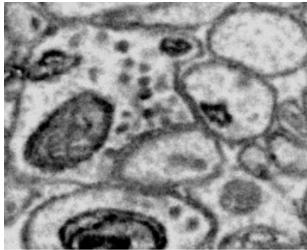


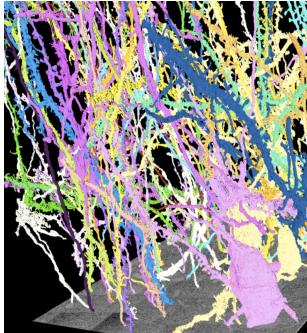
DANIEL HAEHN

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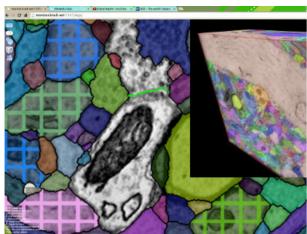
+1.617.701.root
haehn@ieee.org
<http://danielhaehn.com>



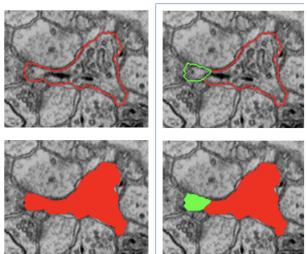
A slice of connectomics image data showing neurons.



Selected three-dimensional neuron reconstructions in a 100 micron cube of rat cortex.



The web-based and interactive proofreading software Dojo.



Guided Proofreading reduces error correction to simple yes/no decisions.

I am a connectomics and visualization researcher who investigates how neurobiology and data science can help advance the understanding of visual cortex inspired machine learning.

Connectomics

In connectomics we create a map of the mammalian brain at nano-scale. For this one must acquire image stacks of the brain of a rat using electron microscopy. These images are of such high resolution that individual neurons (nerve cells) and their connections (synapses) are then visible.

Once these images are acquired, machine learning algorithms then classify cell structures and connections within these massive (terabytes or petabytes) images as manual processing is, thus far not possible.

Understanding the wiring of the brain, curing mental and neurological diseases, and deriving new artificial intelligence methods are ultimate goals. While these goals are far from achieved, the current developmental milestones are a fully processed 100 micron cube followed by its' extension to a 1 millimeter cube of brain tissue [7, 6].

Proofreading

Currently, the automatic classification of cells and connections is far from absolute. Humans are still needed to double-check the results and this task is called proofreading. In 2014 we published Dojo¹, which is an interactive proofreading software that enables proofreading for untrained individuals recruited from all walks of life. All of the results and data that have been gathered from the published user study can be found in The Proofreading Benchmark². [3]

We discovered that the majority of time spent during interactive proofreading is looking for errors. To reduce this, we developed the Guided Proofreading system. The artificial intelligence within our system suggests potential errors and corrections to a user thus speeding up the proofreading task. Our results have demonstrated our trained classifier is also able to perform proofreading automatically up to a certain threshold. For increased performance, the Guided Proofreading³ user interface simplifies error correction by humans to a yes/no decision. [2]

Visualization

Brain data is beautiful and not only at a nano-scale resolution. In 2012 we developed XTK⁴, the first web-based visualization framework for medical imaging data such as MRI scans. This framework quickly became an established collaborative effort with over twenty international contributors which powers many projects world-wide. [4]

One example of these projects is our award-winning software, Slice:Drop⁵, a web-based viewer that supports many different medical imaging formats. Not only clinicians but researchers, as well as patients, now use this viewer daily. The software visualizes data without requiring any server uploads and leverages the local graphics card for accelerated rendering. [5]

In turn, Connectomics data is much larger in size thus making visualization more difficult. We have successfully applied new processing strategies to overcome these challenges and have developed the MBeam viewer for the Zeiss MultiSEM 505 microscope. This software allows neuroscientists to view the high resolution images immediately

¹<http://rhoana.org/dojo/>

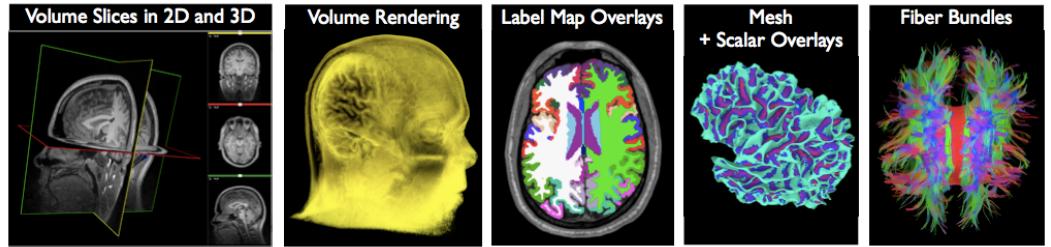
²<http://github.com/haehn/proofreading/>

³<http://rhoana.org/guidedproofreading/>

⁴<http://goXTK.com/>

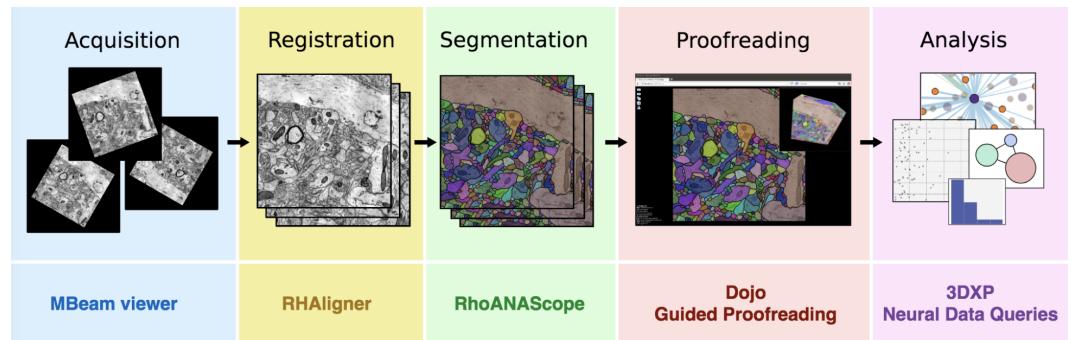
⁵<http://slicedrop.com/>

after acquisition. This process has been so successful that Zeiss, the manufacturer of the microscope, installed the MBeam viewer internally.



The Slice:Drop viewer supports different 2D and 3D visualizations of medical imaging data directly in the web-browser.

From an engineering standpoint, the MBeam viewer along with Dojo, our proofreading software, provide overlapping functionality such as the processing of data for transfer and visualization. To avoid duplication, we have now developed Butterfly, a system for scalable data management which unifies logic and visualization. As a result we can now create visualizations of large scientific datasets for every step of the connectomics processing pipeline. [1]



Our Butterfly application suite includes specifically targeted visualizations for every step of the connectomics cannot and is fully extendable for future visualizations.

In addition, we have recently added the Neural Data Queries interface to the Butterfly platform, allowing semantic queries of neurons and their synaptic connections. This functionality is a core component in evaluating the performance of our connectomics pipeline for the Machine Intelligence from Cortical Networks (MICrONS) effort, a \$100 million research program backed by the Intelligence Advanced Research Projects Activity (IARPA).

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