Connectomics Large-scale synaptic-resolution brain mapping in academiaindustry collaborations.

Michał Januszewski Google Research



TEAMS >

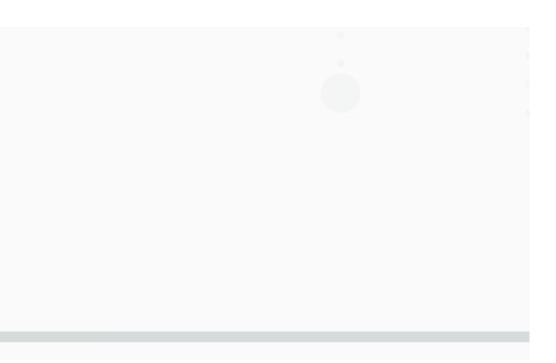
Connectomics

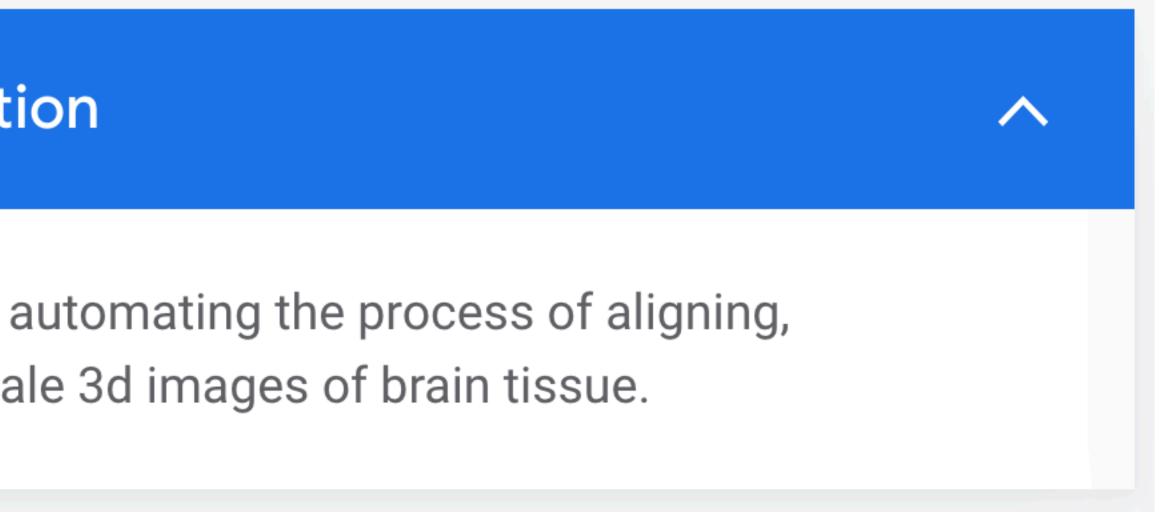
Our goal is to leverage Google expertise and resources to advance understanding of the structure and function of the brain.

Automated 3d Brain Reconstruction

We develop algorithms and software for automating the process of aligning, segmenting, and annotating petabyte-scale 3d images of brain tissue.

https://research.google/teams/connectomics/





TEAMS >

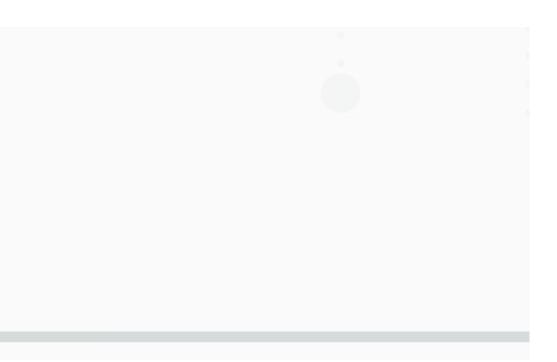
Connectomics

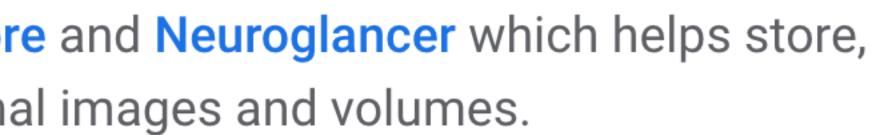
Our goal is to leverage Google expertise and resources to advance understanding of the structure and function of the brain.

Visualization and Infrastructure

We develop software such as TensorStore and Neuroglancer which helps store, process, and visualize large n-dimensional images and volumes.

https://research.google/teams/connectomics/

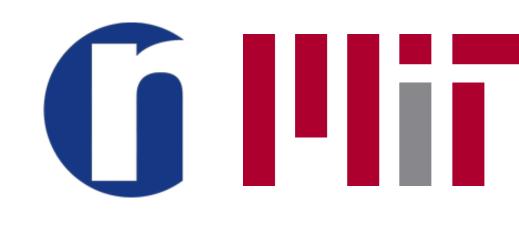




Connectomics @ Google

- Tim Blakely
- Sven Dorkenwald
- Viren Jain
- Michał Januszewski
- Laramie Leavitt
- Peter Li
- Jeremy Maitin-Shepard

Academic Collaborators



max planck institute of neurobiology



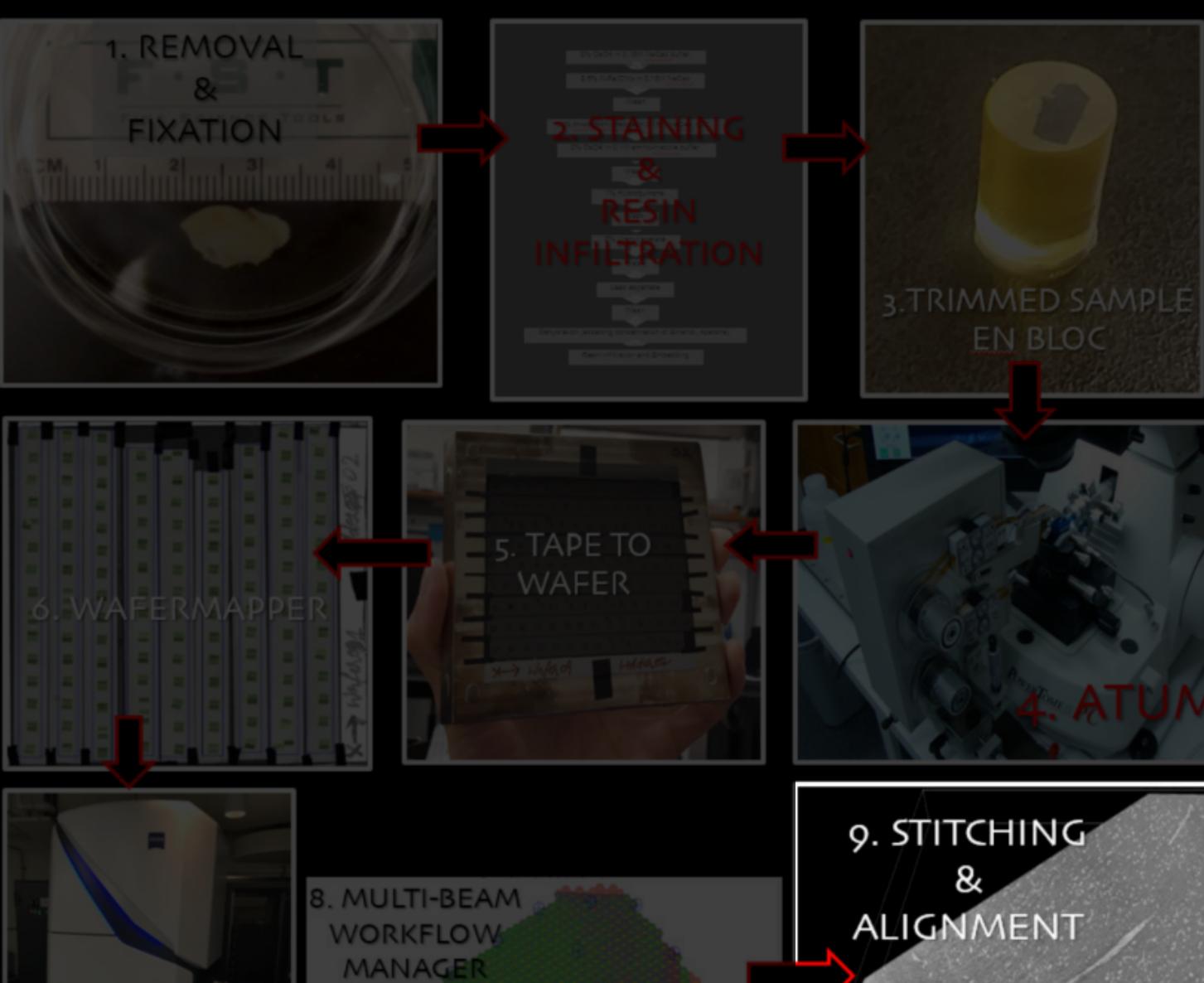


Fly EM



HARVARD **UNIVERSITY**





MULTI-BEAM SEM

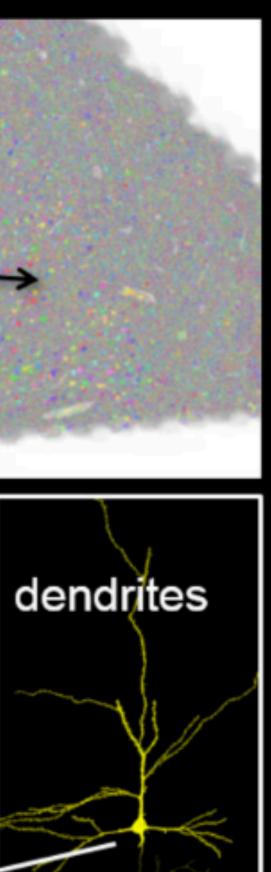


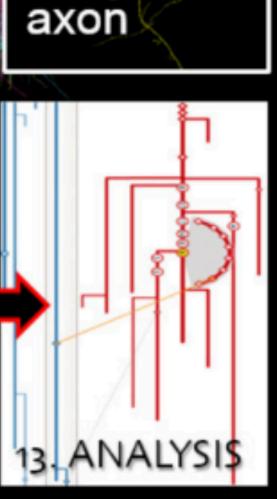
11. RENDERING

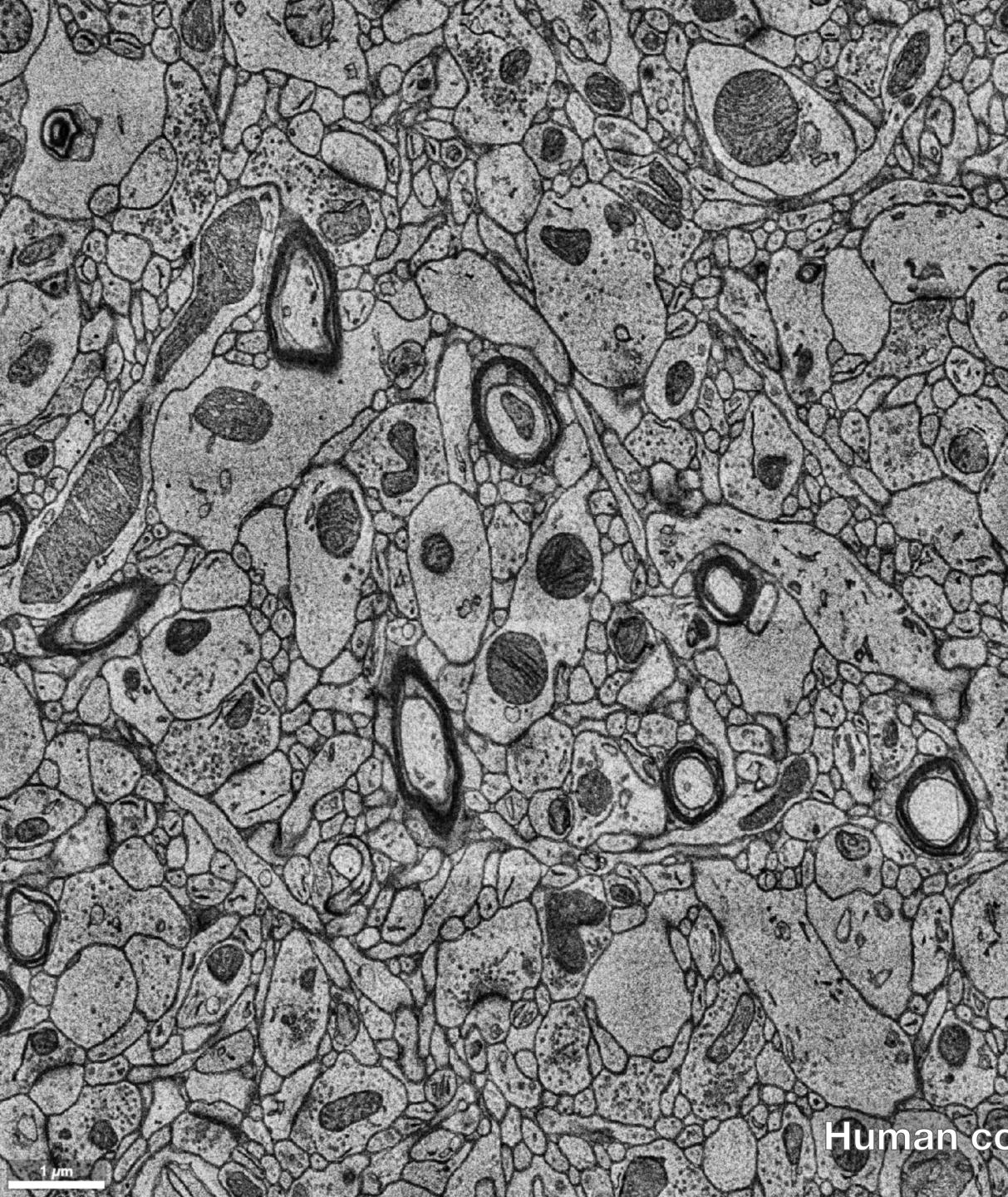
SYNAPSE

ANNOTATIO

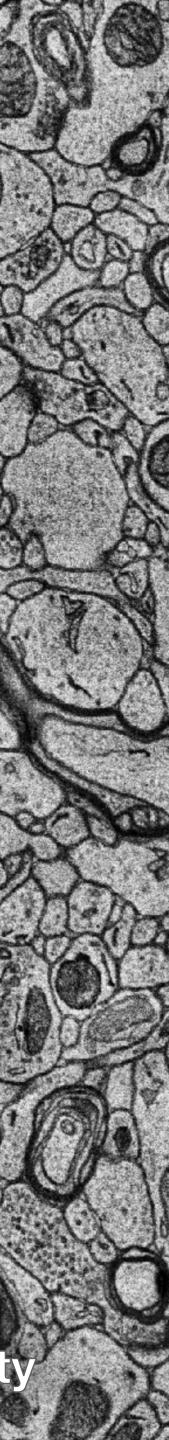
Courtesy of Jeff Lichtman, Harvard University

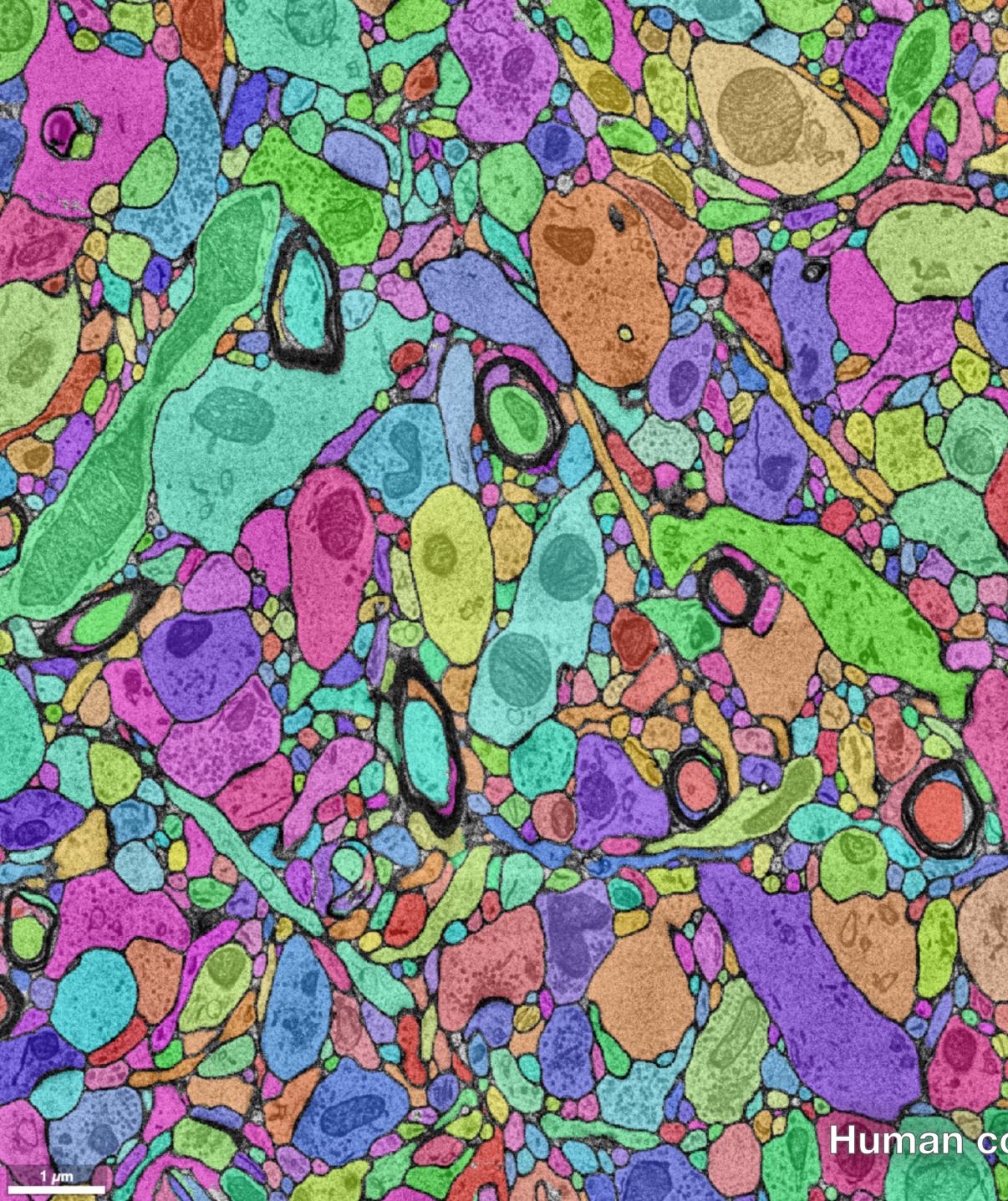




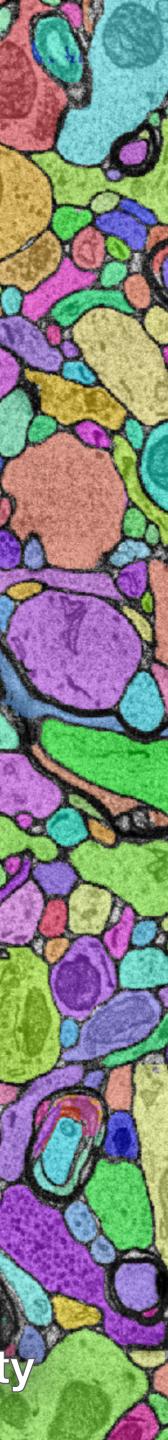


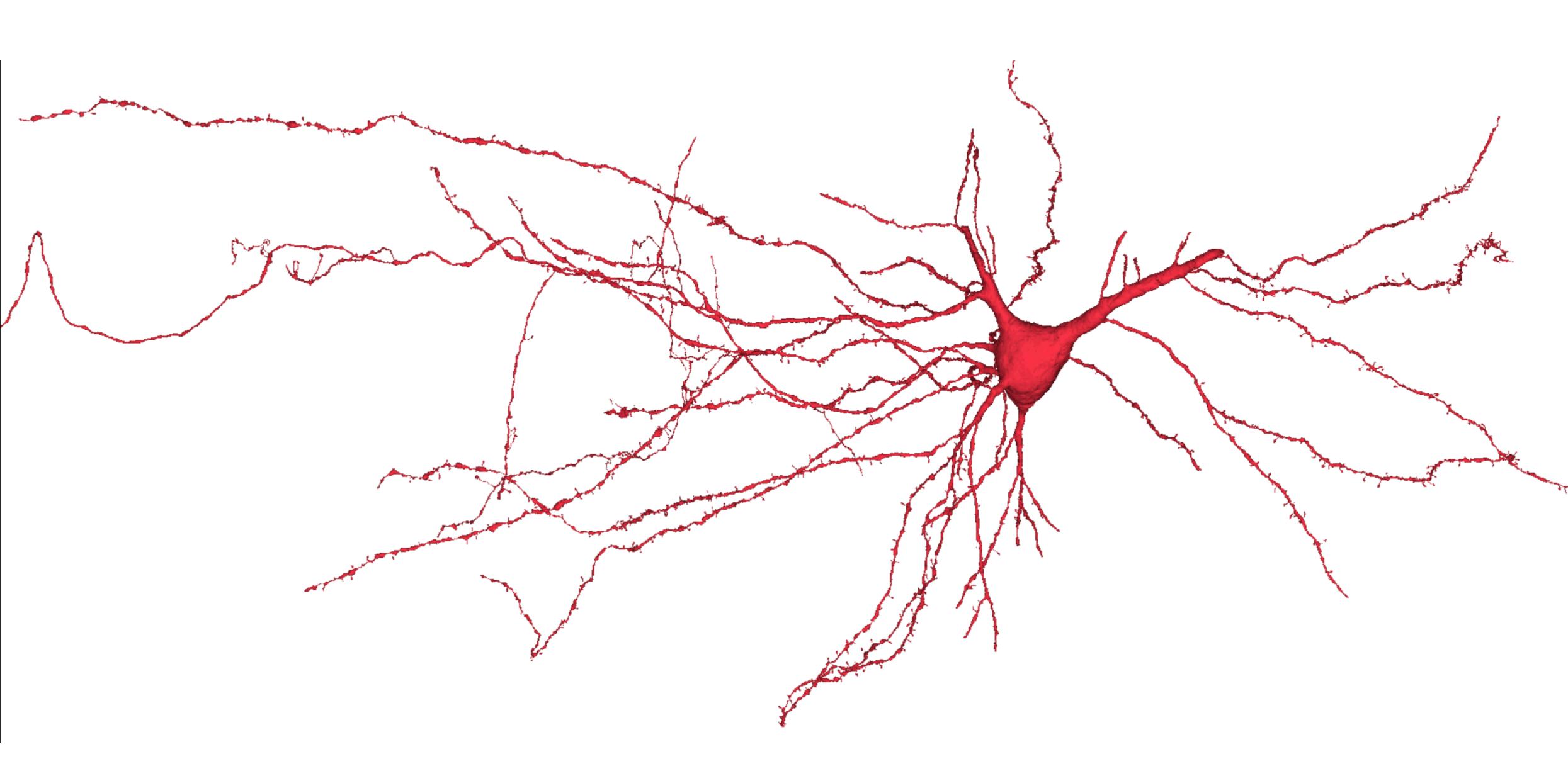
Human cortex, ATUM mSEM, Lichtman Lab, Harvard University



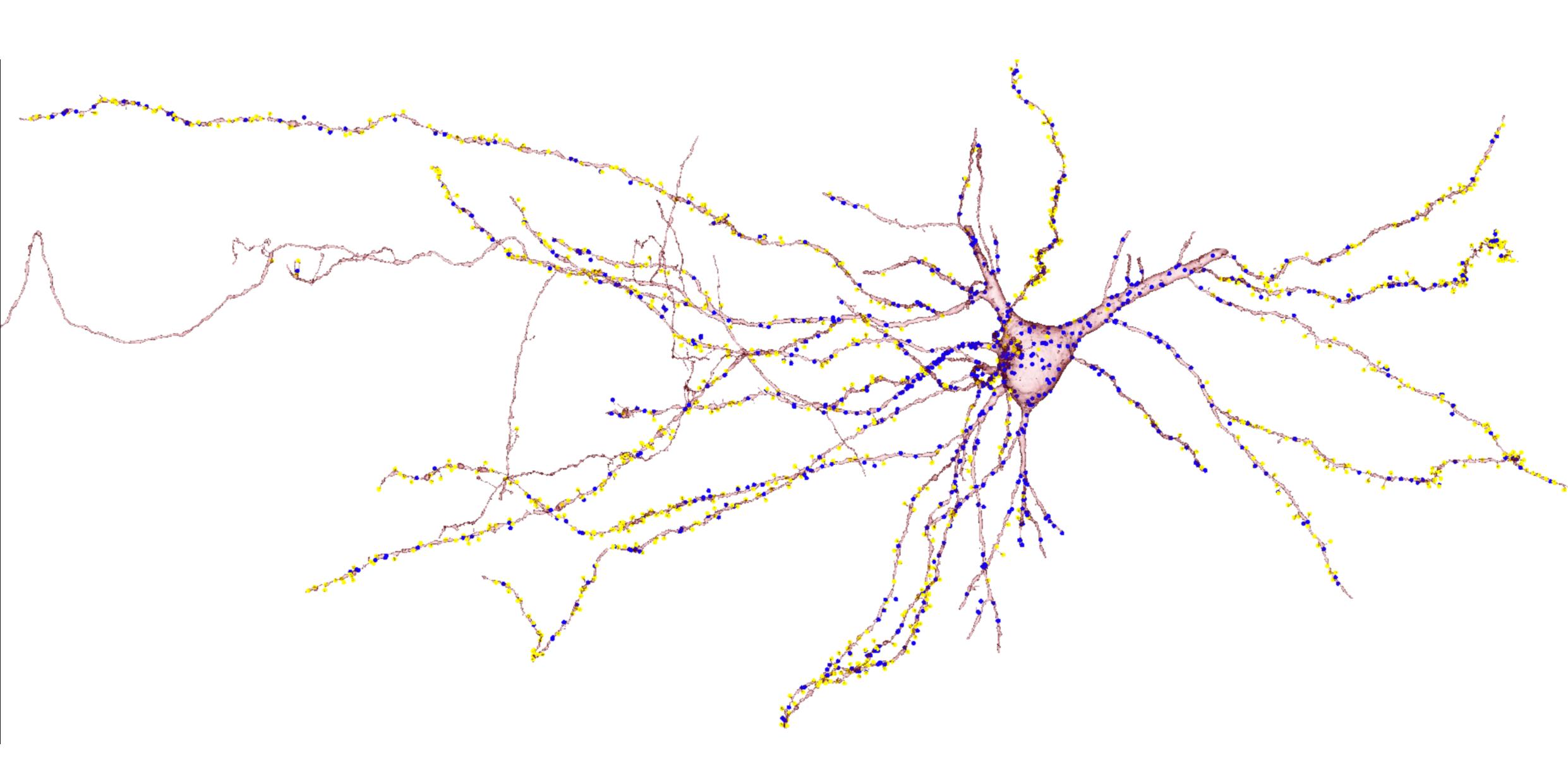


Human cortex, ATUM mSEM, Lichtman Lab, Harvard University

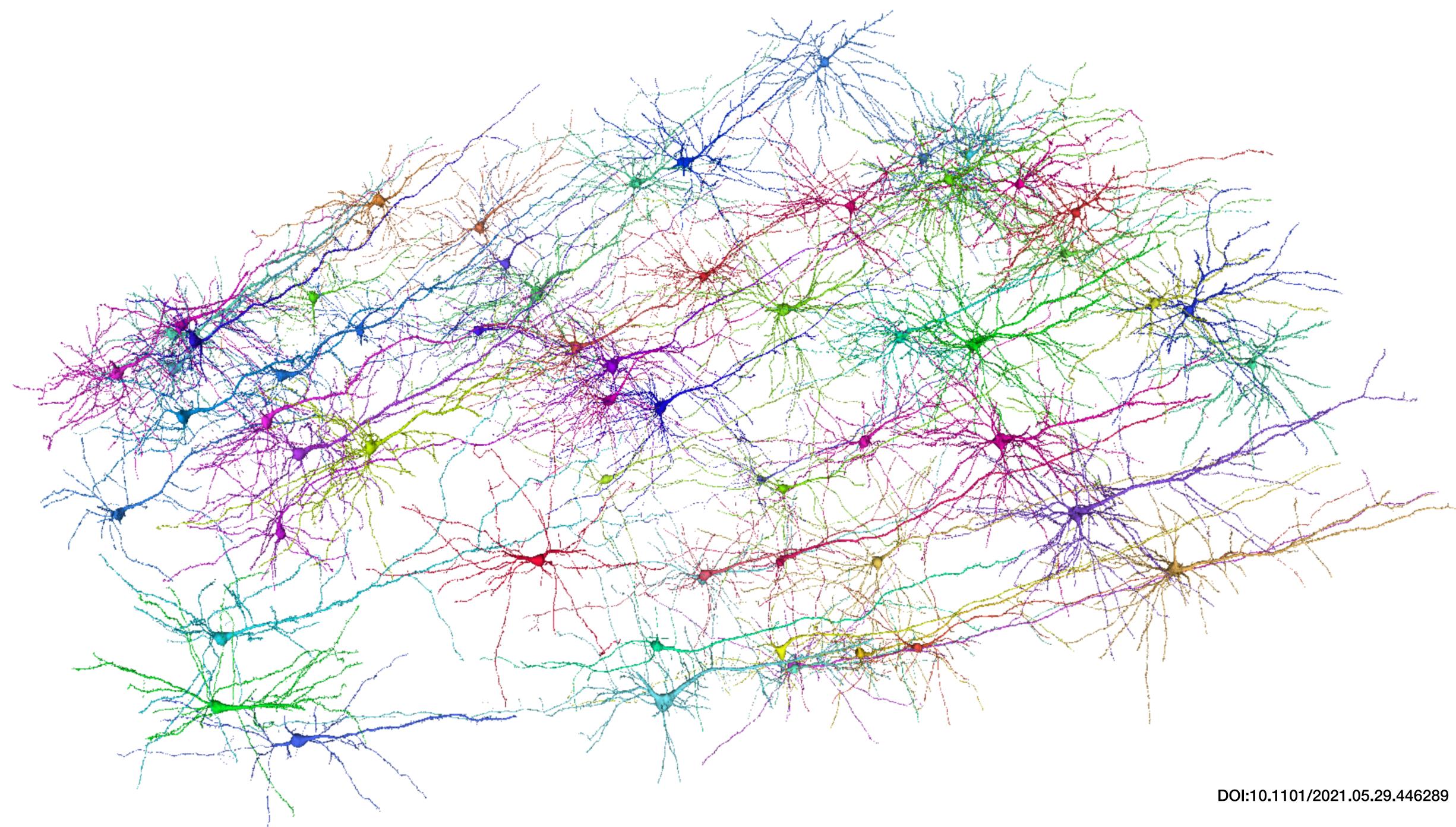






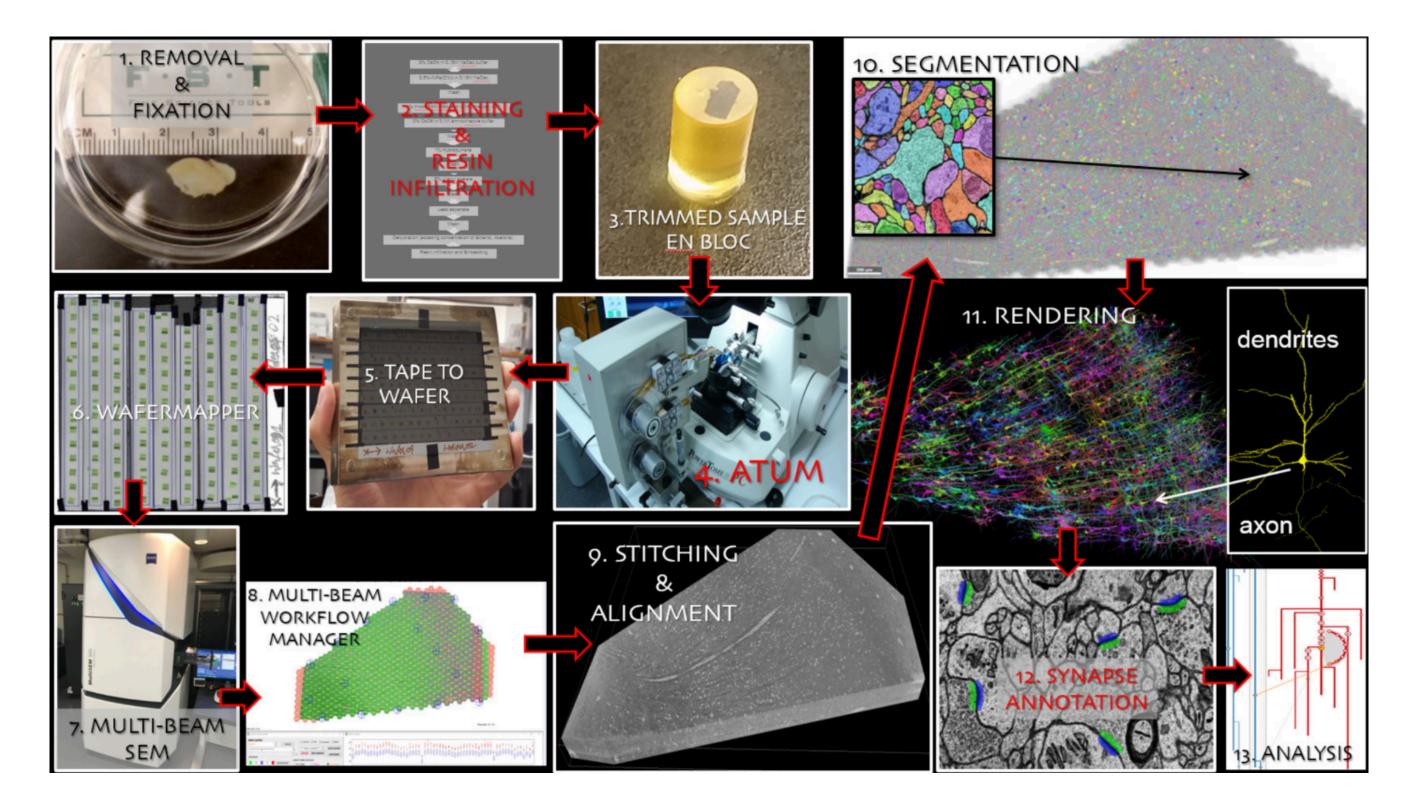






Why a collaboration?

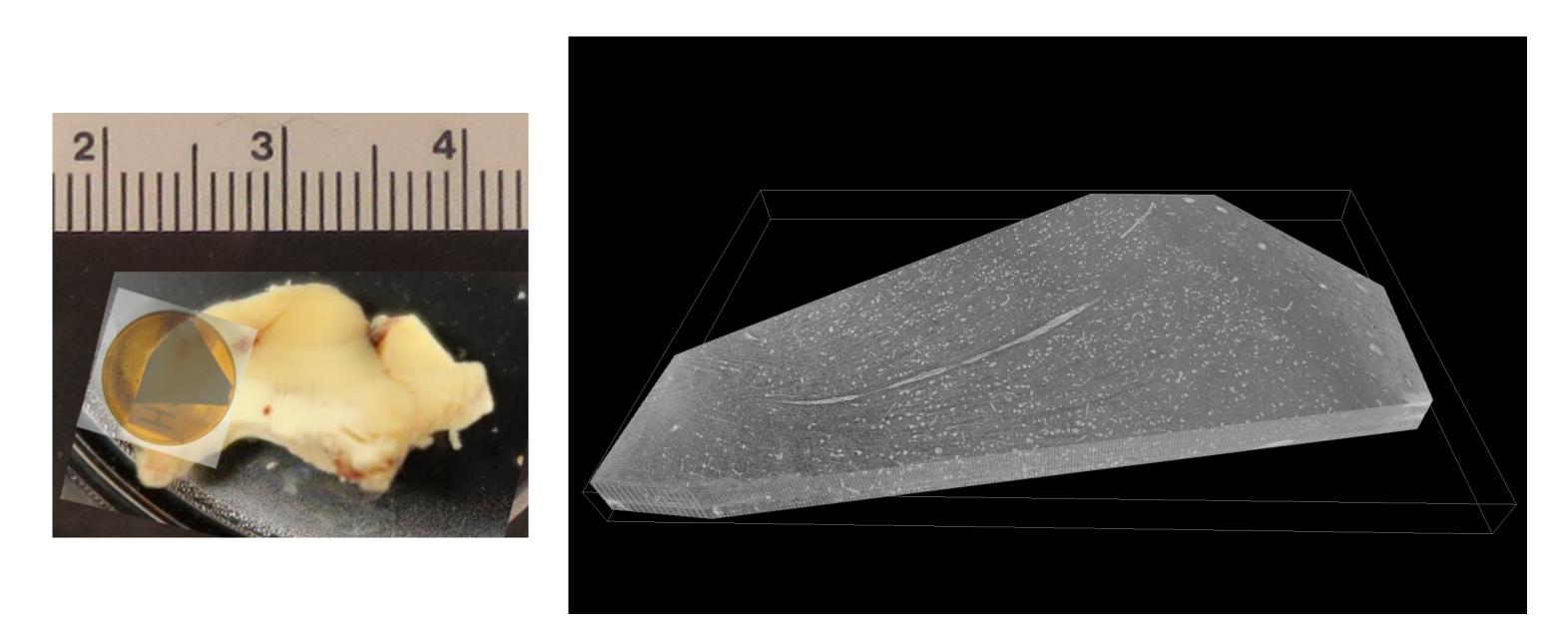
- Common goal.
- Large-scale, complex project.
- Complementary expertise.
- Sufficient shared understanding of the involved domains.



h01: 1 mm³ of human cortex

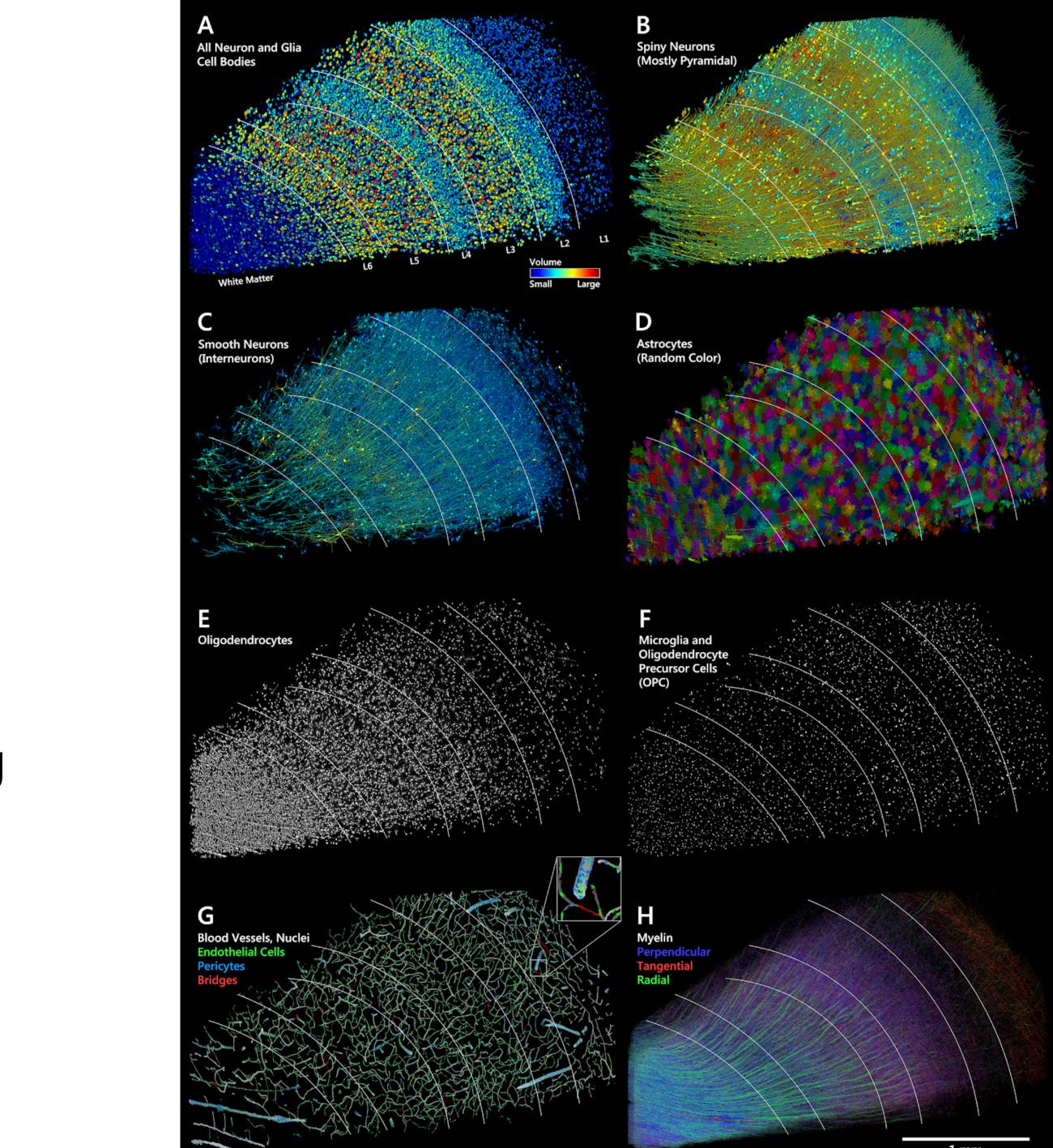
- Collaboration with Lichtman lab, Harvard University
- 5,000 sections
- 326 days of imaging time
- 1.4 PB of imagery
- 57,216 cells
- 133.7M synapses
- Available online: <u>https://h01-release.storage.googleapis.com/landing.html</u>

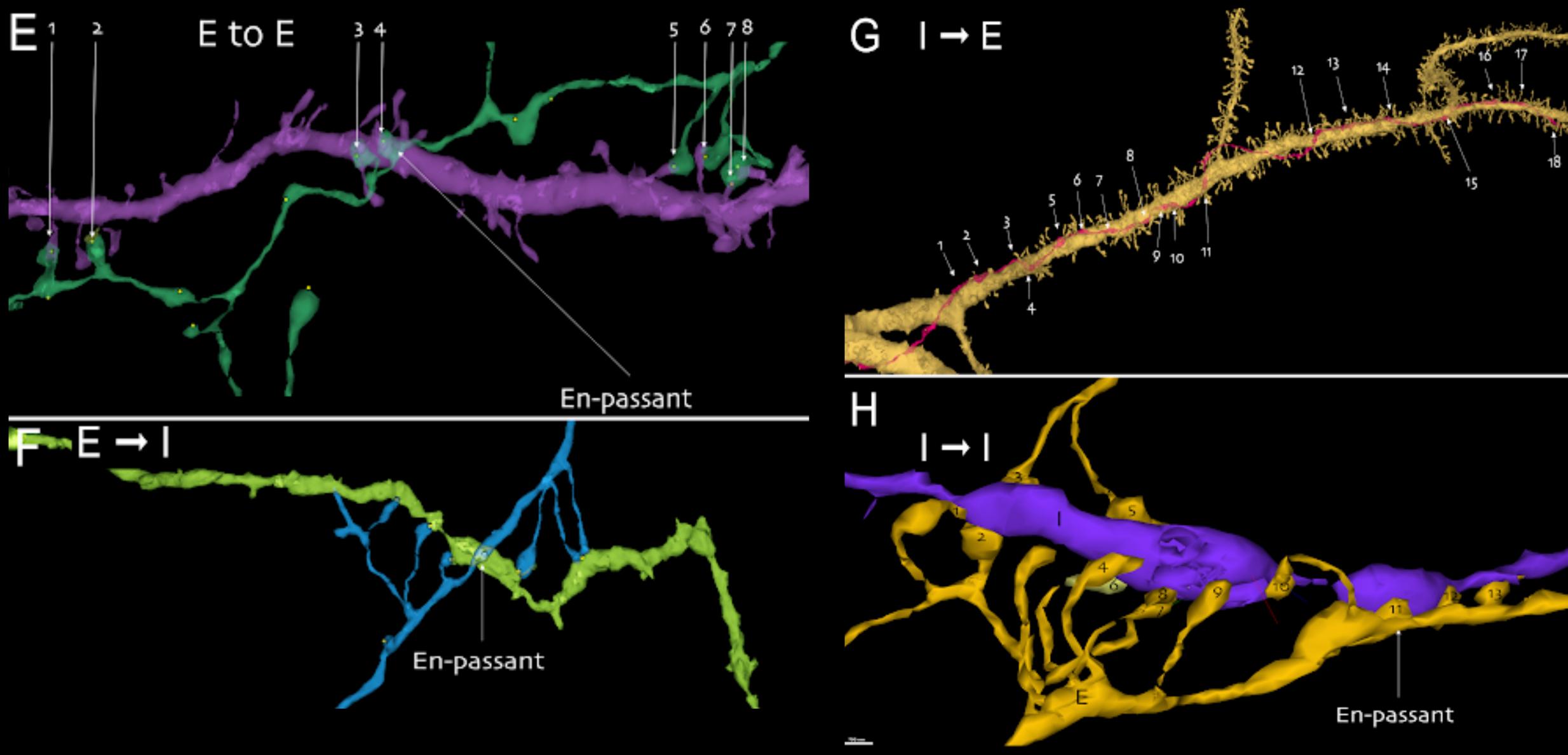
Shapson-Coe, Alexander, et al. "A connectomic study of a petascale fragment of human cerebral cortex." *bioRxiv* (2021) DOI: 10.1101/2021.05.29.446289

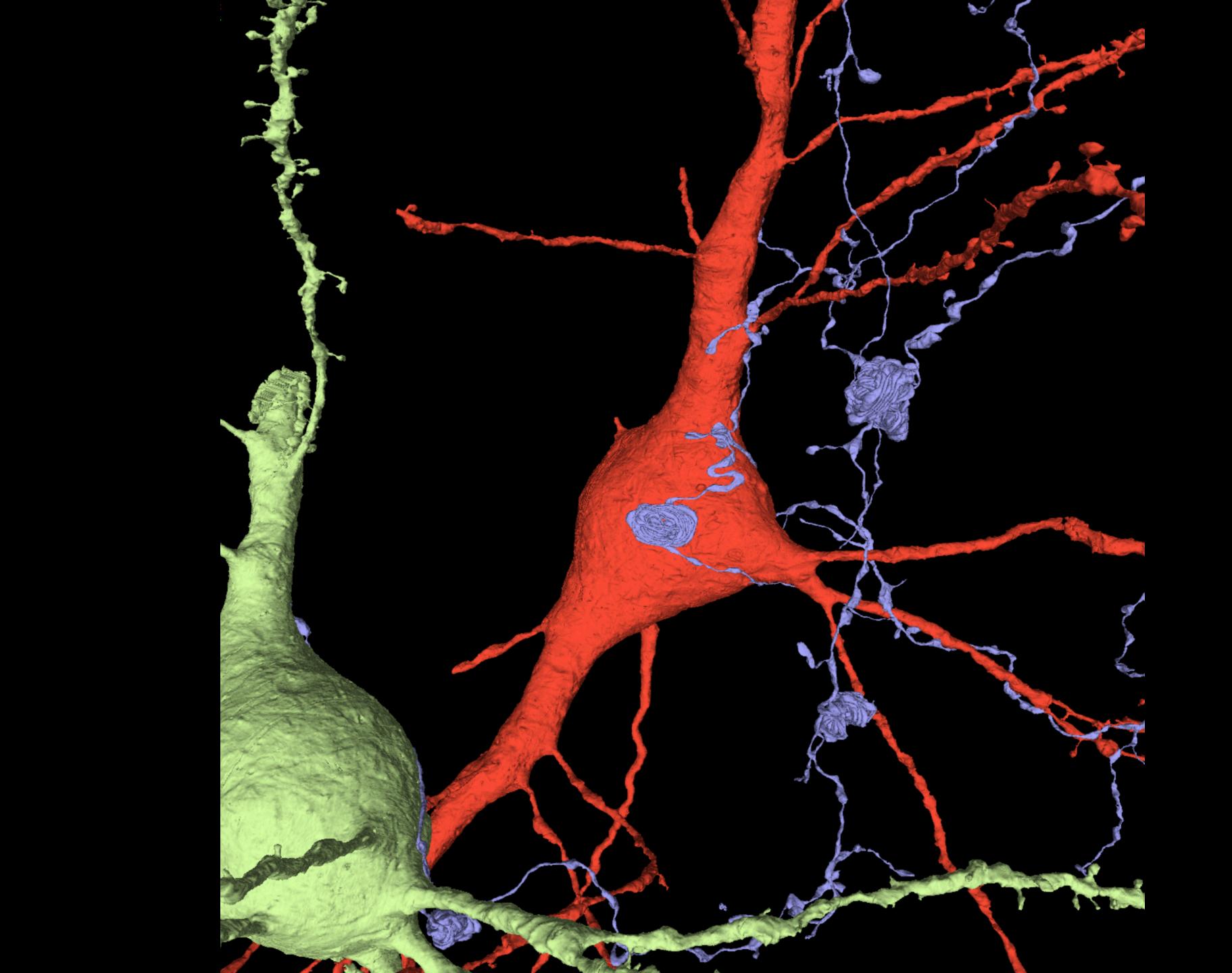


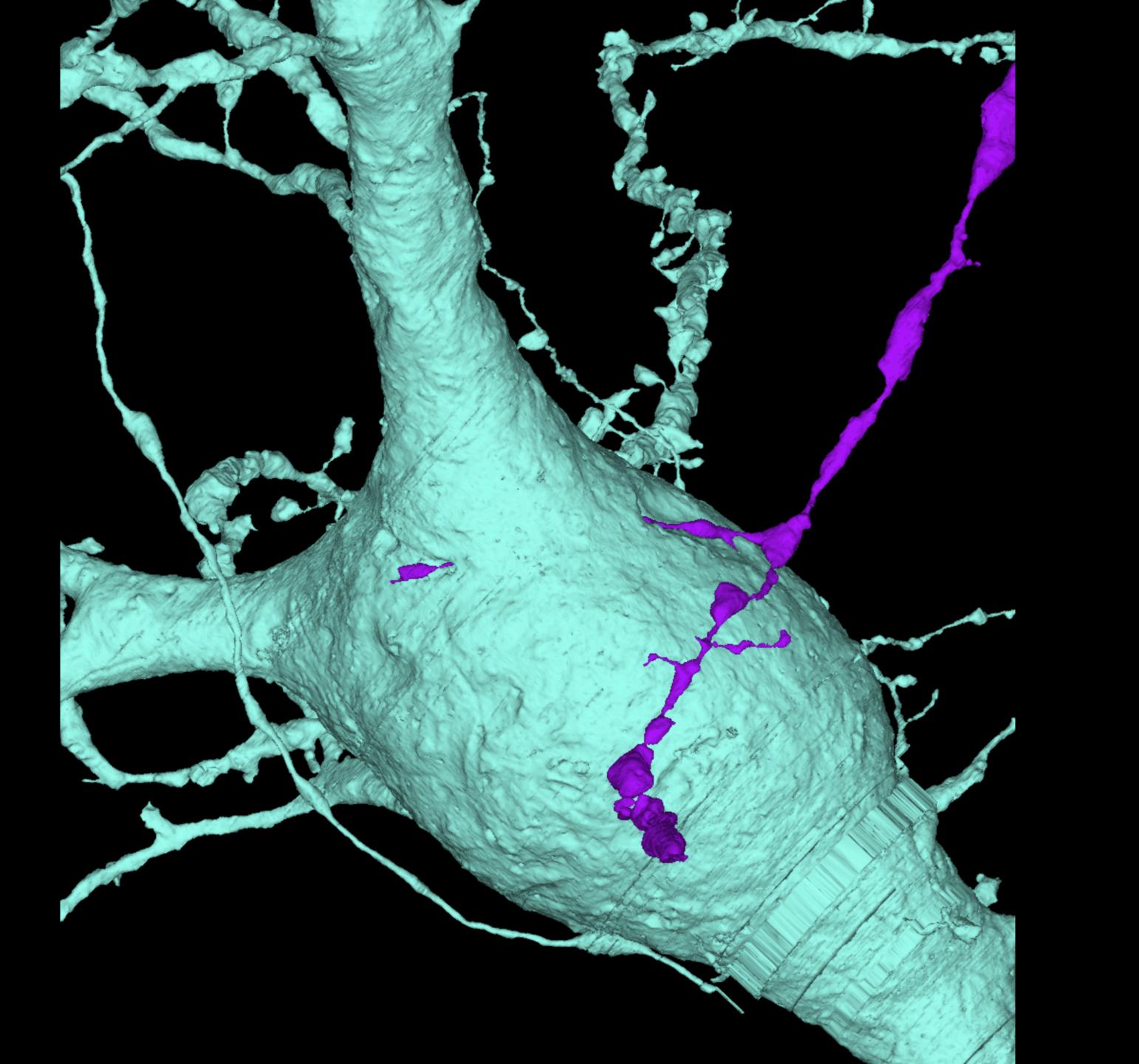
Initial findings

- Complete cell census;
 ~2:1 glia:neuron ratio.
- Presence of axons with unusual morphology ("whorls").
- Chandelier interneurons innervating each other's axon initial segments.
- Presence of rare multi-synaptic contacts.

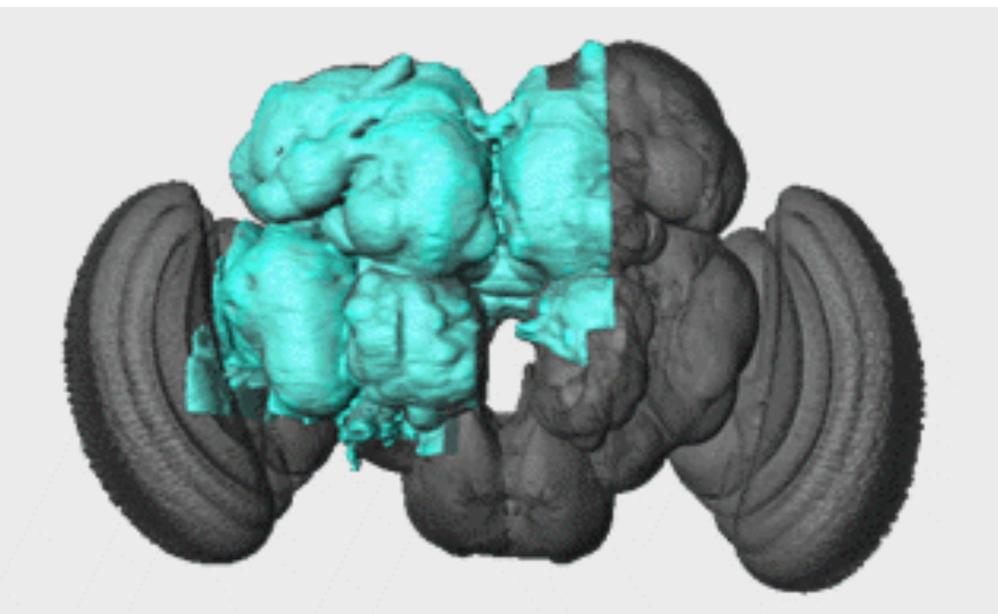








Hemibrain

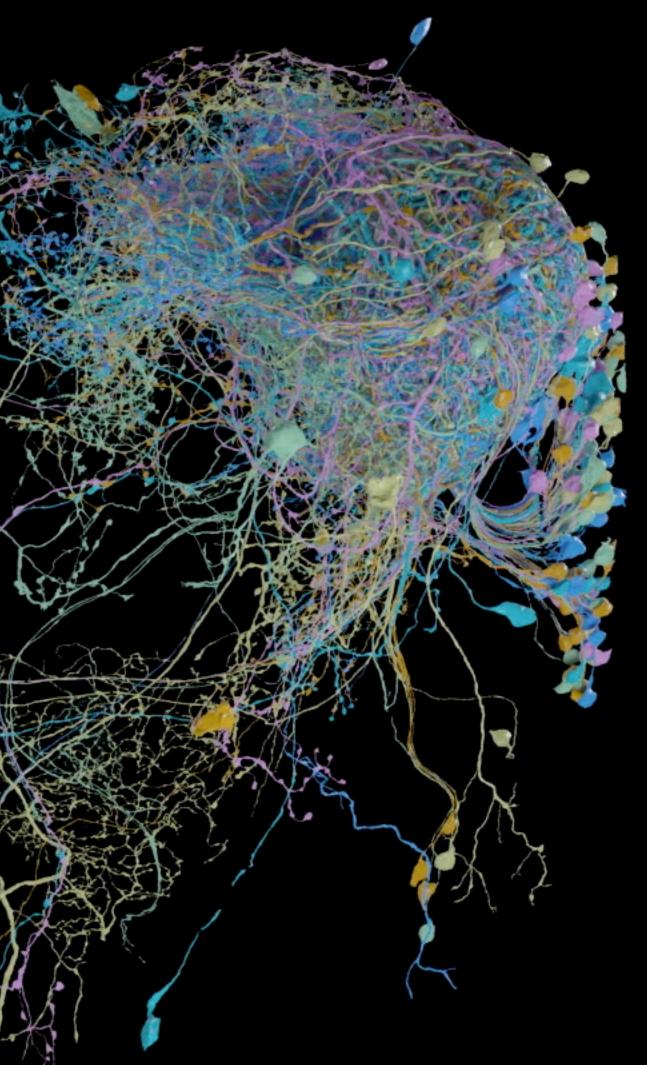


The hemibrain dataset encompasses the part of the fly brain highlighted here in blue. This region includes neurons involved in learning, navigation, smell, vision, and many other functions. Central part of the Drosophila brain
25,000 neurons
50 person-years of proofreading
Public resource: <u>https://www.janelia.org/project-team/flyem/hemibrain</u>

Details in:

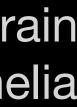
Scheffer, Louis K., et al. "A connectome and analysis of the adult Drosophila central brain." *Elife* 9 (2020): e57443.

Olfactory



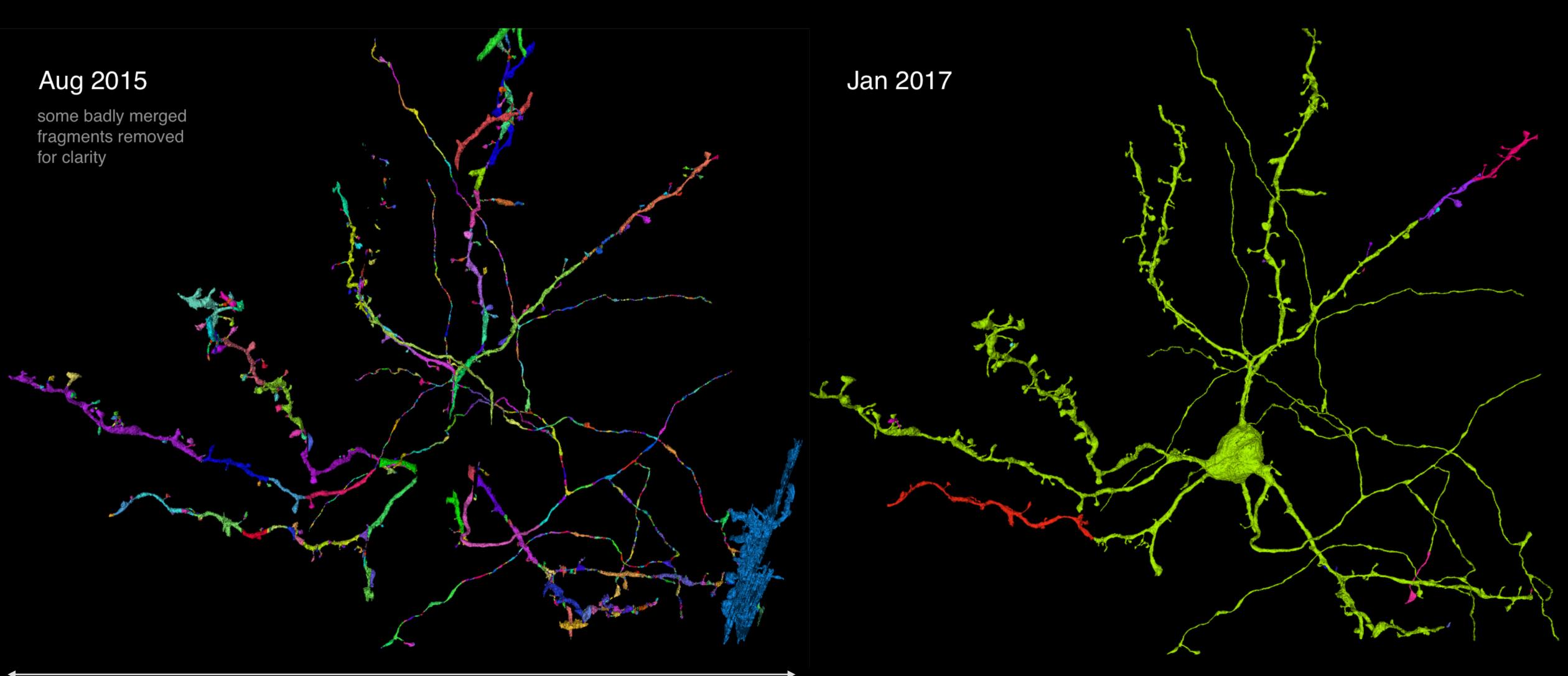
A LEC

Drosophila hemibrain Google Connectomics & FlyEM, HHMI Janelia



It should be kept in mind that although most of the currently operating systems make extensive use of the computer for bookkeeping, 3-D display, and data analysis, they still require the slow manual input of graphical information. However, it seems quite clear that the rapid advances in electronics will make more and more automation possible at a reasonable cost. Within a few years we can expect that systems will be available that can easily recognize and digitize some features automatically, leaving for the investigator only those cases that are difficult or ambiguous. The greater speed with which the analysis can then be done should make possible a great increase in the use of such systems for both basic research and practical problems, such as those of the clinical pathologist. Thus two quite separate issues will be involved in future developments of this technique: (a) the technical problems associated with increasing automation and reducing equipment cost; and (b) the expanded exploration of ways in which these techniques can be applied to new and different scientific as well as clinical problems

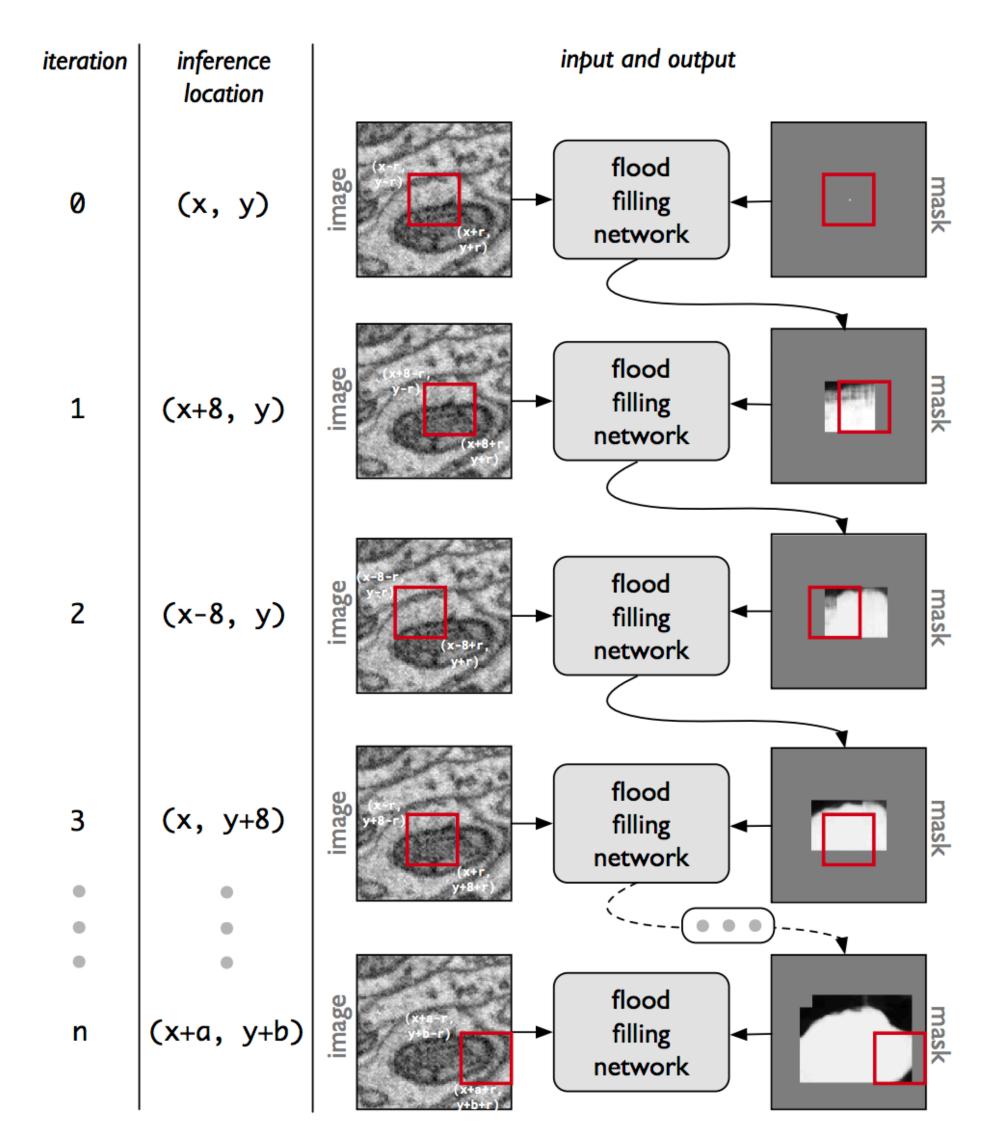
Macagno, Levinthal, Sobel (1979)

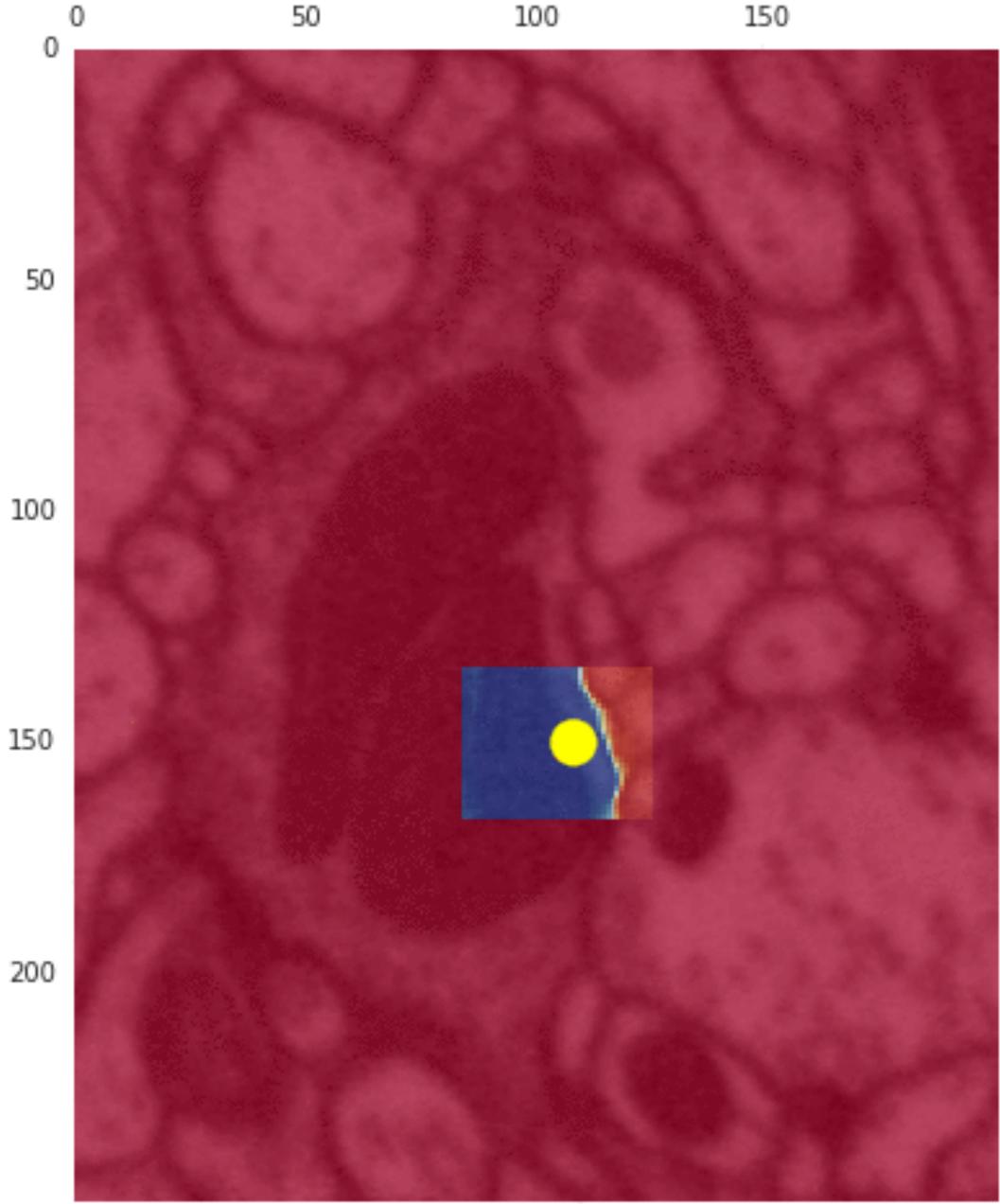


100 µm

J0126: Zebra Finch Area X Jörgen Kornfeld, Winfried Denk, MPI of Neurobiology 9x9x20 nm SBEM data

Flood-Filling Networks



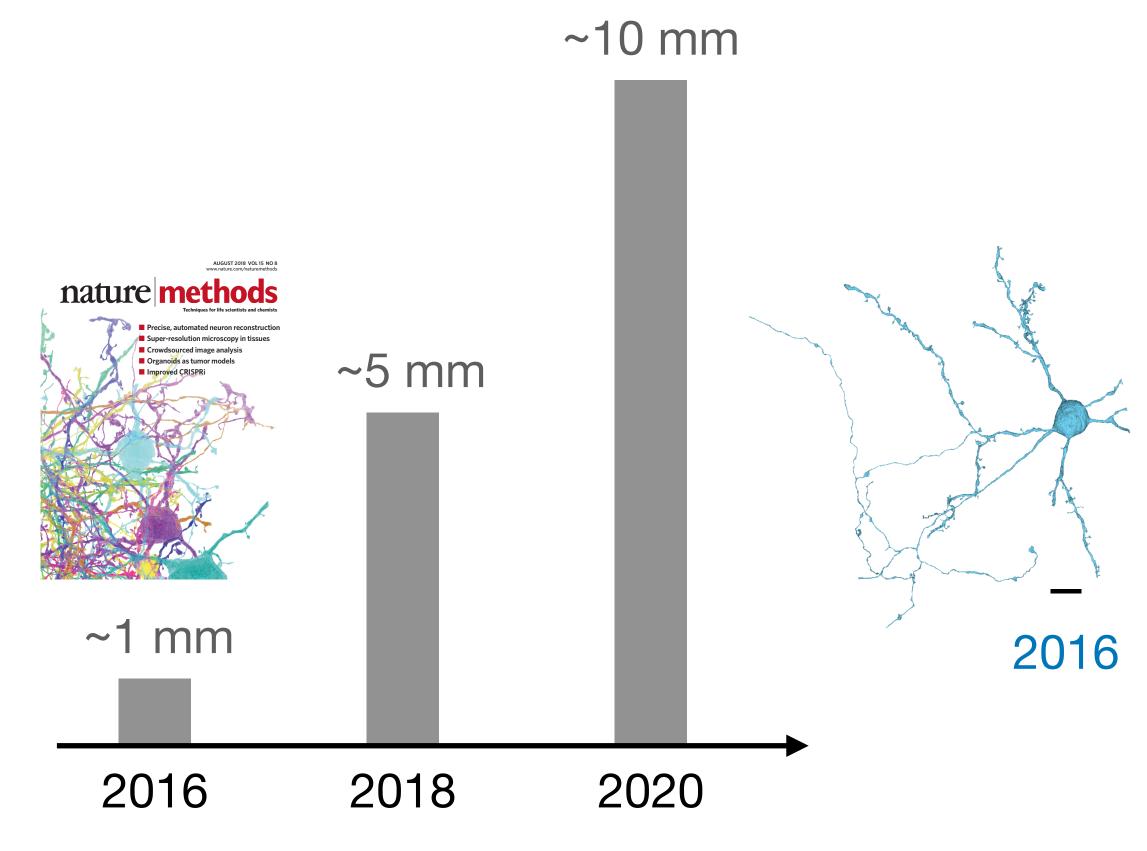




J0126: zebra finch Area X (Jörgen Kornfeld, Winfried Denk, MPI of Neurobiology) 9x9x20 nm SBEM data, ~[100 µm]^3

Reconstruction quality

Expected Run Length (ERL): how far can a system automatically trace from a randomly selected point before encountering a reconstruction error?



Nat Methods 15, 605–610 (2018) DOI: <u>10.1038/s41592-018-0049-4</u>



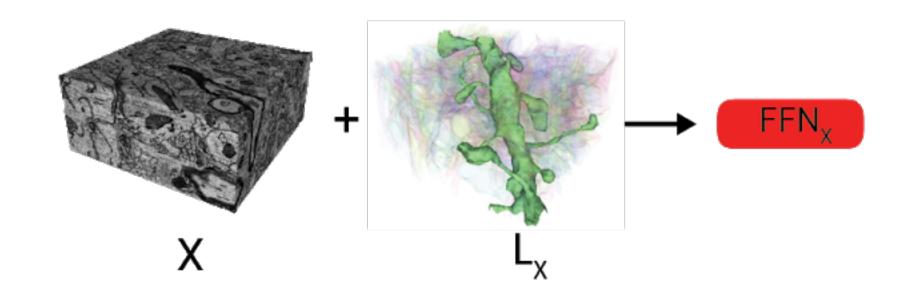




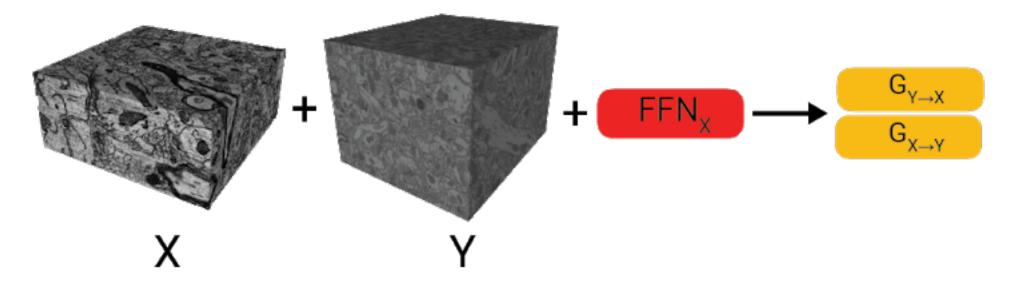
SECGAN: Segmentation-Enhanced CycleGAN

Train FFN on Volume X

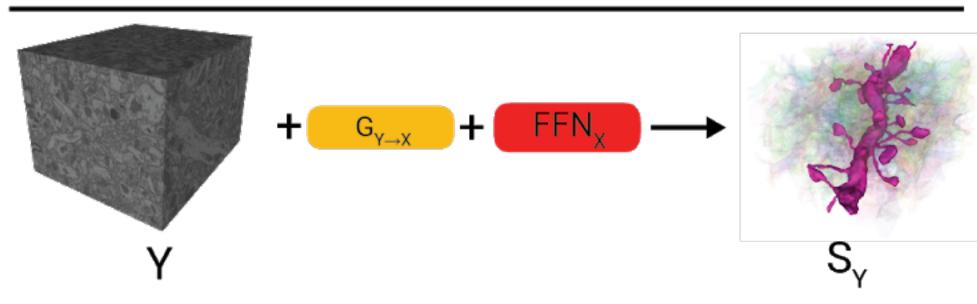
а



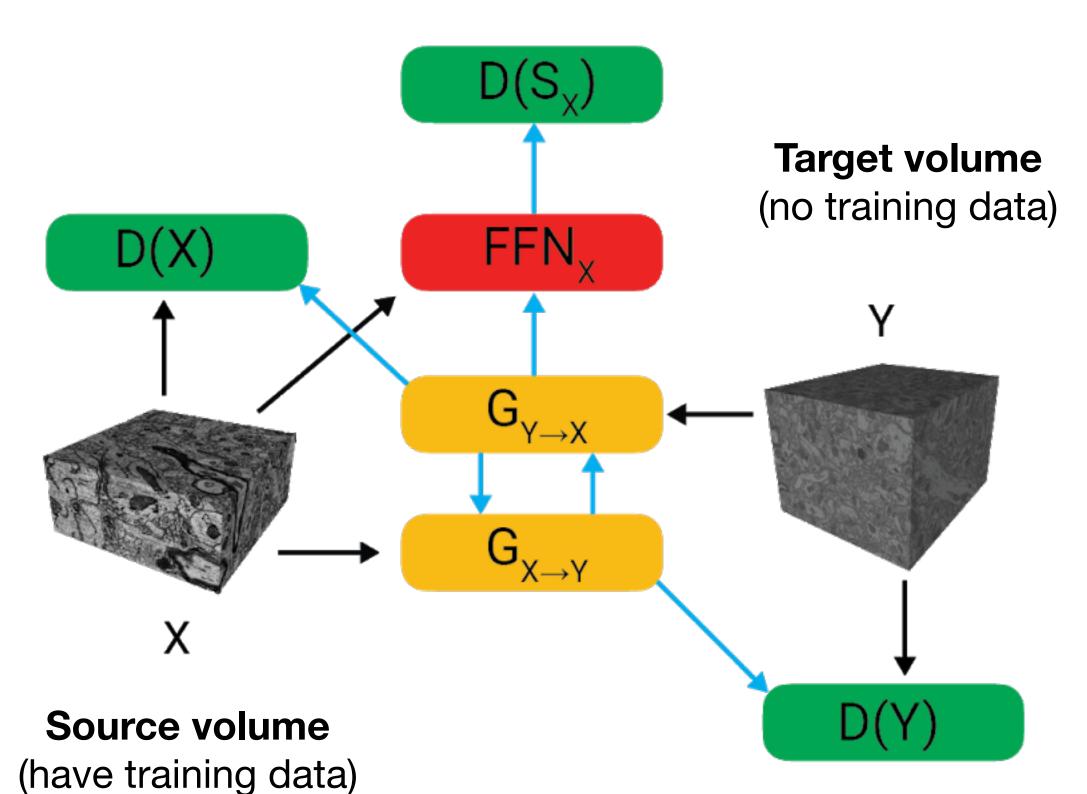
Train Segmentation-Enhanced CycleGAN



Inference on Volume Y



b

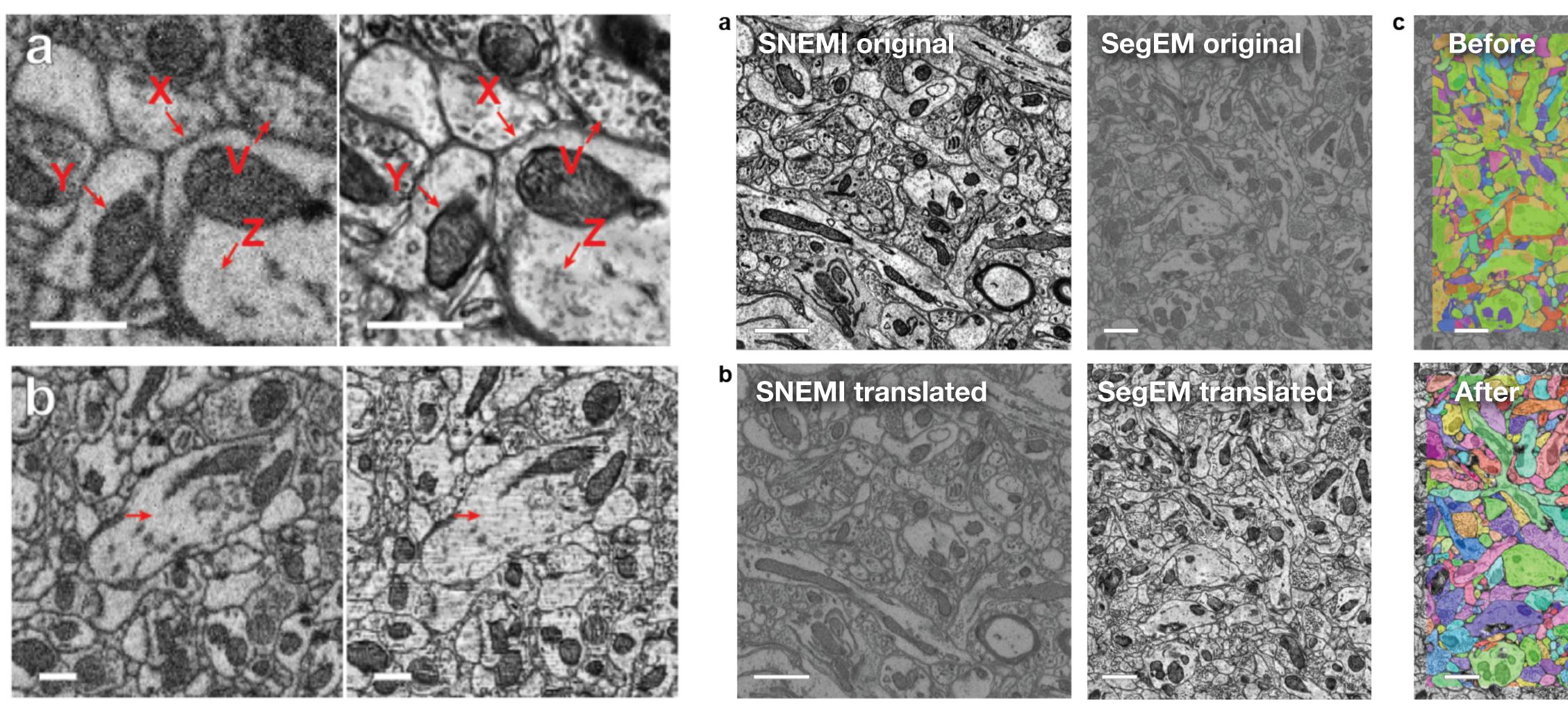


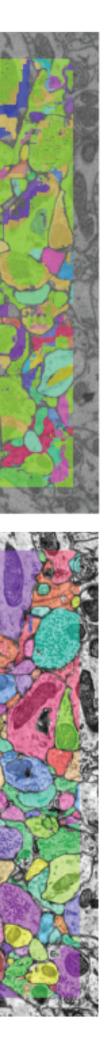
DOI: 10.1101/548081

Sample results

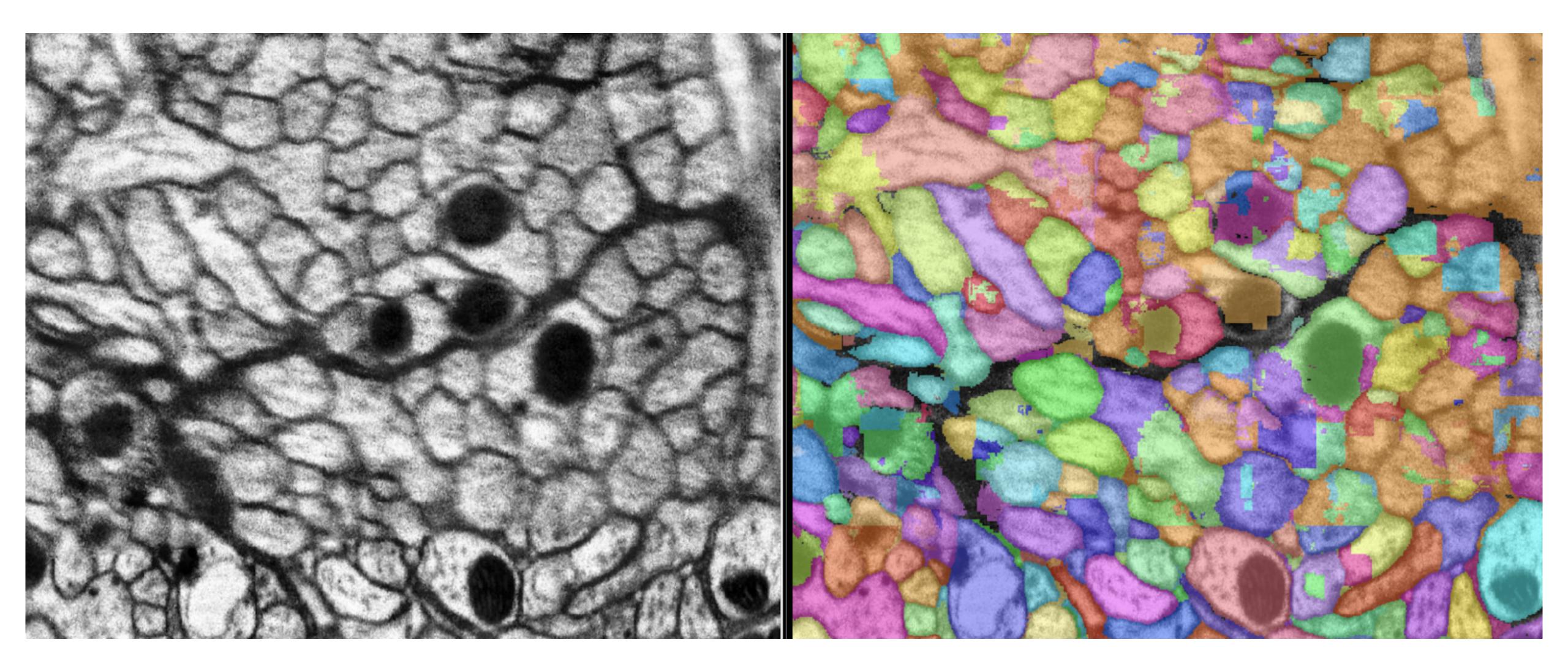
original

translated

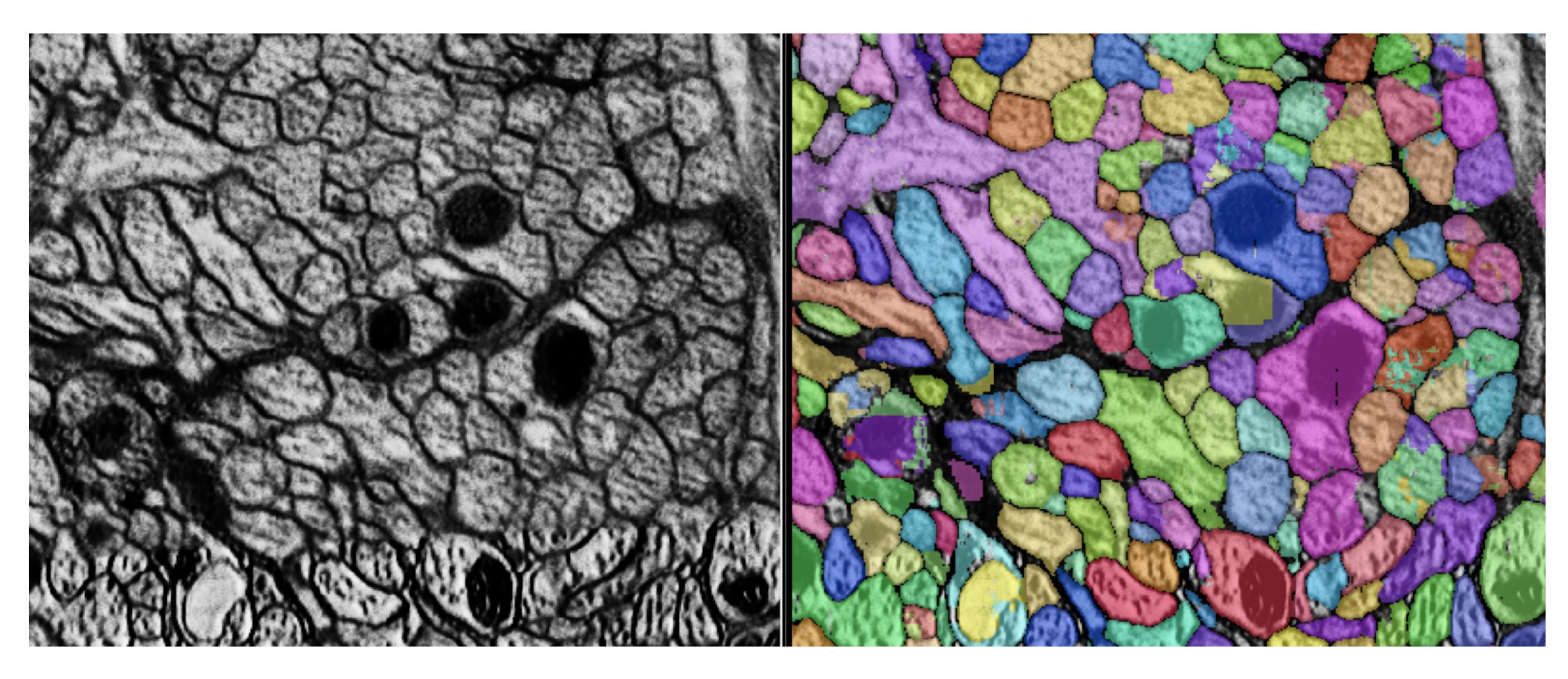




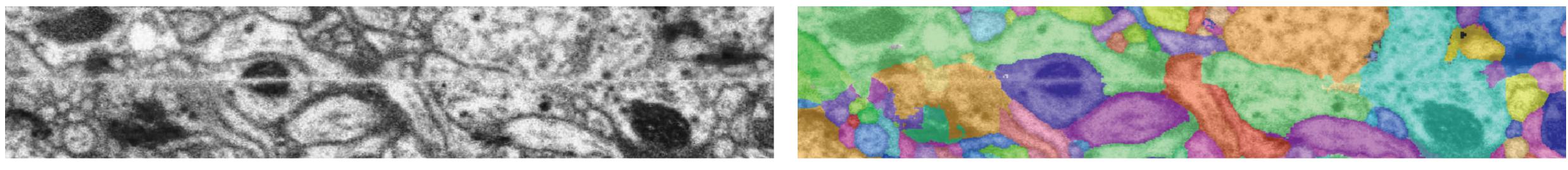
Applications: image correction

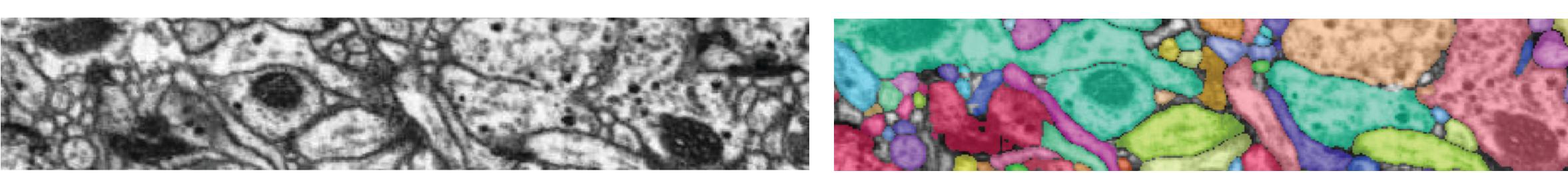


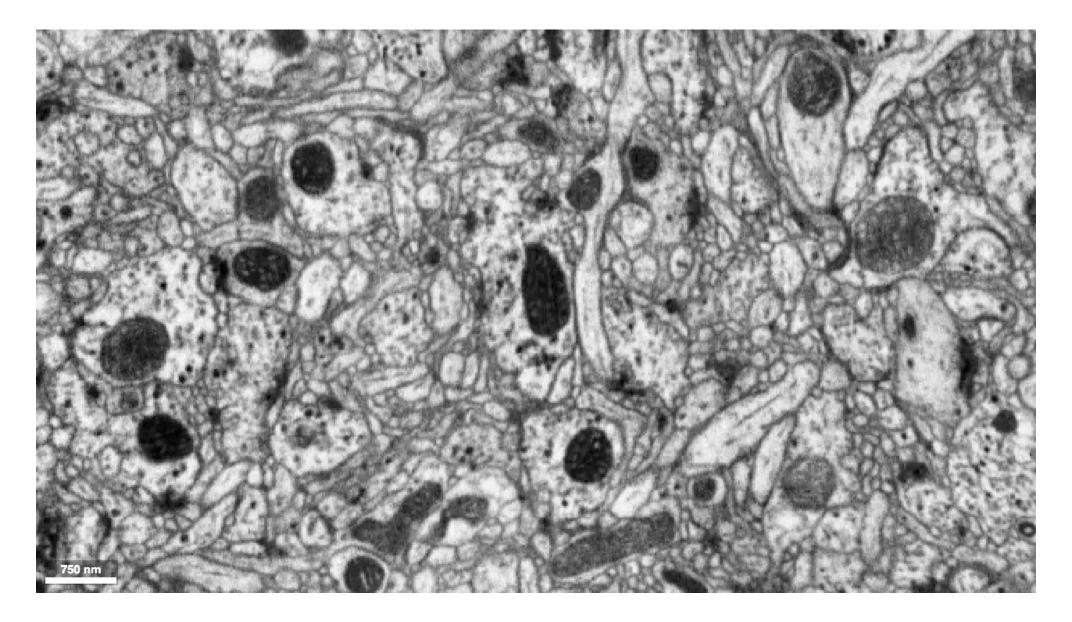
Applications: image correction

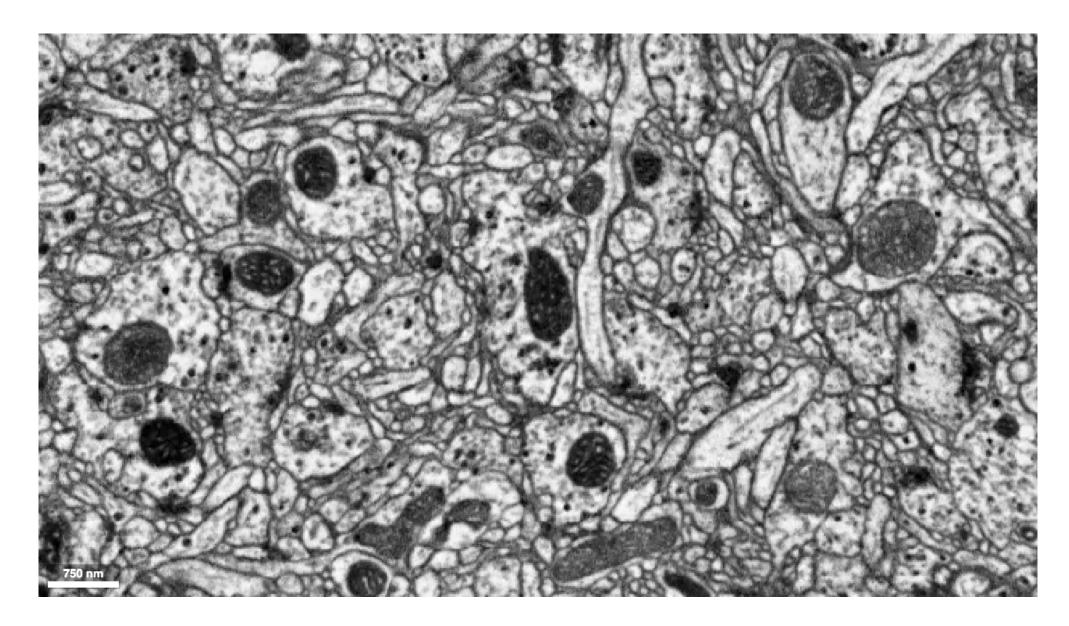


Applications: image restoration











Summary

- Connectomics demands extreme accuracy and scale. Customized ML approaches make this possible.
- Successful projects bring together lots of complementary expertise to a single collaboration.
- More about our work:

Open source code:



- https://research.google/teams/connectomics
- https://github.com/google/neuroglancer (WebGL-based N-d data browser)
- https://github.com/google-research/sofima (alignment & stitching of large volumes)
 - <u>https://github.com/google/tensorstore</u> (N-d data storage library)

mjanusz@google.com