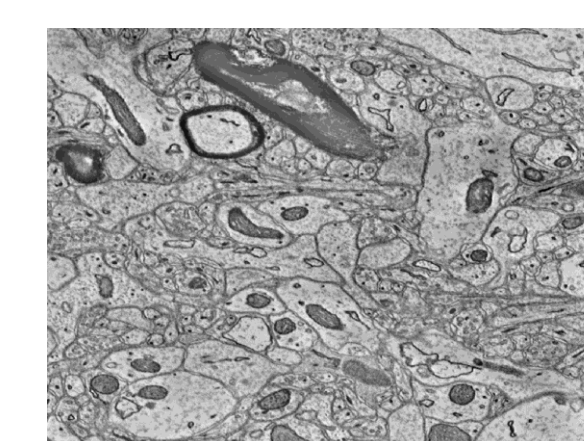


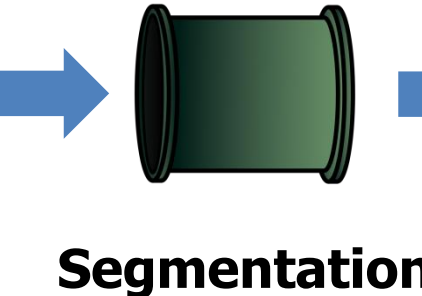
Overview

Computer vision research in the field of connectomics focuses on developing automated or semi-automated solutions to reconstruct a wiring diagram (i.e., brain graph). Most existing work has focused on segmentation, rather than constructing a graph for inference tasks. When considering this objective, one of the largest sources of error is dendritic shaft-spine fragmentation, which leads to significant connectivity errors.

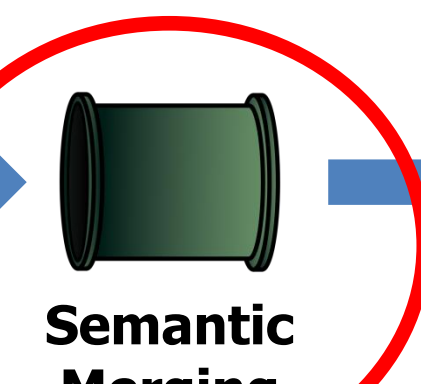
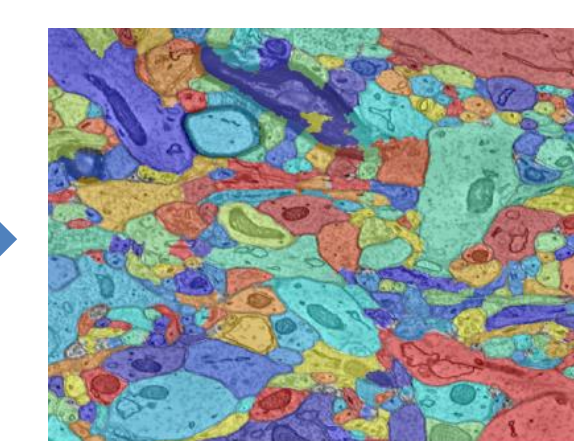
We present a fully automated method to more accurately recover the neuronal graph of the brain by improving these linkages, leveraging semantic information and computing graph-aware optimizations.



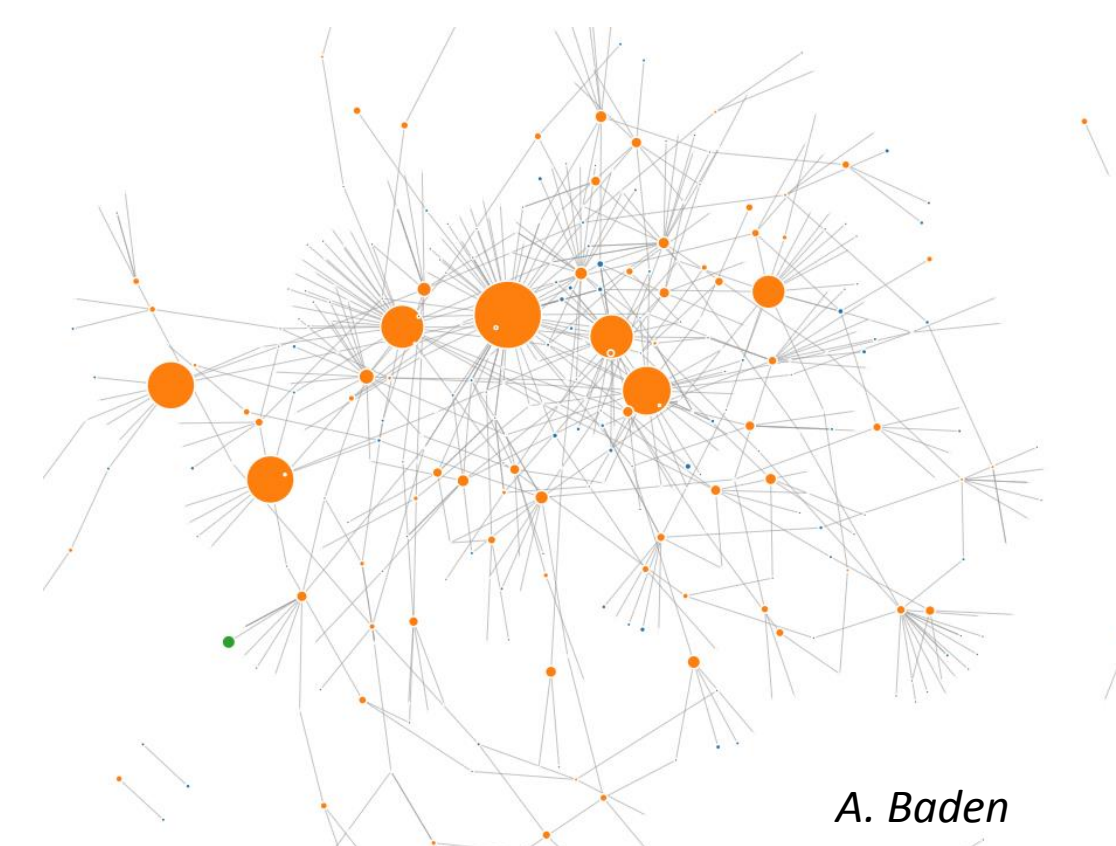
B. Kasthuri



Segmentation

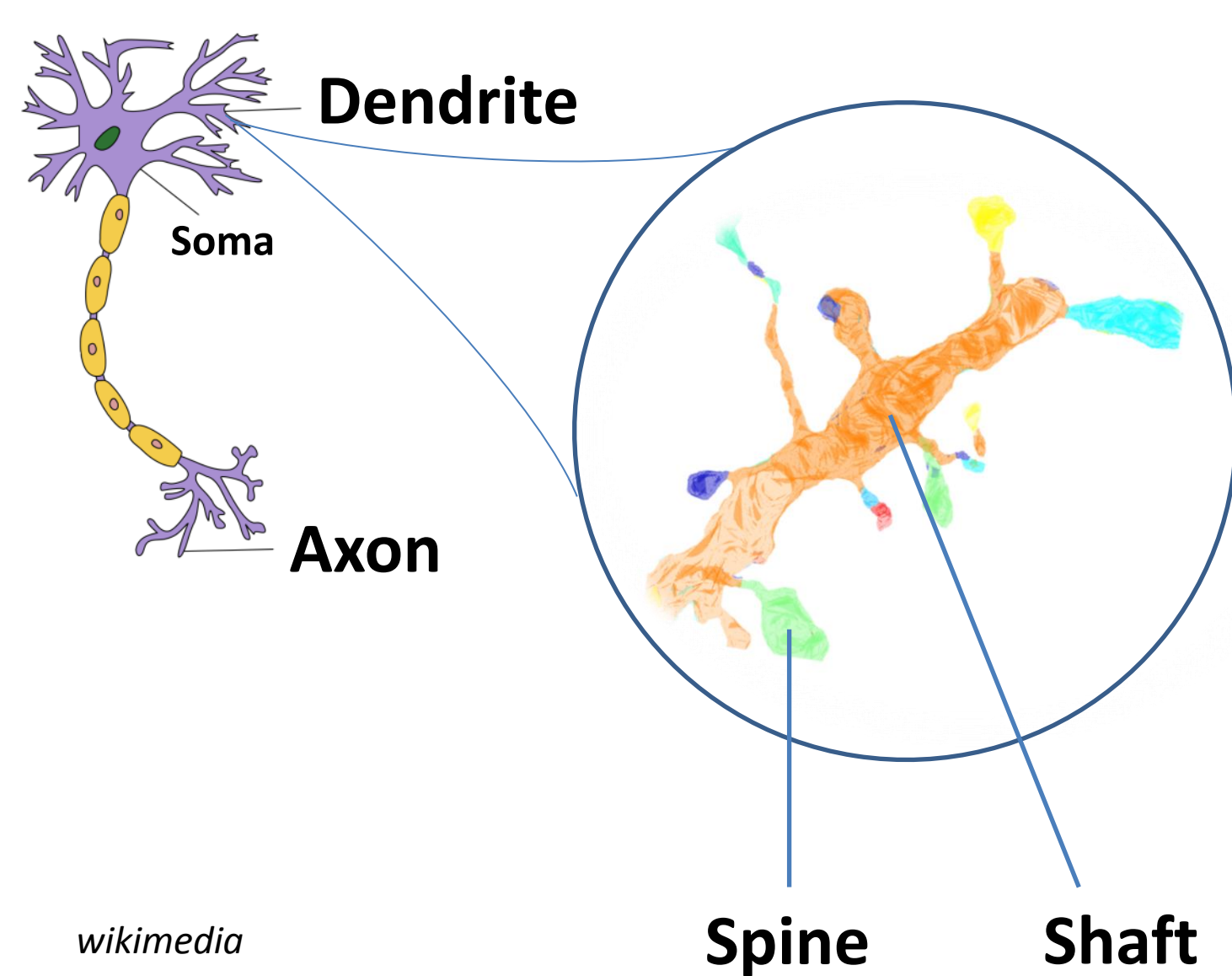


Semantic Merging

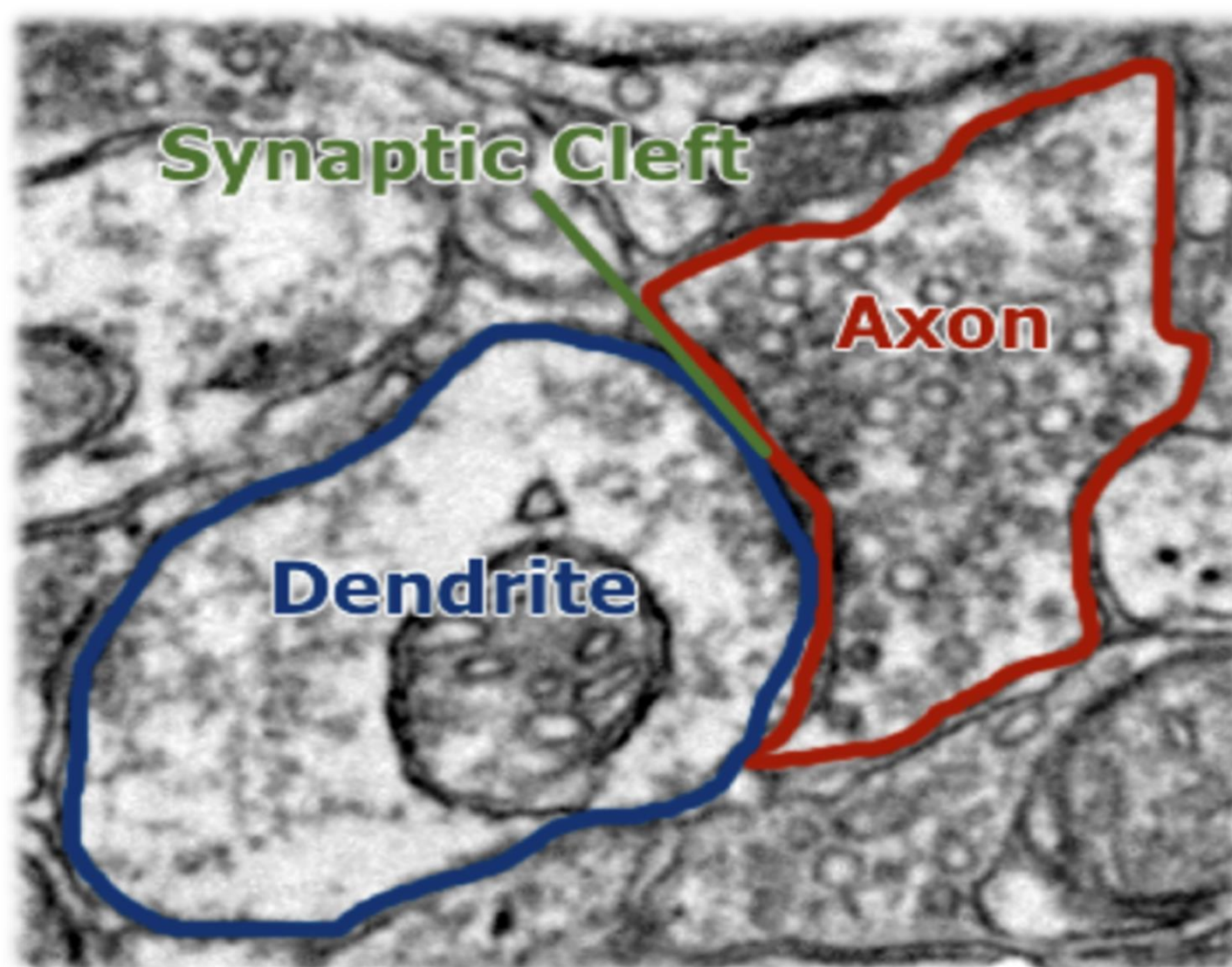


A. Baden

Neuroscience Primer



wikimedia

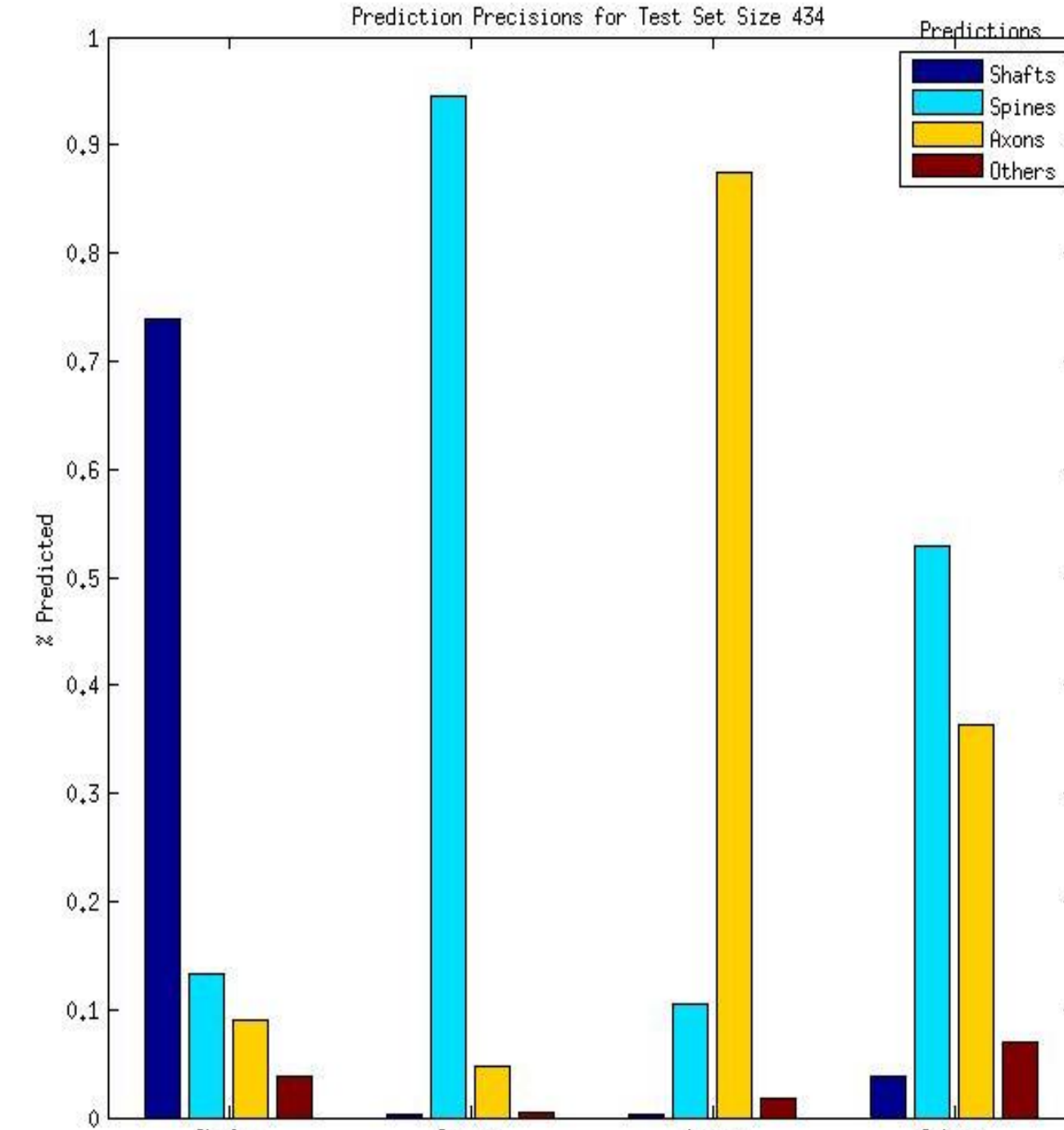
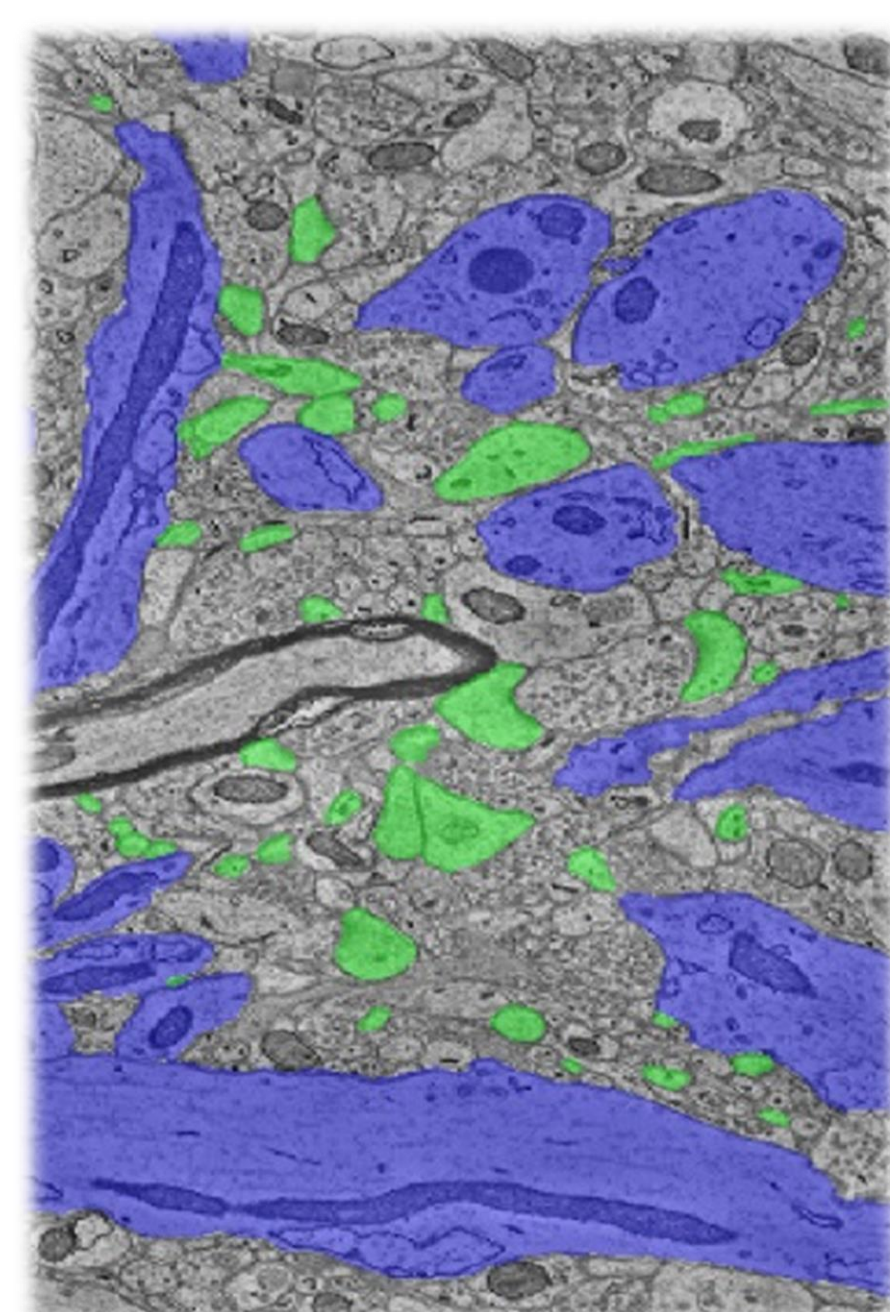


D. Bock

Merging Dendritic Spines to Shafts

Finding Spines & Shafts

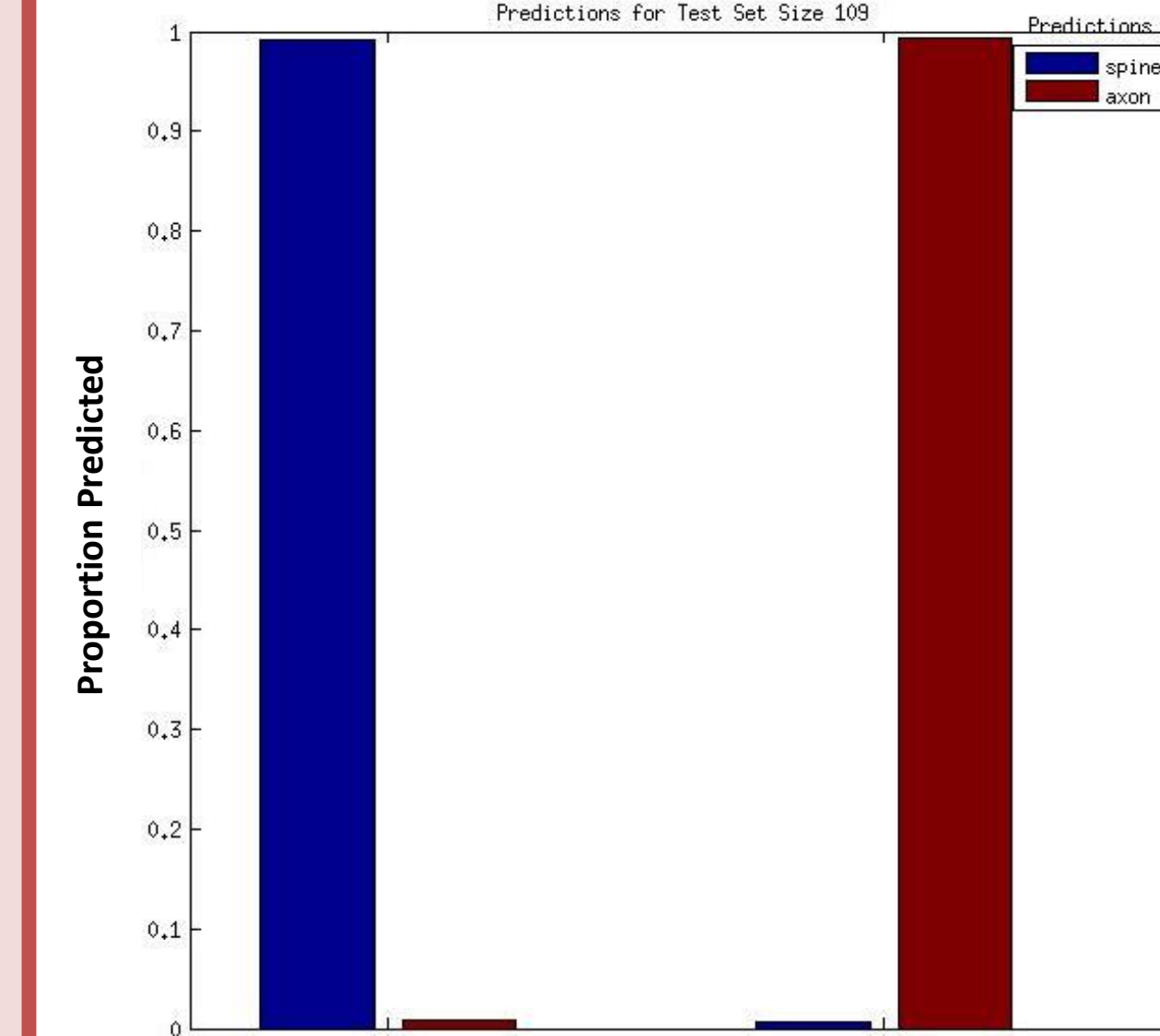
Semantic Classifier



Random Forest Features:

- Voxel intensity statistics
 - Histogram
 - Percentiles
 - Entropy
- D2 shape descriptor
- Segment size

Synapse Context



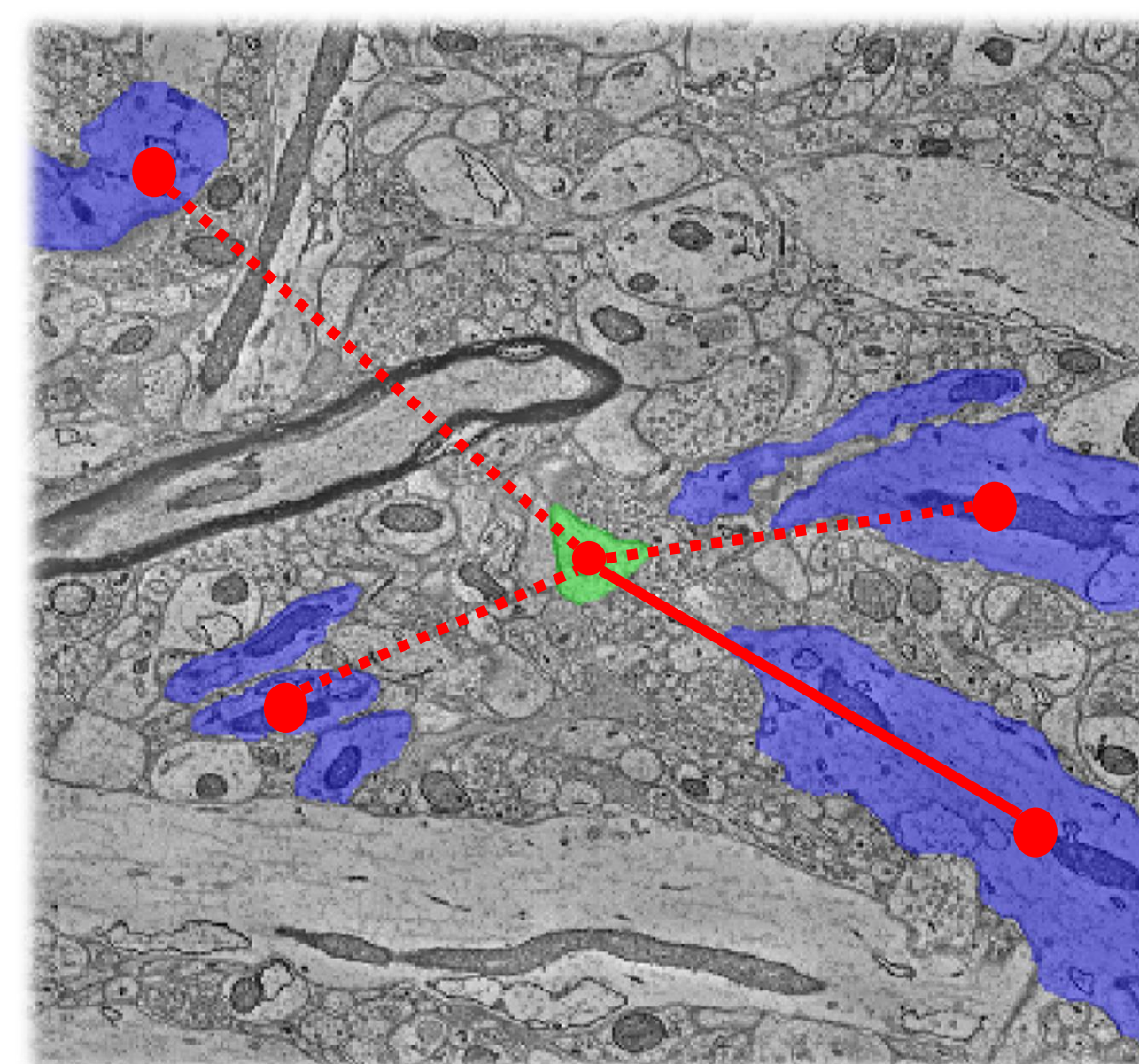
Axon-dendrite partnership prediction (cross-validated) : **99.26%**

Spine-Shaft Merge

For each orphan spine:

- Gather candidate shafts from within ~0.5 micron radius (biologically motivated)
- Calculate spine major axis vector using spine point furthest from its synapse
- Construct tree rooted at the spine spanning all candidate shafts
- Use random forest (RF) or conditional random field (CRF) to learn/predict matching parent shaft

Spine Neighborhood Tree



Features

Nodes:

- Semantic classifier votes
- Size

Edges (pairwise):

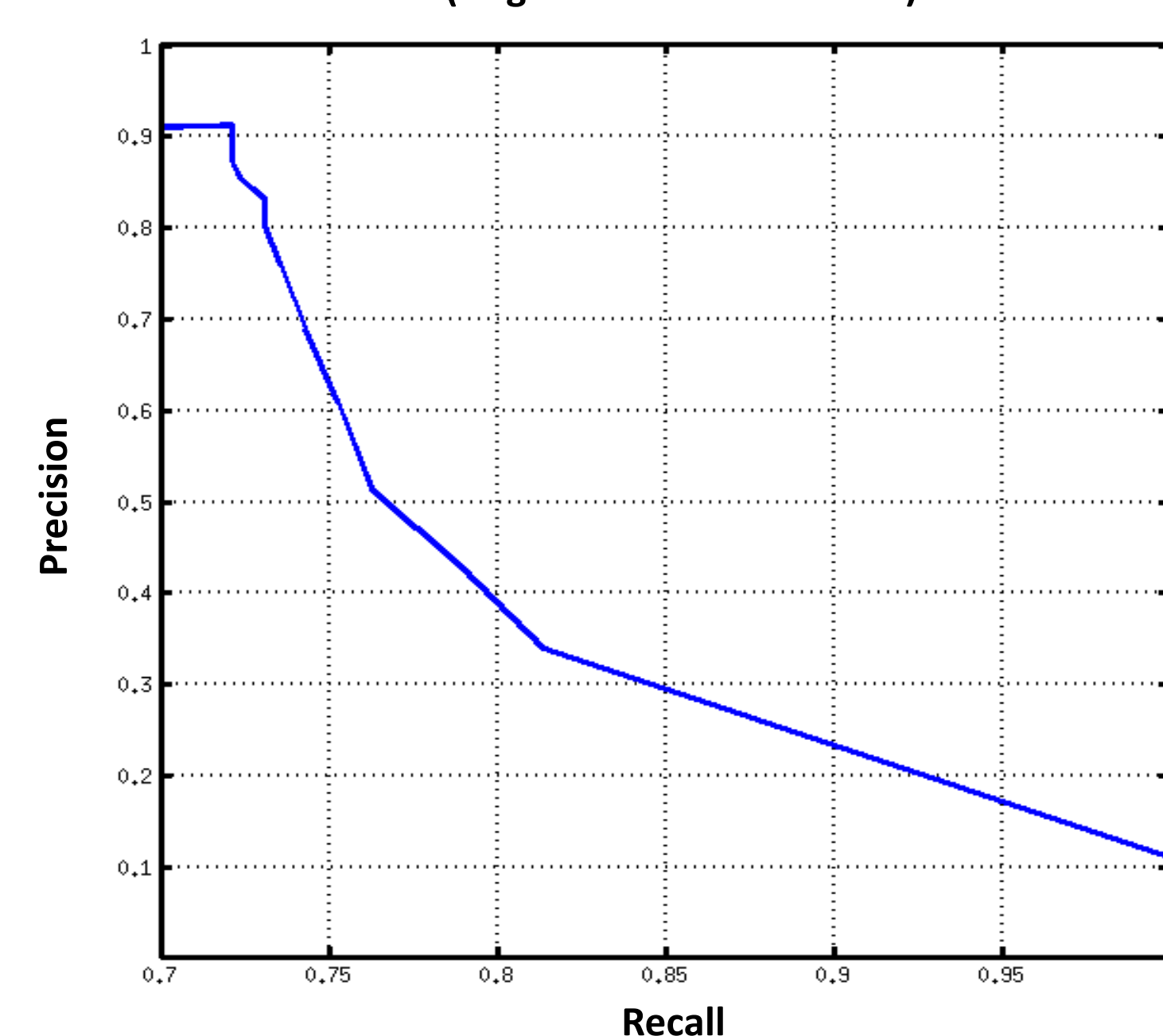
- Min distance between segments
- Alignment (using spine major axis vector)

Graph Assessment



A. Baden

Random Forest Parent Shaft Inference (fragmented manual truth)



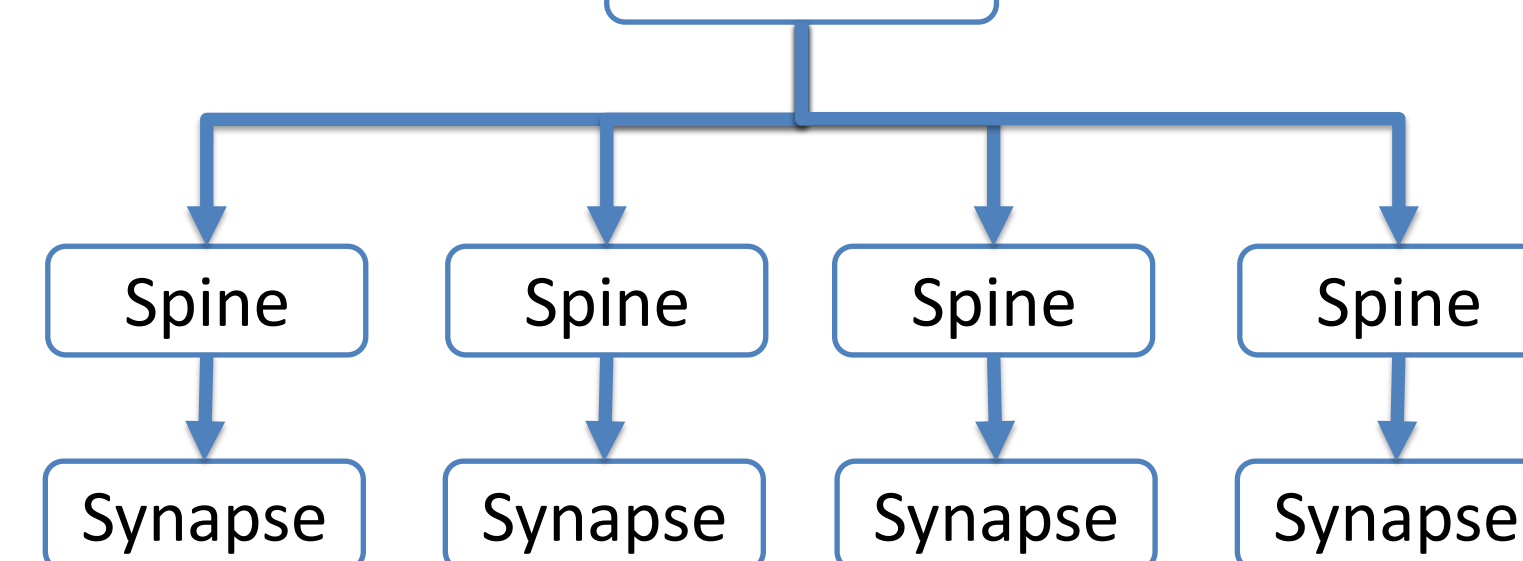
- Using only the few features listed, an operating point exceeding 0.9 precision, 0.7 recall was obtained
- Inclusion of additional pairwise features may result in a more comprehensive model
- CRF implementation can capture more structural context than baseline RF

Towards a Grammar Framework

- Brain tissue can be labeled with a small number of known nouns
 - soma, dendrite, spine, axon, bouton, synapse
- Known neuronal structure can be leveraged (e.g., terminal/non-terminal nodes, semantic links)
- Motifs and constraints exist at multiple scales



Dendrite



Future Work

- Continue graphical model (i.e. CRF) development to consider additional constraints and structural information
- Apply framework to computer vision generated segments
- Assess results using additional error metrics

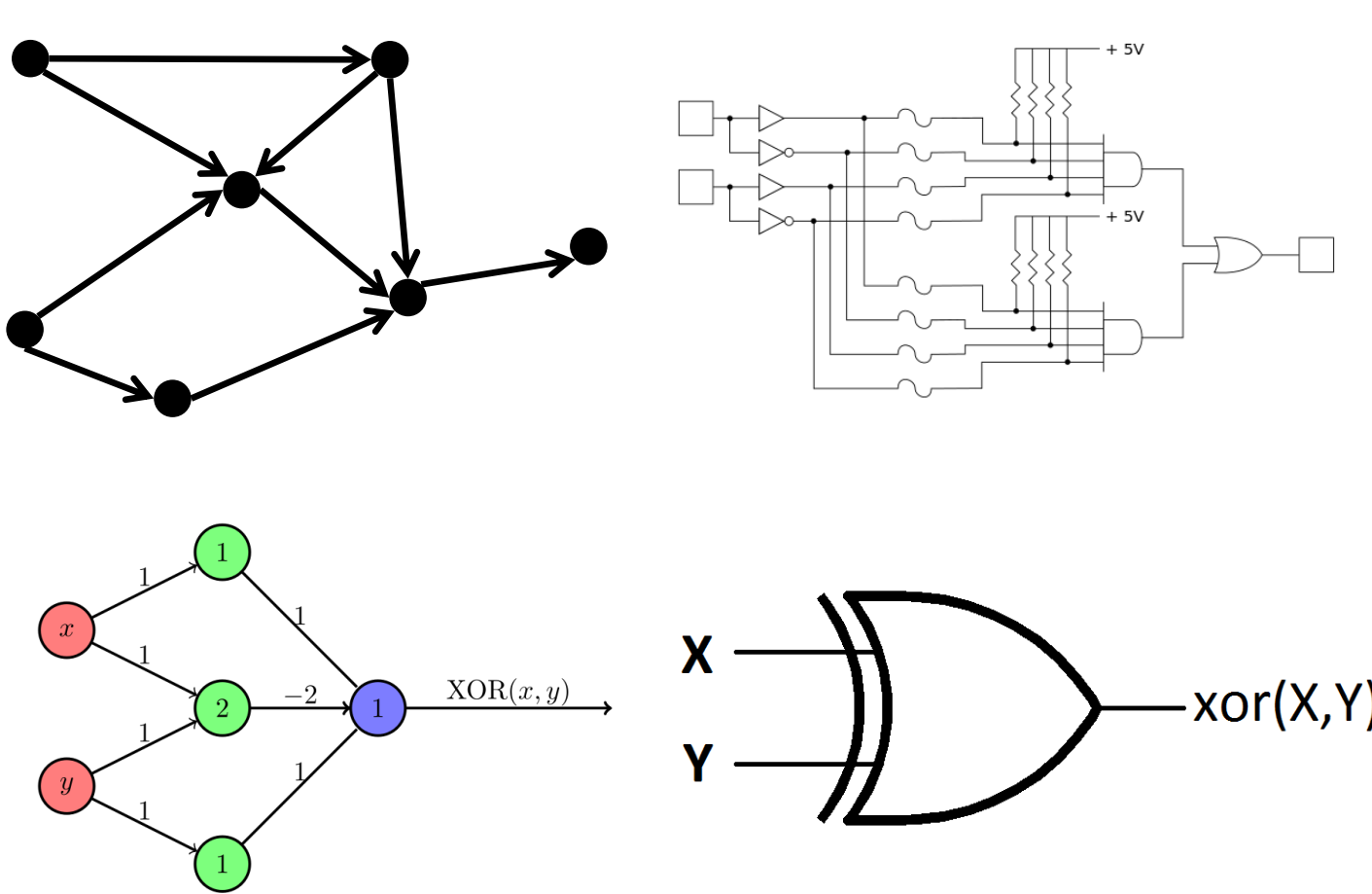
Acknowledgements

- ✓ Alex Baden
- ✓ Bobby Kasthuri
- ✓ Dean Kleissas
- ✓ Colin Lea
- ✓ Marysol Encarnación
- ✓ OpenConnectome Project Team

References

- [1] D. D. Bock, W.-C. A. Lee, A. M. Kerlin, M. L. Andermann, G. Hood, A. W. Wetzel, S. Yurgenson, E. R. Soucy, H. S. Kim & R. C. Reid, "Network anatomy and in vivo physiology of visual cortical neurons," *Nature*, 2011.
- [2] A. Vazquez-Reina, M. Gelbart, D. Huang, J. Lichtman, E. Miller, H. Pfister, "Segmentation Fusion for Connectomics," *IEEE ICCV* 2011.
- [3] C. Sommer, C. Straehle, U. Köthe, F. A. Hamprecht, "Ilastik: Interactive Learning and Segmentation Toolkit," *8th IEEE International Symposium on Biomedical Imaging*, 2011.
- [4] V. Jain, S. Turaga, K. Briggman, M. Helmstaedter, W. Denk, H. S. Seung, "Learning to Agglomerate Superpixel Hierarchies," *NIPS* 2011.
- [5] A. Lucchi, K. Smith, R. Achanta, G. Knott, P. Fua, "Supervoxel-based segmentation of mitochondria in EM image stacks with learned shape features," *IEEE transactions on medical imaging*, Feb. 2012.
- [6] W.-K. Jeong, J. Beyer, M. Hadwiger, R. Blue, C. Law, A. Vazquez-Reina, C. Reid, J. Lichtman, H. Pfister, "SSECRIT and NeuroTrace: Interactive Visualization and Analysis Tools for Large-Scale Neuroscience Datasets," *IEEE Computer Graphics & Applications*, '11.
- [7] D. Kleinfeld, A. Bharioke, P. Blinder, D. D. Bock, K. L. Briggman, D. B. Chklovskii, W. Denk, M. Helmstaedter, J. P. Kaufhold, W.-C. A. Lee, H. S. Meyer, K. D. Micheva, M. Oberlaender, S. Prohaska, R. C. Reid, S. J. Smith, S. Takemura, P. S. Tsai, and B. Sakmann, "Large-Scale Automated Histology in the Pursuit of Connectomes," *Journal of Neuroscience*, vol. 31, no. 45, pp. 16125-16138, Nov. 2011.
- [8] W. R. Gray, J. A. Bogovic, J. T. Vogelstein, B. A. Landman, J. L. Prince, R. J. Vogelstein, "Magnetic Resonance Connectome Automated Pipeline," *IEEE Pulse EMBS*, 2012.
- [9] I. Dinov, J. D. Van Horn, K. M. Loeve, R. Magsipoc, P. Petrosyan, Z. Liu, A. Mackenzie-Graham, P. Eggert, D. S. Parker, and A. W. Toga, "Efficient, Distributed and Interactive Neuroimaging Data Analysis using the LONI Pipeline," *Frontiers in Neuroinformatics*, 2009.
- [10] J. G. White, E. Southgate, J. N. Thomson, S. Brenner, "The Structure of the Nervous System of the Nematode *Caenorhabditis Elegans*," *Phil. Trans. Royal Soc. London*, 1986.
- [11] N. Kasthuri, K. Hayworth, J. C. Tapia, R. Schalek, S. Nundy, J. W. Lichtman, "The brain on tape: Imaging an Ultra-Thin Section Library (UTSL)," *Society for Neuroscience Abstracts*, 2009.
- [12] S. Saalfeld, A. Cardona, V. Hartenstein, P. Tomančák, "CATMAID: collaborative annotation toolkit for massive amounts of image data," *Bioinformatics*, 2009.
- [13] R. Burns, et al., "The Open Connectome Project Data Cluster: Scalable Analysis and Vision for High-Throughput Neuroscience," *SSDBM*, 2013. Accepted.

Motivation



- Structural motifs can explain neural functionality (form following function)
- Supplement analyses of neurological illnesses/impairments
- Provide an architecture to inform brain-computer interface techniques
- Repeated structures may be synthesizable for novel artificial intelligence applications



openconnectome.me