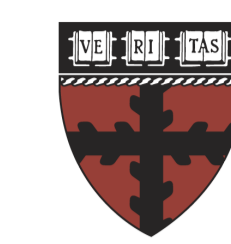
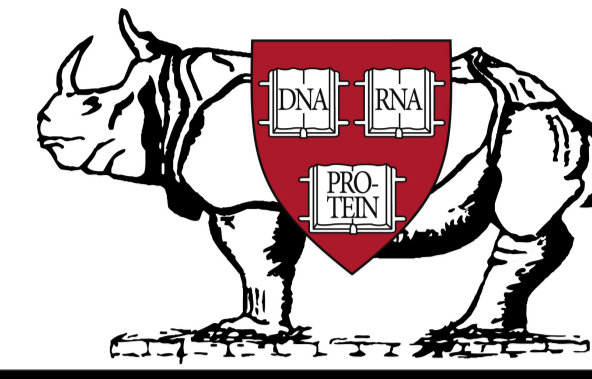


Mojo 2.0: Connectome Annotation Tool

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Available online at <http://www.rhoana.org/>

Introduction

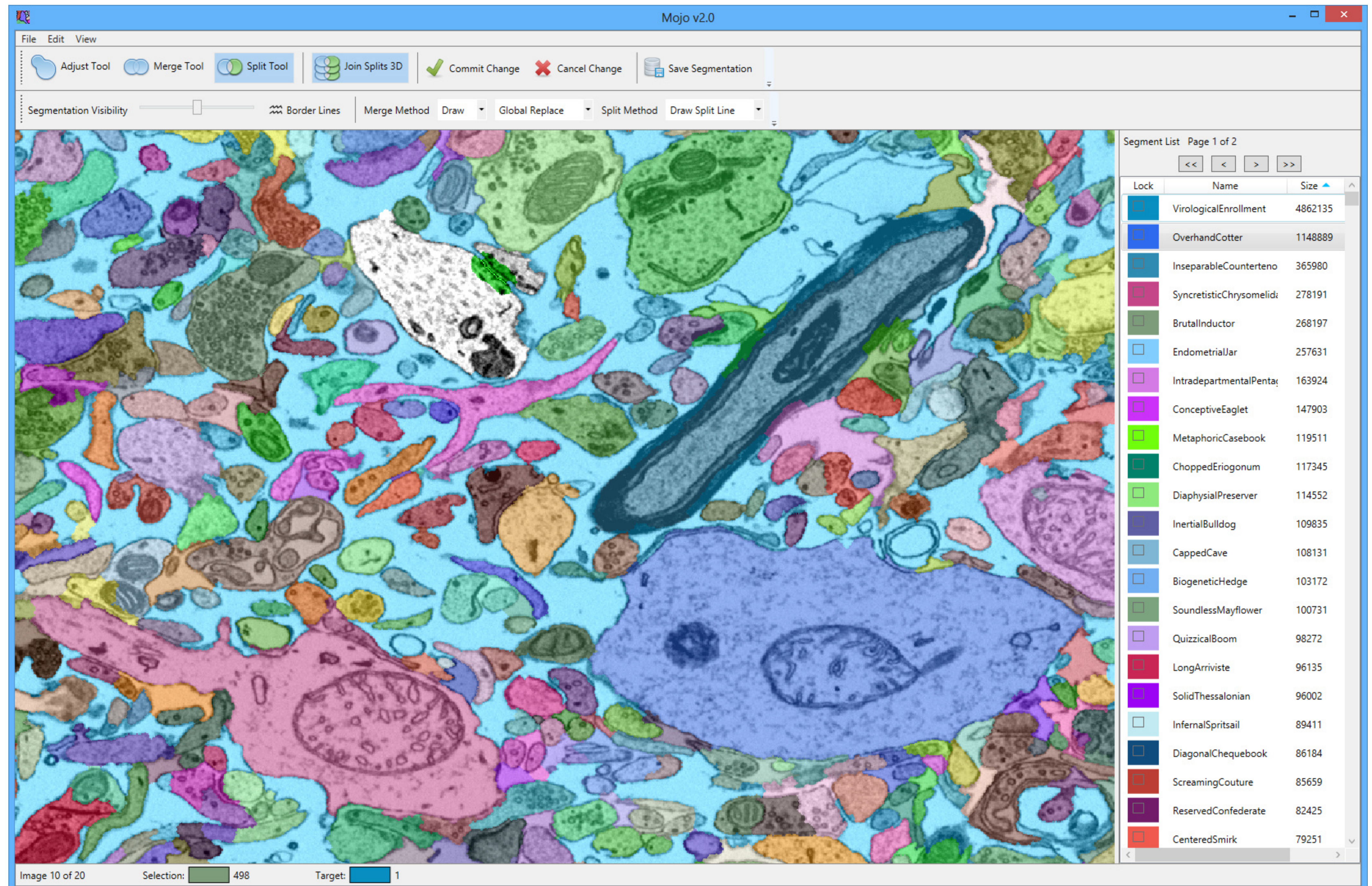
A connectome is the wiring diagram of connections in a nervous system. Mapping this network of connections is necessary for discovering the underlying architecture of the brain and investigating the physical underpinning of cognition, intelligence, and consciousness [1, 2, 3]. It is also an important step in understanding how connectivity patterns are altered by mental illnesses, learning disorders, and age related changes in the brain.

Fully automatic computer vision techniques are available to segment electron microscopy (EM) connectome data. Currently we use the Rhoana pipeline to process images, but results are still far from perfect and require additional human annotation to produce an accurate connectivity map [4].

Here we present Mojo 2.0, an open source, interactive, scalable annotation tool to correct errors in automatic segmentation results.

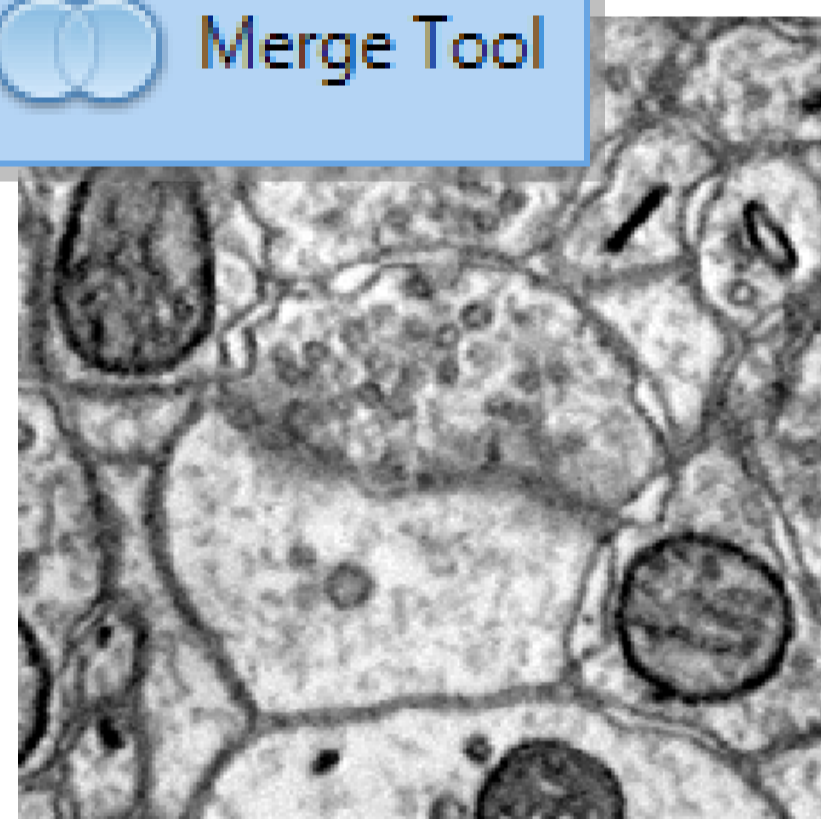
Mojo Features

- Interactive annotation tool
- Smart scribble interface for split and merge operations
- Scalable up to TB scale volumes
- Entire segmentation pipeline including Mojo is open source and available online: <http://www.rhoana.org/>

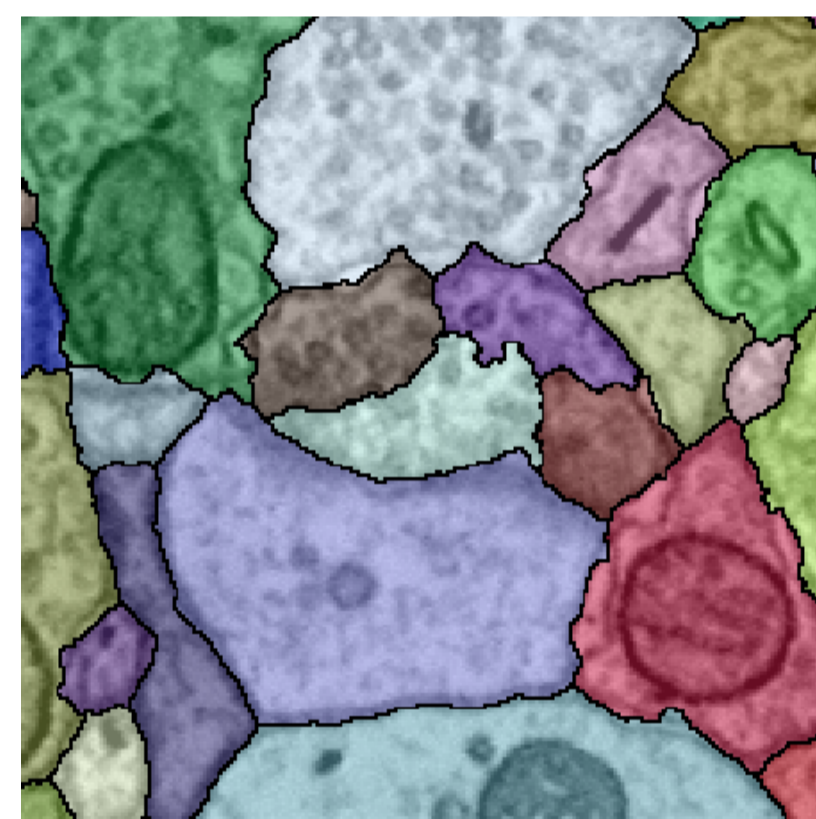


The Mojo interface displaying an EM section from mouse cortex, approximately 7.5x5µm.

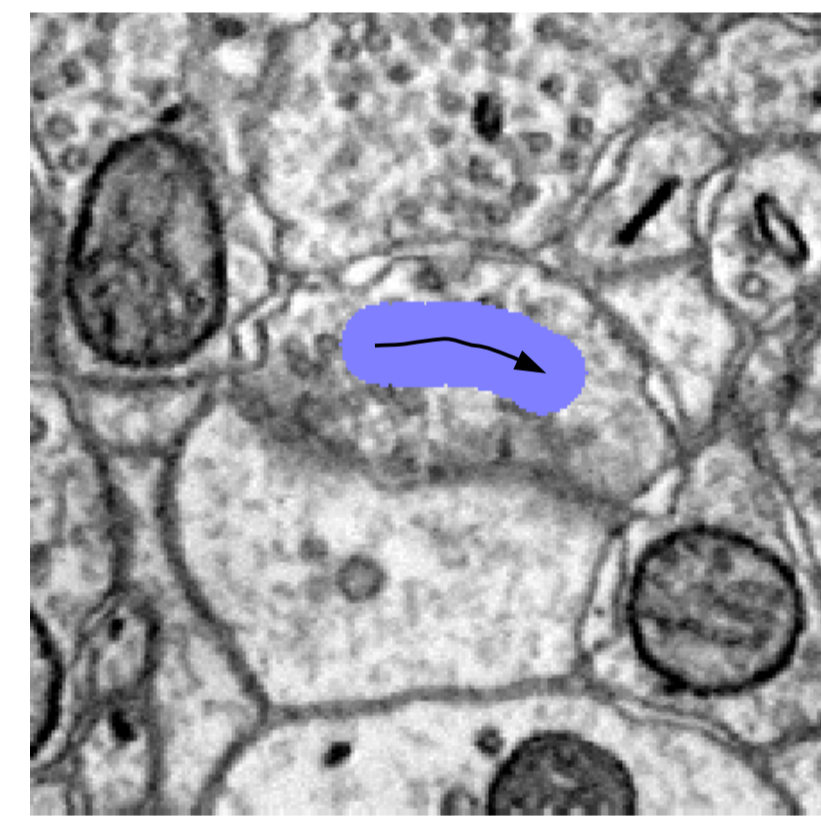
Merge Tool



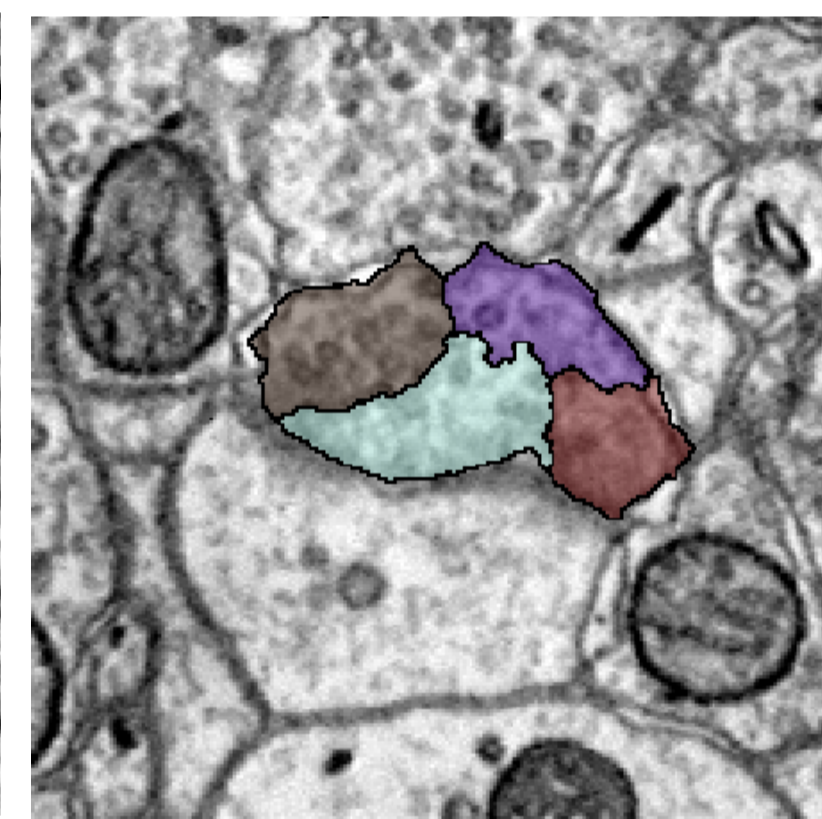
Original Image
1.3x1.3µm



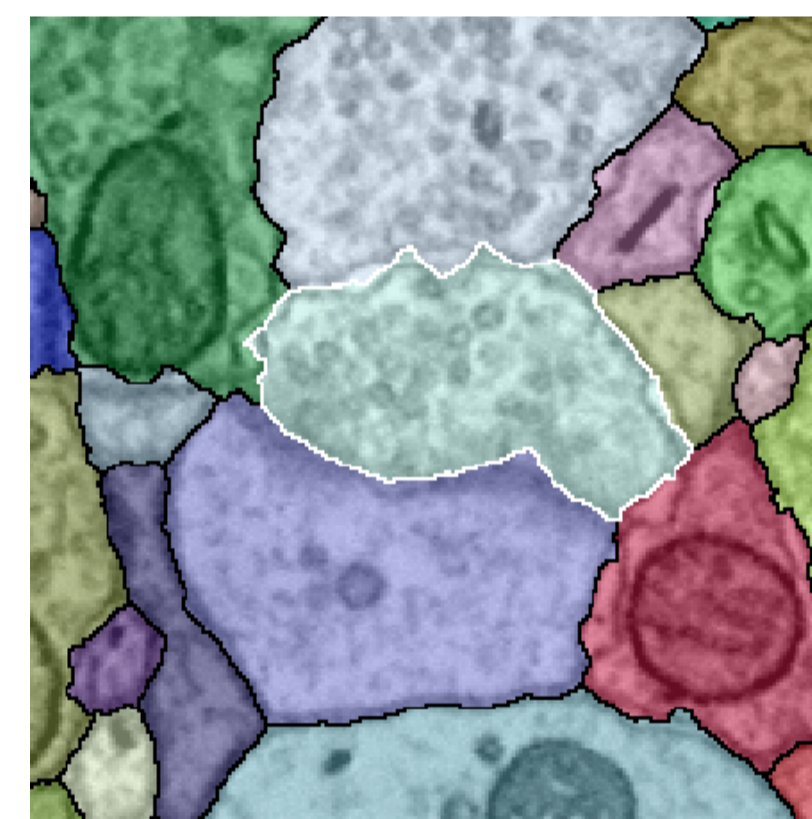
Initial
segmentation



User scribbles
over segments to
be merged

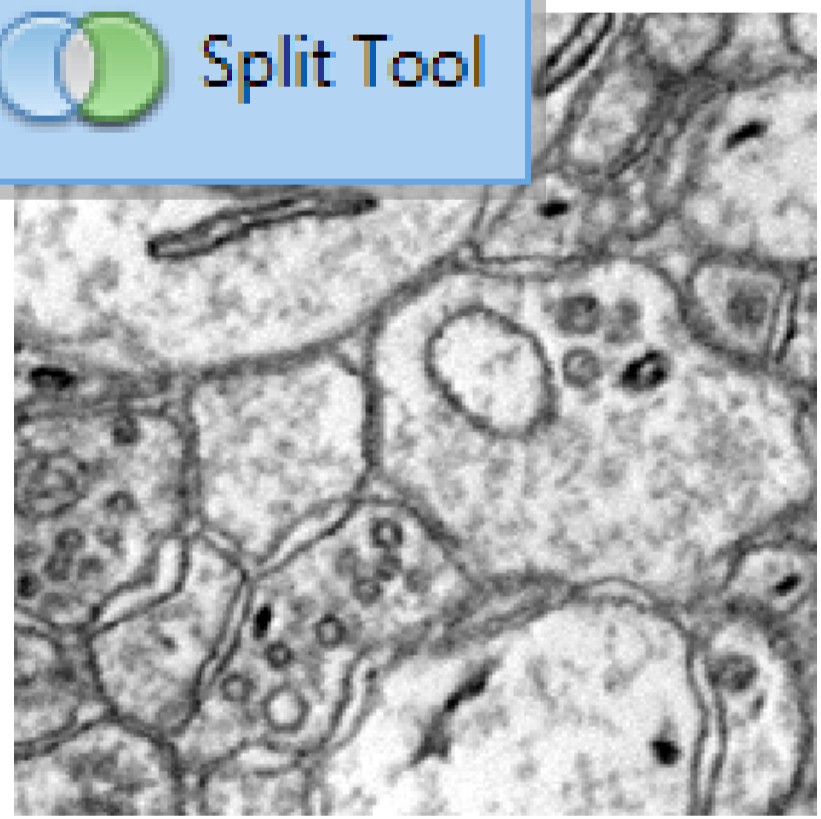


Segments touched
by the user's scribble
are merged

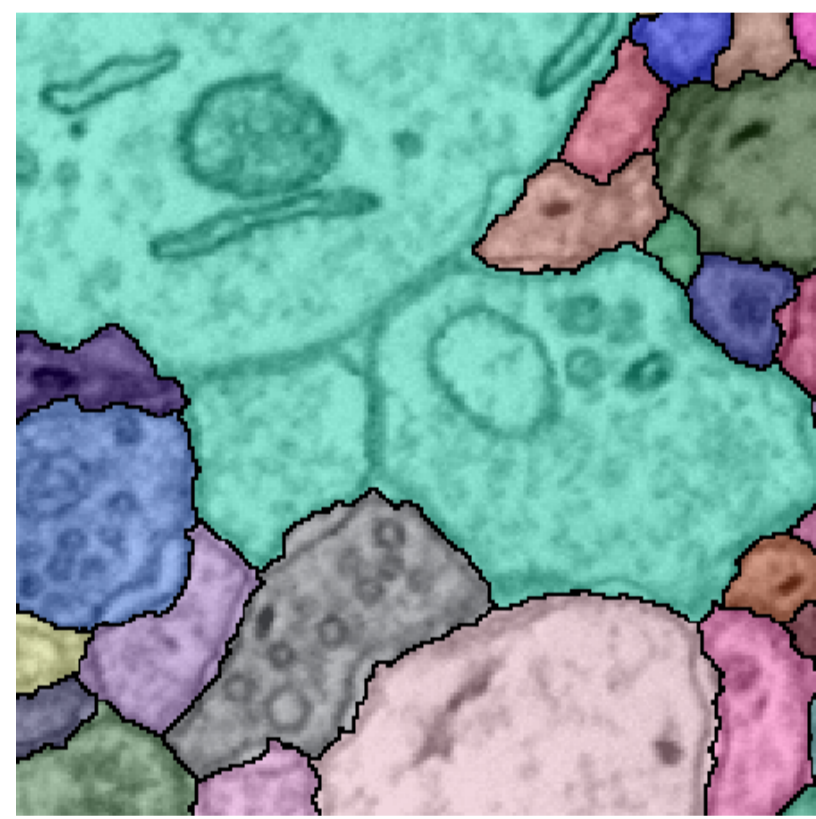


Corrected
segmentation

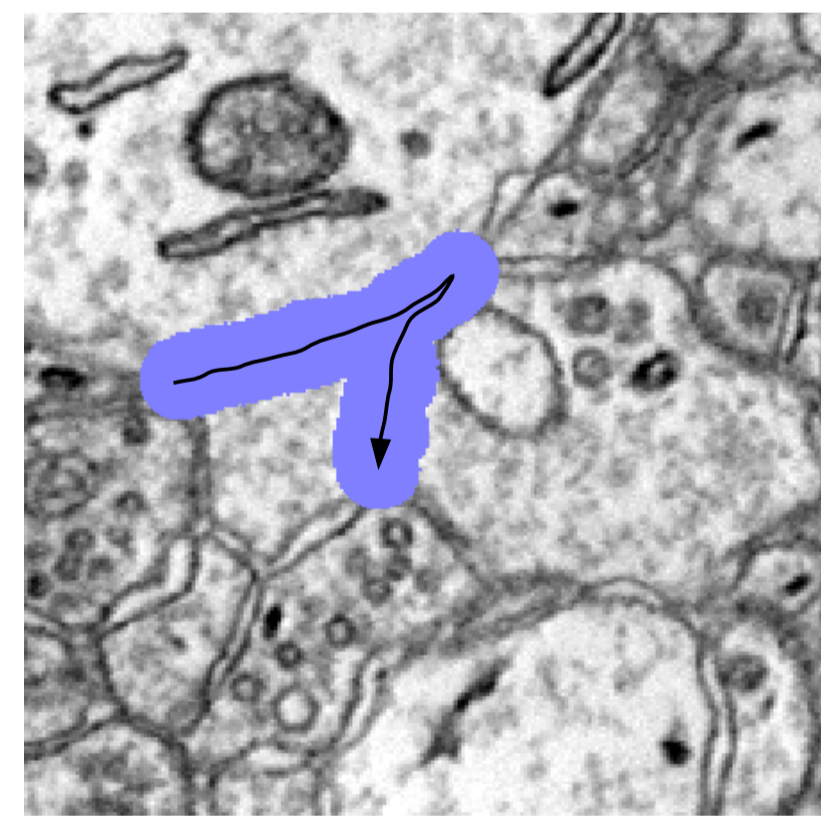
Split Tool



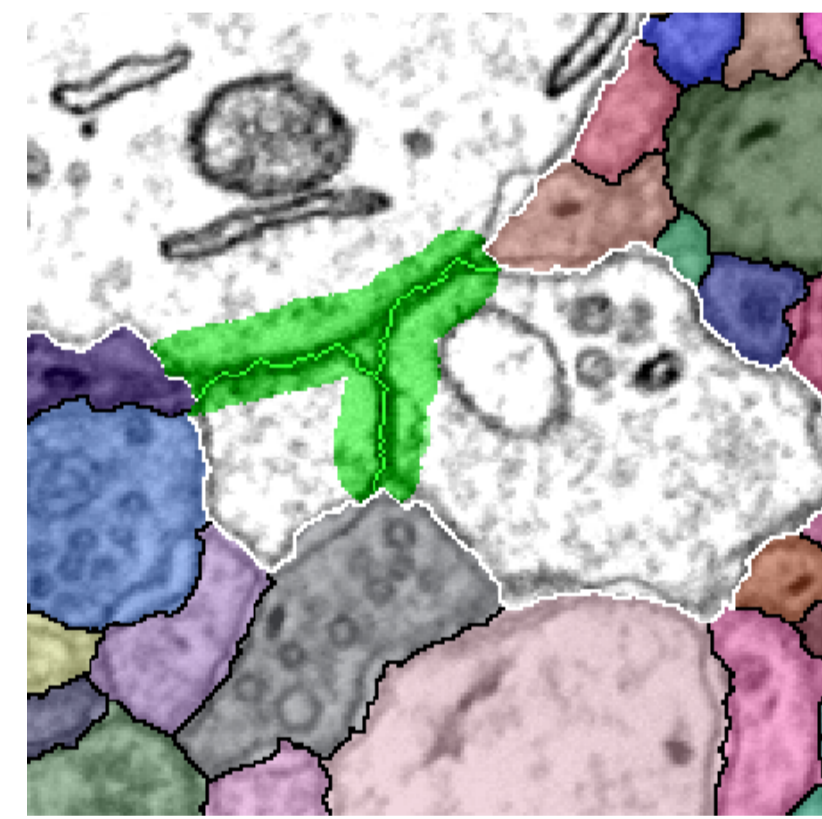
Original Image
1.3x1.3µm



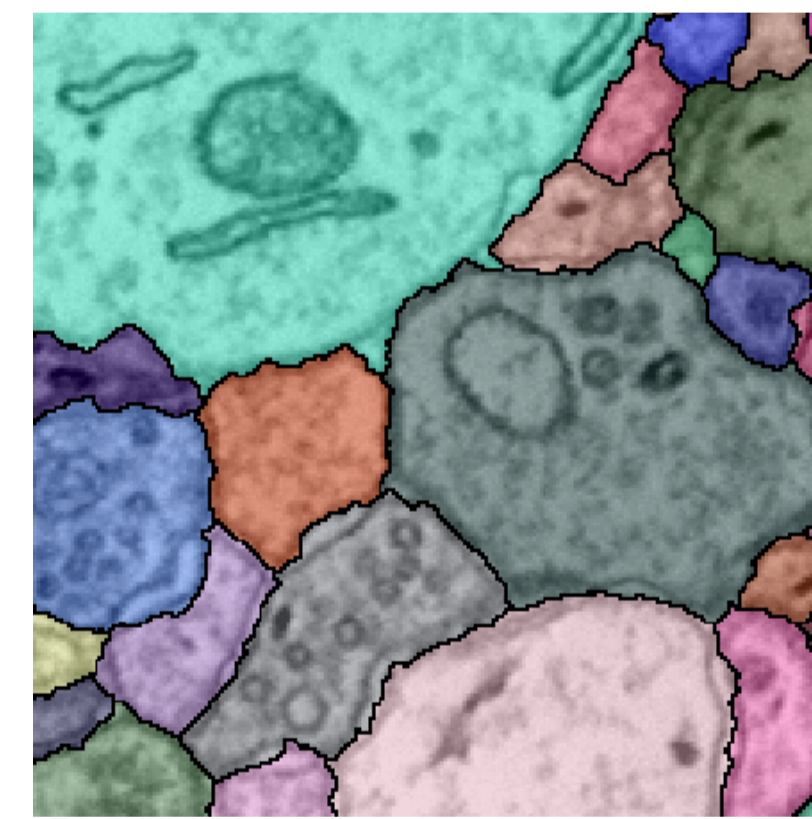
Initial
segmentation



User scribbles
over membrane to
be split



Display overlay
and predicted split
boundary

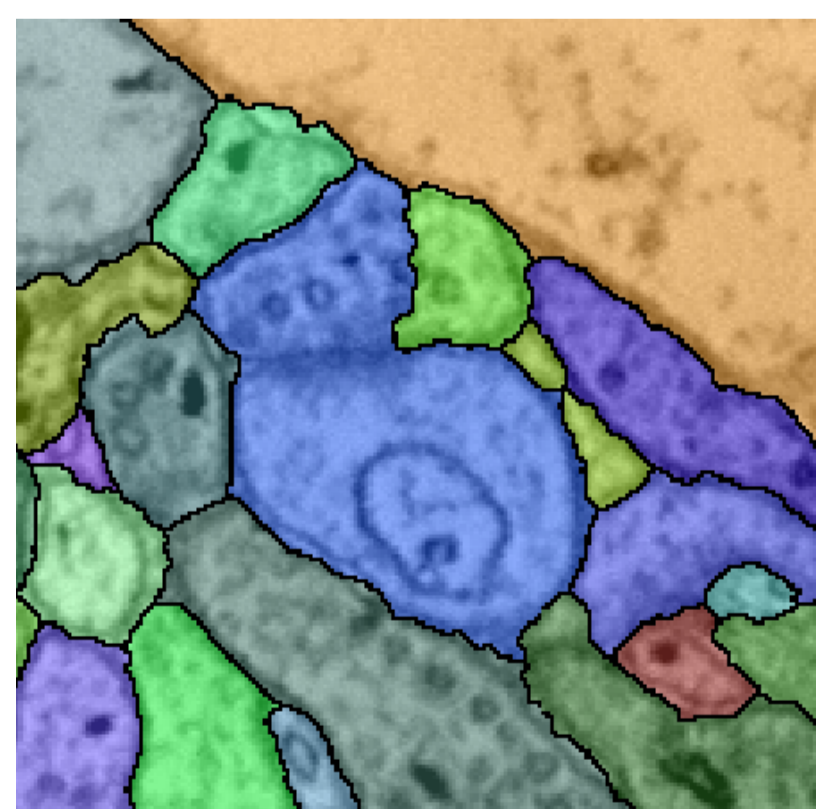


Corrected
segmentation

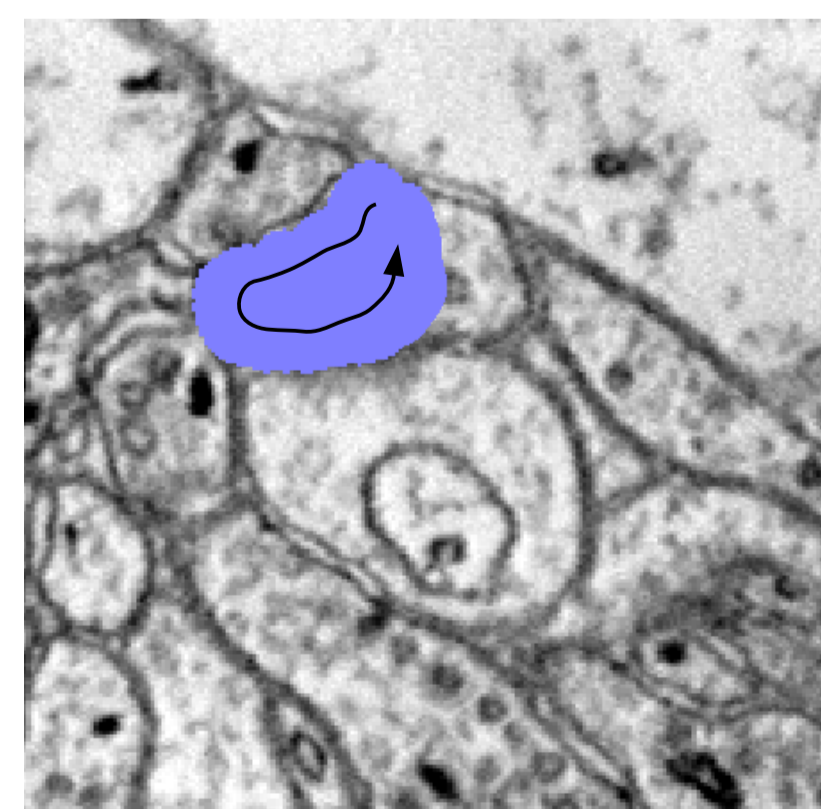
Adjust Tool



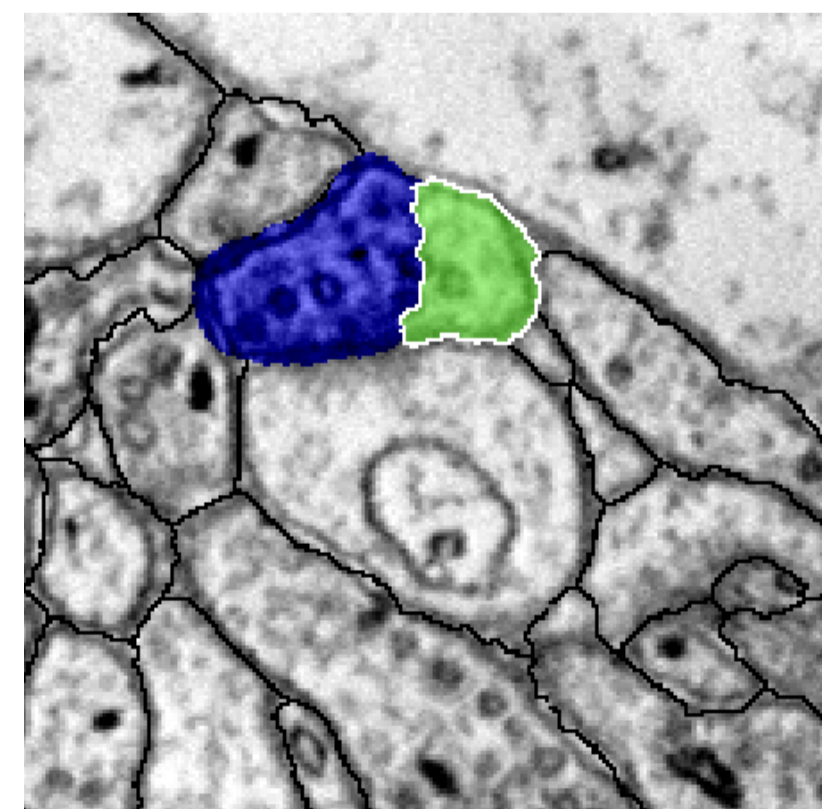
Original Image
1.3x1.3µm



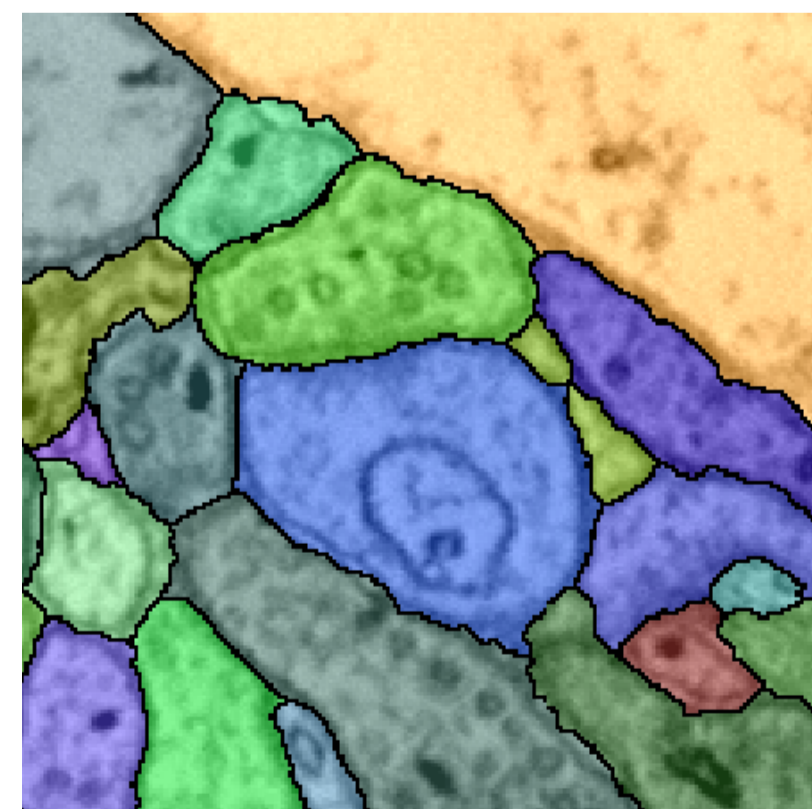
Initial
segmentation



User scribbles
over region to add



Display overlay

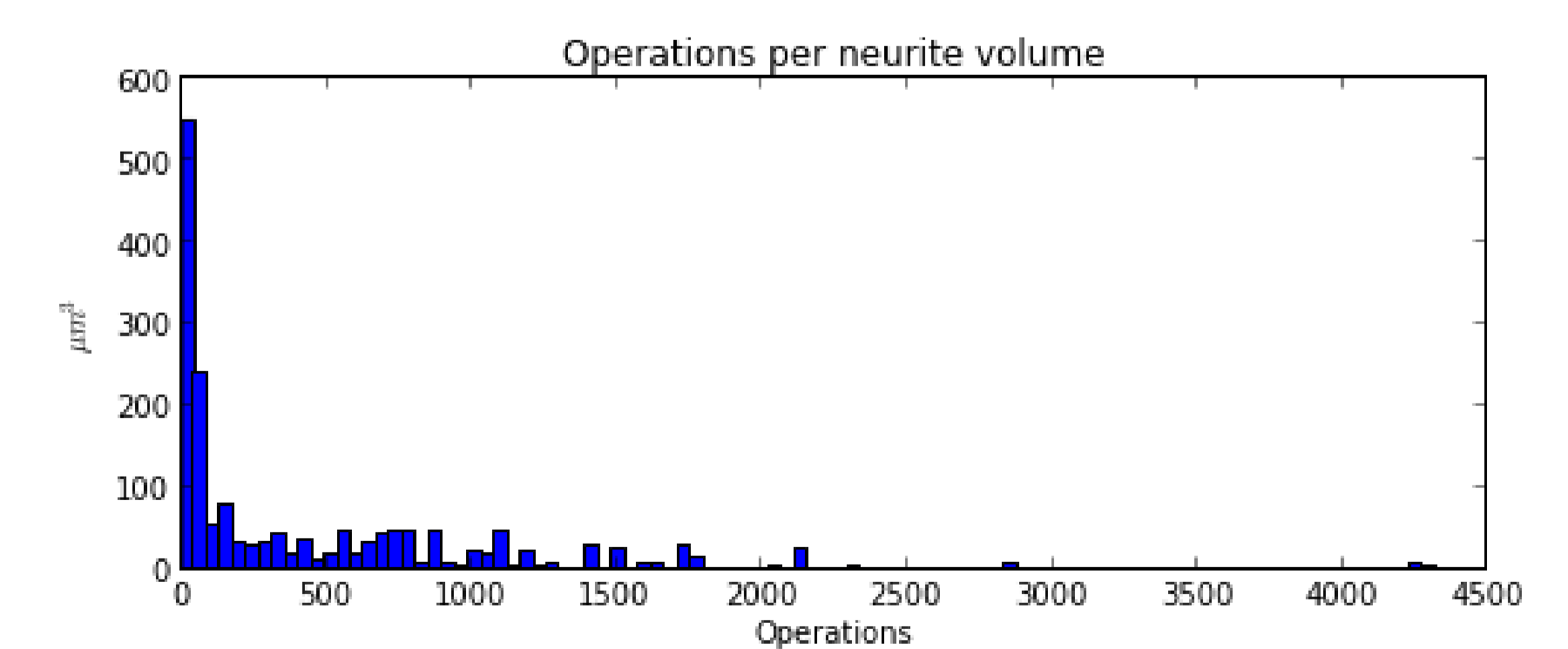
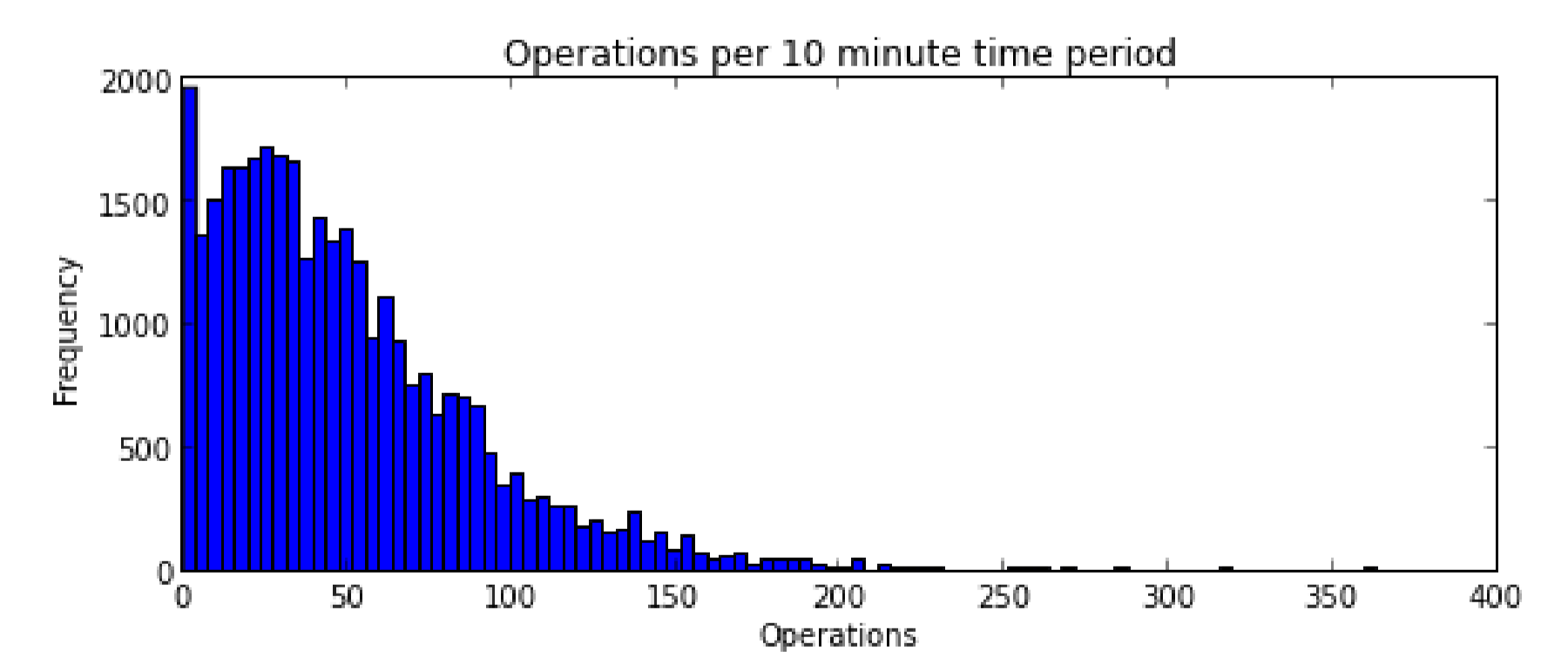
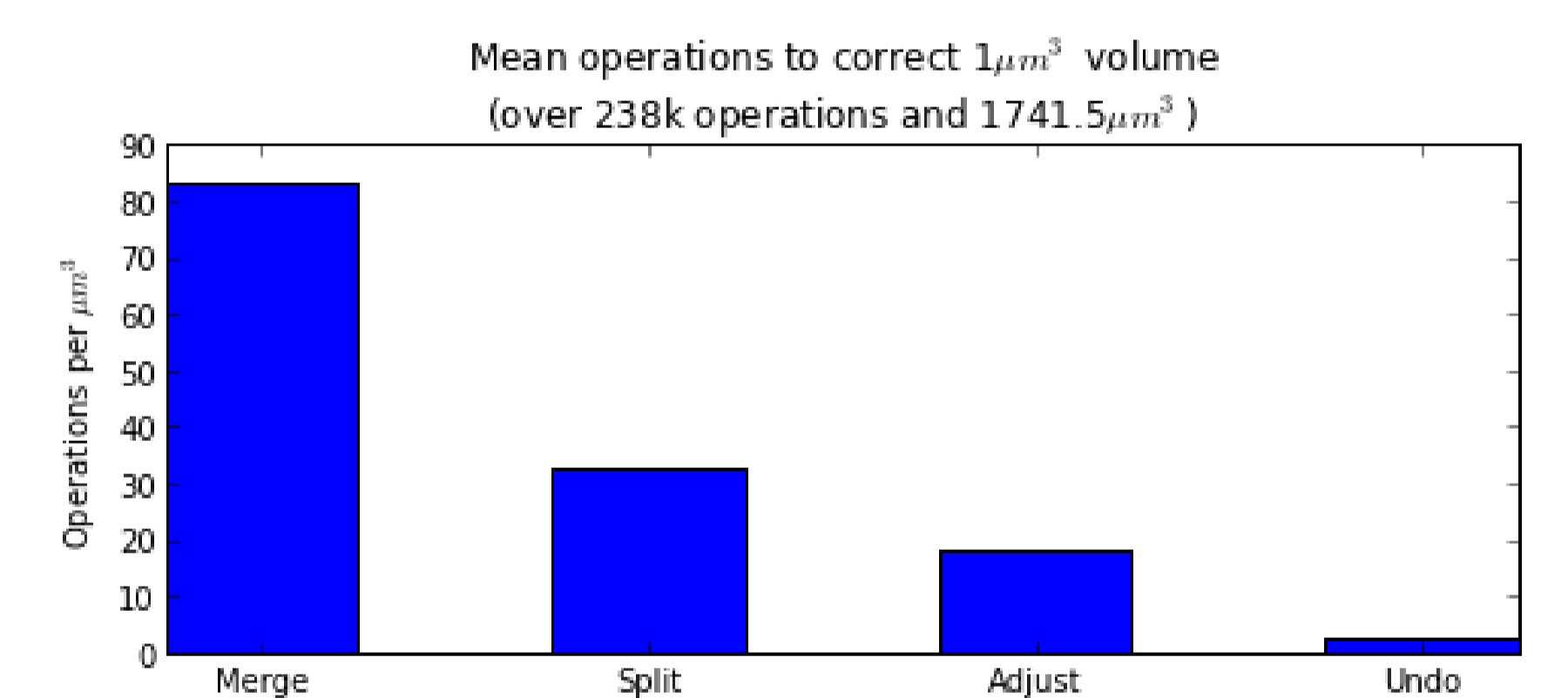


Corrected
segmentation

Annotation Results

A mouse brain cortex dataset was annotated with the Rhoana image processing pipeline and corrected using Mojo.

Partial annotations over two sub volumes totaling 2123µm³ were made by novice users. On average, 1µm³ was annotated in 15 minutes and required 126 edit operations. This compares favorably to estimates of manual tracing times which range between 0.1-1µm³ per hour [5].



Acknowledgments

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References

- [1] Narayanan Kasthuri and Jeff W. Lichtman. Neurocartography. *Neuropsychopharmacology*, 35(1):342–343, 2010.
- [2] Jeff W. Lichtman and Joshua R. Sanes. Ome sweet ome: what can the genome tell us about the connectome? *Current Opinion in Neurobiology*, 18(3):346–353, 2008.
- [3] H Sebastian Seung. Reading the book of memory: Sparse sampling versus dense mapping of connectomes. *Neuron*, 62(1):17–29, 2009.
- [4] Verema Kaynig, Amelio Vazquez-Reina, Seymour Knowles-Barley, Mike Roberts, Thouis R. Jones, Narayanan Kasthuri, Eric Miller, Jeff W. Lichtman, and Hanspeter Pfister. Large Scale Automatic Reconstruction of Neuronal Processes from Electron Microscopy Images. *IEEE Transactions on Medical Imaging* (under review).
- [5] Yuriy Mishchenko. Automation of 3D reconstruction of neural tissue from large volume of conventional Serial Section Transmission Electron Micrographs. *J Neurosci Methods*, 176(2): 276–289, 2009