

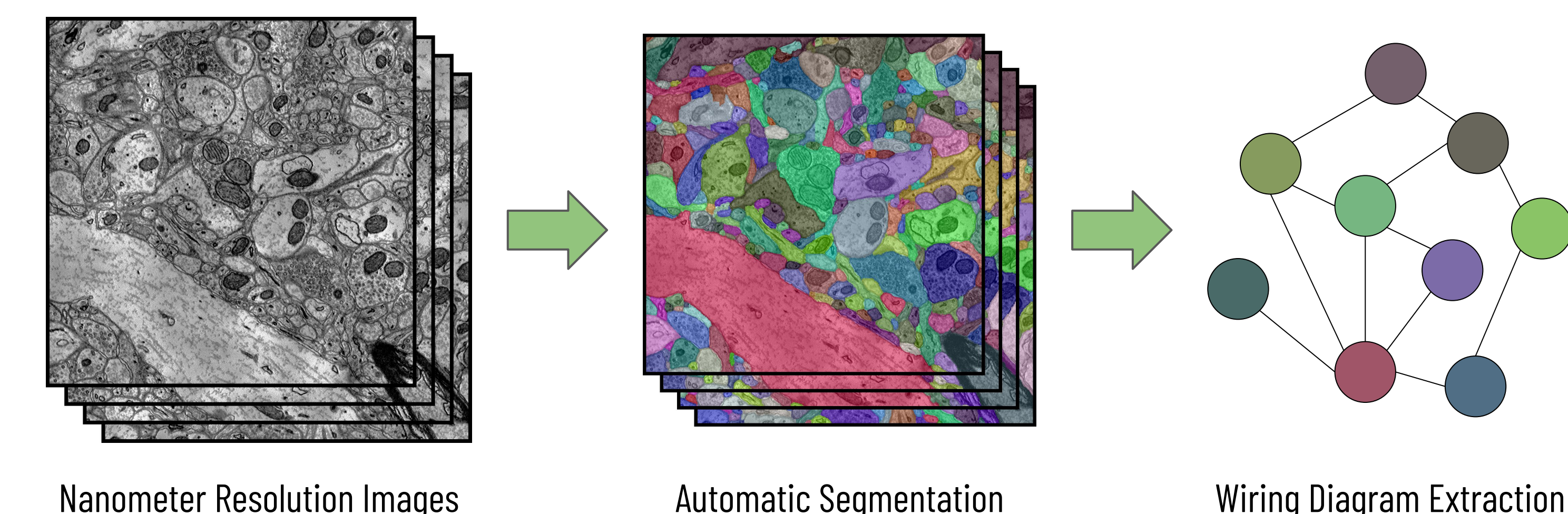
# Biologically-Constrained Graphs for Global Connectomics Reconstruction

Brian Matejek, Daniel Haehn, Haidong Zhu, Donglai Wei, Toufiq Parag, Hanspeter Pfister



Harvard John A. Paulson  
School of Engineering  
and Applied Sciences

The goal of connectomics is to extract the neural wiring diagram from high-resolution images of brain tissue.

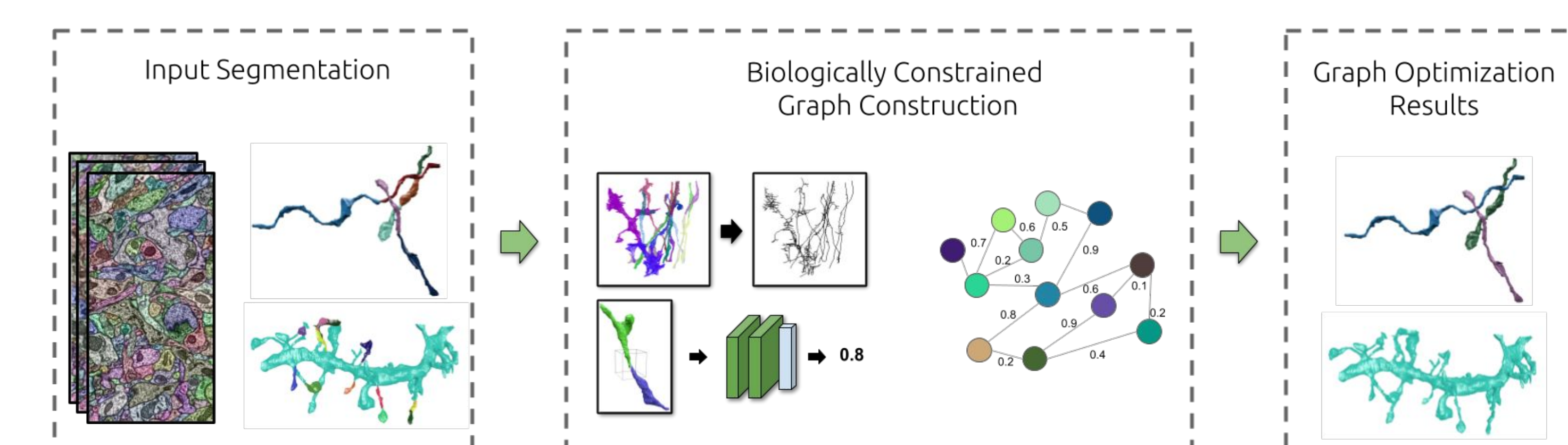


Current pipelines typically oversegment the image stack producing numerous *split errors*.

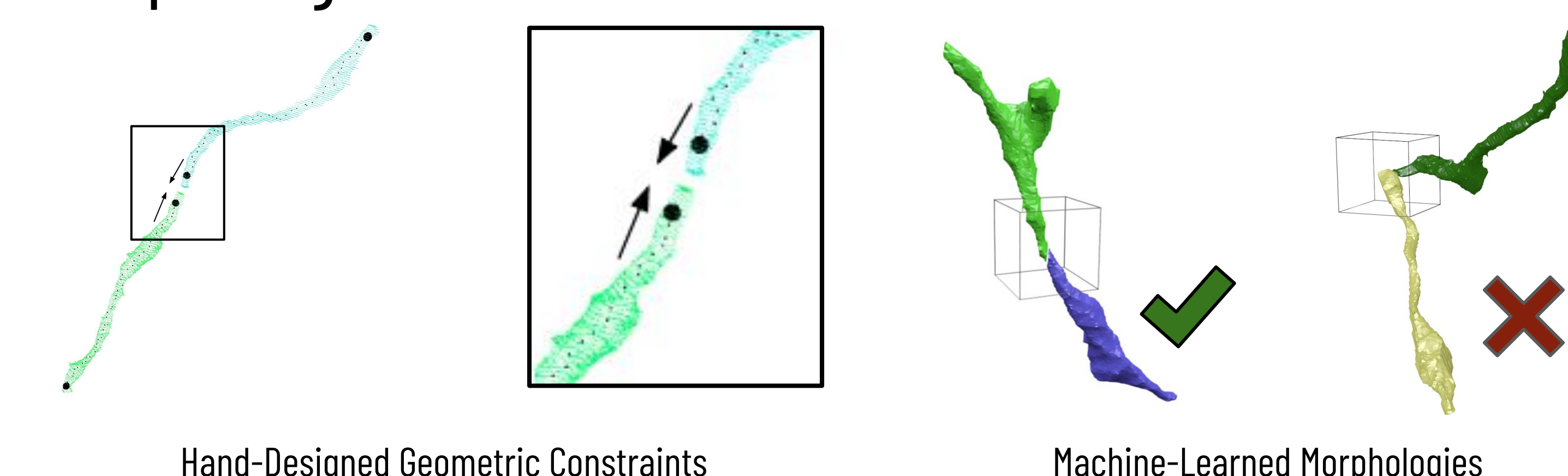


Three example neuronal processes that were each split into multiple segments.

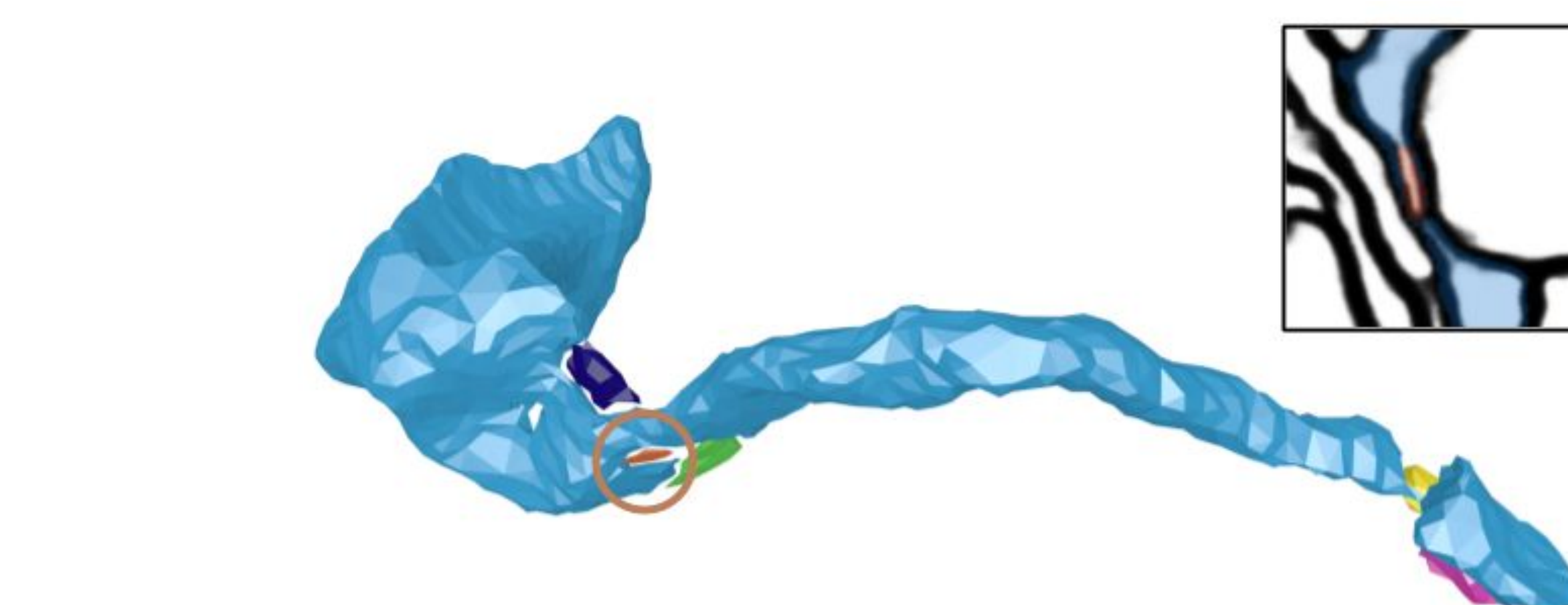
We refine these input segmentations and leverage global context by reformulating the error correction process as a graph partitioning one.



During graph construction, we employ hand-designed geometric constraints and machine-learned morphologies.

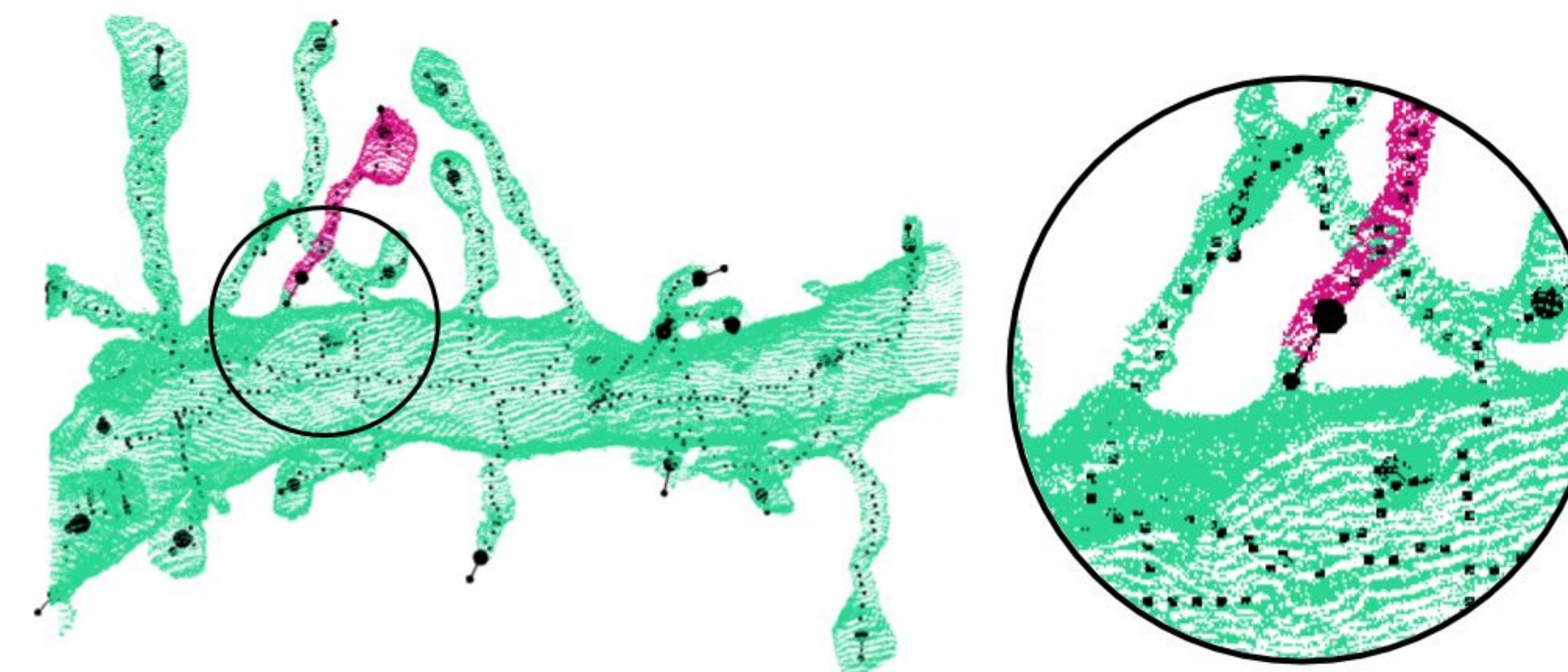


We greatly reduce the number of nodes by identifying biologically implausible segments and training a CNN to merge them with other nearby segments.



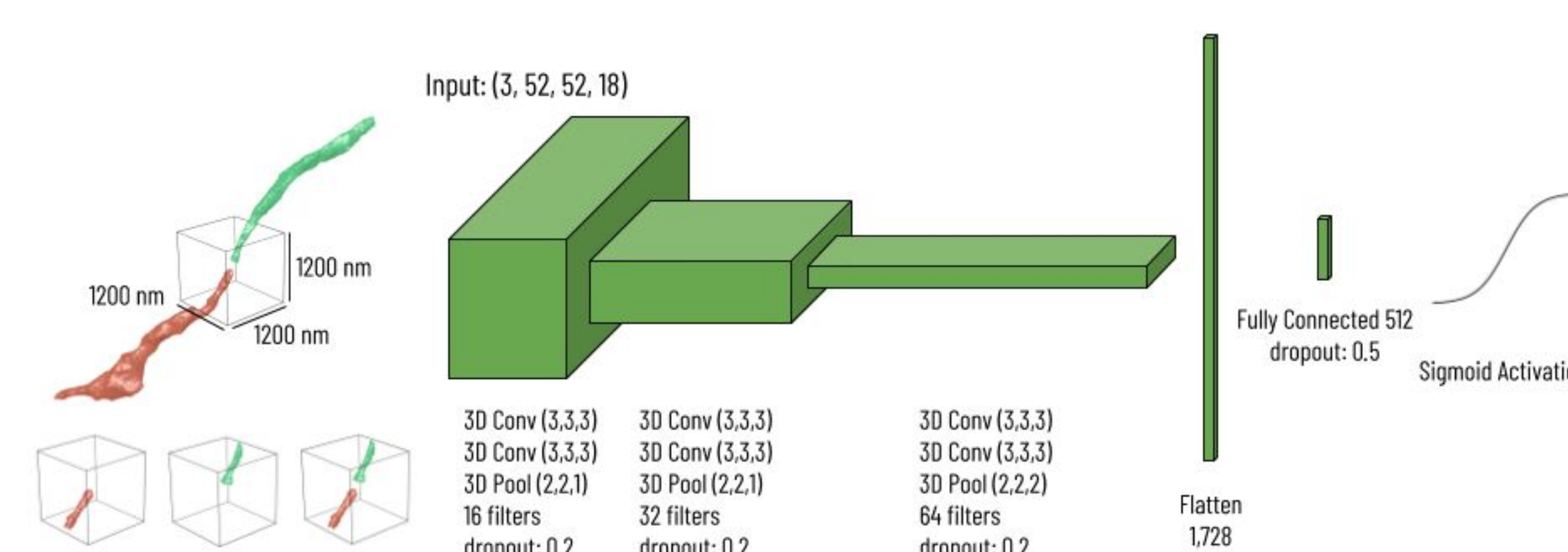
Restricting which segments have corresponding nodes reduces the running time of graph partitioning.

We generate skeletons of the remaining segments to identify potential split errors quickly; each split error corresponds to an edge in our graph.



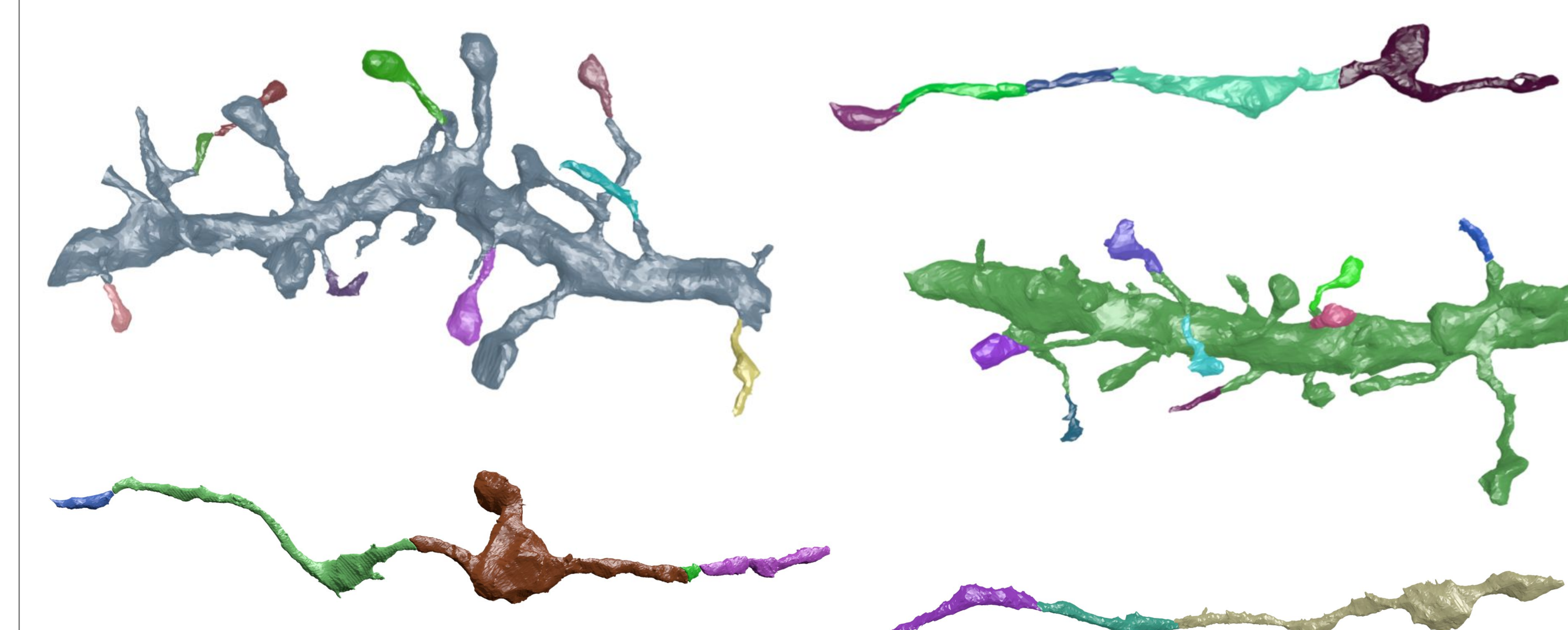
We only generate edges when a skeleton ends in the direction of another segment.

A 3D CNN examines the region around a potential split error to produce a probability that two segments belong to the same neuronal process.



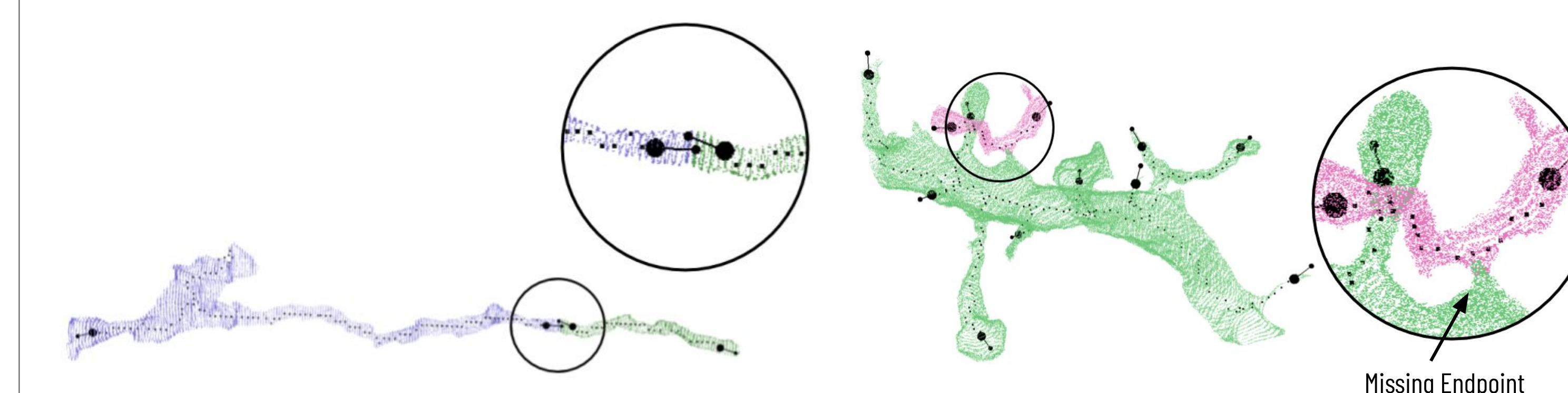
These probabilities correspond to edge weights for our graph, which we partition using a lifted multicut solver.

We evaluate our method on four testing datasets with two different state-of-the-art input segmentation methods and reduce the variation of information by 21.3% on average.



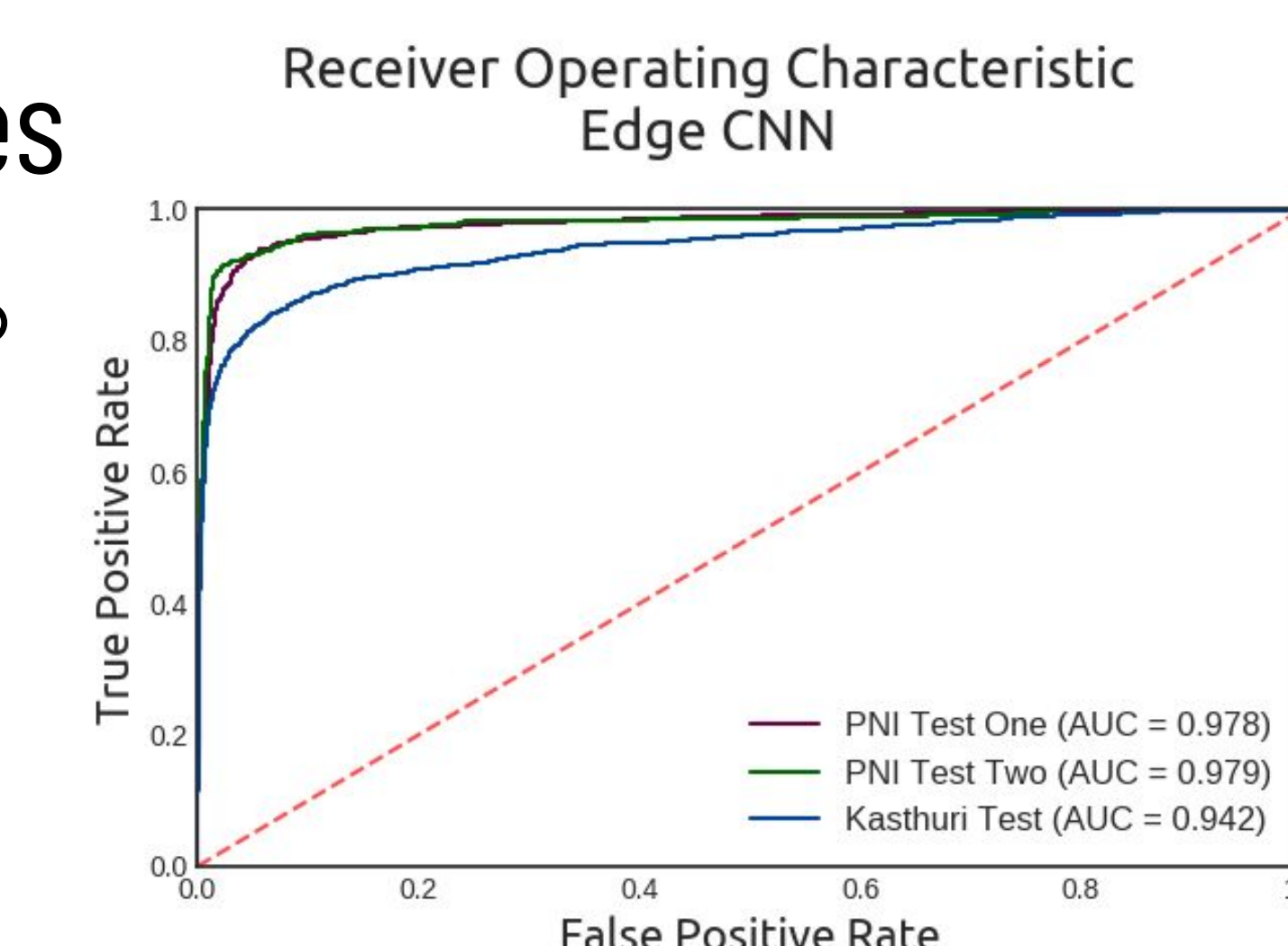
Five neuronal processes where we correct all split errors.

Our edge generation strategy recalls 80% of split errors while reducing the number of edges in an adjacency graph by over 60%.



Most split errors occur near a skeleton endpoint (left), although around 20% of split errors are missed (right).

Our CNN achieves accuracies of 96.4%, 97.2%, and 93.4% on three datasets when predicting if two segments belong to the same neuron.



Source code is available at  
<https://www.rhoana.org/biologicalgraphs>

This research was supported in part by NSF grants IIS-1447344, IIS-1607800, and IARPA contract DI6C00002.