with Rand Error

- *Rand error* - fraction of pixels pairs that belong to same region (connected component) in one segmentation but not other
- Able to:
 - Give score as decimal
- Improvements:
 - Solve accuracy issues
 - Generate visualization



Working with Warping Error

- *Warping error* - fraction of topologically-relevant boundary labeling errors
- Able to:
 - Give accurate score as decimal
- Improvements:
 - Generate visualization
 - Improve speed (currently ~ 10 min to run)



Conclusions



Results

- Wrote program able to compare two segmentations with pixel, rand, and warping error
 - Visualize/export pixel error
- Applied application to expansion microscopy data
 - Converted segmentations to common format (TIFF image)
- Ongoing: Collaborating with Boyden Lab researchers to provide feedback for algorithms

Future Plans

- Visualize results of Rand and Warping error
 - Provide better feedback for algorithm developers
- Add capability to evaluate multi-cell segmentations
- Automate scoring and improving algorithms



*Multi-cell segmentation courtesy of Nick Barry
(Boyden Lab)*

Sources

- <http://expansionmicroscopy.org/15.01.chen.FULL.pdf>
- <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2975605/#S7title>
- imagej.net/Topology_preserving_warping_error
- https://www.sfn.org/~media/SfN/Documents/Short%20Courses/2011%20Short%20Course%20II/2011_SC2_Seung.ashx

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