Deep Learning for the Connectome

Seymour Knowles-Barley1,2, Thouis R. Jones1,2, Josh Morgan2, Dongil Lee2, Narayanan Kasthuri2, Jeff W. Lichtman2 and Hanspeter Pfister1.

1Harvard University, School of Engineering and Applied Sciences, USA. 2Harvard University, Department of Molecular and Cellular Biology, USA.

Introduction

The connectome is the wiring diagram of the nervous system. Mapping this network 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.

In our experiments, brain tissue is microtomed and imaged with an electron microscope at a resolution of 4x4x30nm per voxel. Cell membranes and sub-cellular structures such as mitochondria, synapses and vesicles are clearly visible in the images.

We have developed a fully automatic segmentation pipelines [2] to annotate this data. The requirement of a very high level of accuracy and data rates approaching 1TB a day make this a challenging computer vision task.

Deep Learning

The first and most critical stage of the our segmentation pipeline (www.rhoana.org) is to identify membrane in the 2D images produced by the microscope. We use convolutional neural networks to classify images, trained on a few hand-annotated images. GPU computing greatly reduces the training and classification time for these computationally demanding networks. In this work, we used pylearn2 [5] to apply maxout networks [6] to two connectome data sets.

Results and Performance

Image classification and Rhoana segmentation results are shown in Figure 2. Pixel-wise error rates of 4.27% for 2-class LGN and 4.85% for 3-class ECS were achieved during deep network training on down-sampled, 8nm per pixel input.

Deep network classification is a computationally demanding task requiring millions of floating point operations per pixel output. We benchmark Tesla C2070, Quadro K5000 and Tesla K40c GPU performance and estimate the number of GPUs required to classify images as they are captured by a scanning electron microscope (approximately 0.85TB per day).

Acknowledgements

Thanks to Linda Xu, and students from Masconomet Regional High School for their careful and diligent annotations and to Daniel Berger for 3D rendering.

References