CS 291K - Circuit Reconstruction from EM images

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1 Introduction

Automatic reconstruction of neurons and neuronal connectivity is a central problem in neuroanatomy. This is necessary to efficiently map 3D brain structure and connectivity. We address the problem of 2D segmentation of ssTEM image stacks which is often the first step in the pipeline. To segment biological neuron membranes, we use artificial neural network as a pixel classifier. A Convolutional Neural Network takes raw pixel values in a square window centered around each pixel as input and outputs the probability of that pixel being a non-membrane. The label of each pixel (membrane or non- membrane) is predicted by postprocessing the output of our Convolutional Neural Network.

2 Motivation - How is the brain structured?

Connectomics aims to efficiently map the 3D structure and connectivity in an organism's nervous system. With improvements in imaging systems, a lot of data has been collected, enabling the study of structure and connections. Serial Section Transmission Electron Microscopy has been very successful.

However, analysing the structure and connections from these images is a laborious task requiring expertise in neuroanatomy. Consequently, there has been a lot of interest in automating such analysis. A successful solution would carry great potential to reduce the time spent on manual reconstruction of neuronal circuits in electron microscopy volumes.

There are three major challenges in this problem:

- Segmentation: Assessment of neuron labelings in terms of pixel-based measures
- Synapse detection: Detection of synapses
- Connectivity: Identification of synaptic partners

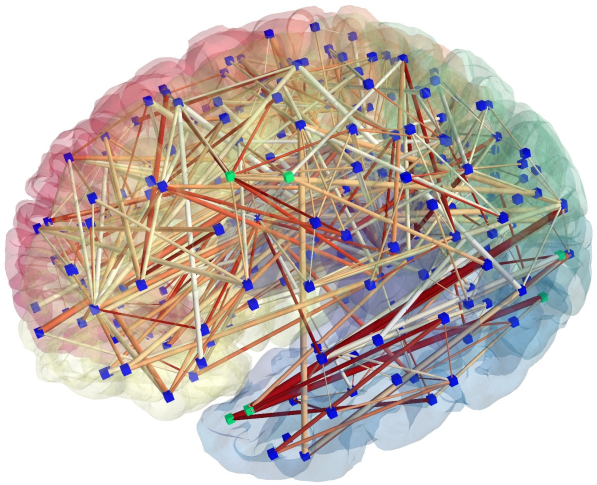
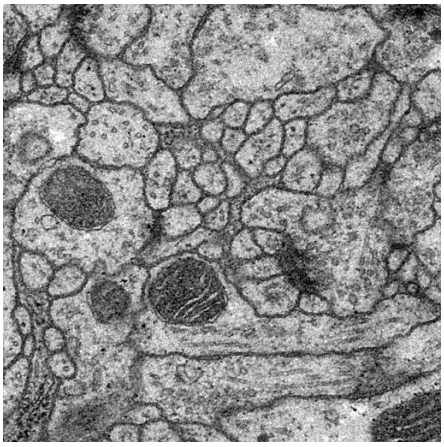
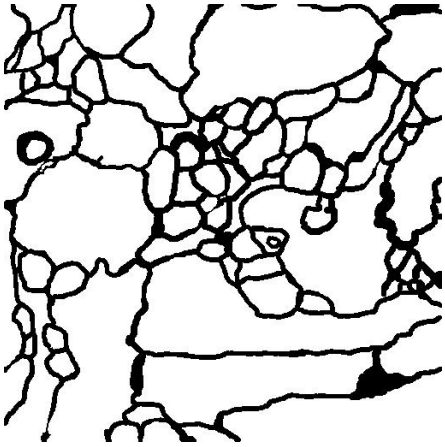


Figure 1: Connectomics

These three are ongoing challenges at the upcoming MICCAI 2016. Our focus for this project has been on 2D segmentation. As 2D segmentation is used as an input for 3D segmentation and reconstruction pipelines, it is an interesting first problem in this domain.



(a) A training image



(b) Corresponding label

Figure 2: Dataset

3 Data Set

Open source datasets are available as part of challenges hosted by ISBI 2012 [3] and MICCAI 2016 [4]. These are from adult Drosophila melanogaster brain tissue, comprising neuron segmentation ground truth and annotations for synaptic connections. The images are representative of actual images in the real-world, containing some noise and small image alignment errors.

For this project, we have used the 2D EM Segmentation Challenge dataset from ISBI 2012. These images are sections from a serial section Transmission Electron Microscopy (ssTEM) data set of the Drosophila first instar larva ventral nerve cord (VNC).The microcube measures 2 x 2 x 1.5 microns approx., with a resolution of 4x4x50 nm/pixel.

The training data comprises of 30 512x512 tif images and binary ground truth labels. The testing data comprises of another 30 512x512 tif images, the ground truth for which is not published.

4 Method

To segment biological neuron membranes, we use artificial neural network as a pixel classifier. Each pixel is classified as membrane or non-membrane. Context is provided by considering a 65x65 window around each pixel.

We used a Convolutional Neural Network that has a series of convolutional layers followed by maxpooling layers. The network is deep enough to learn the deep features required for this task.

In the next section, we detail the architecture of our ConvNet.

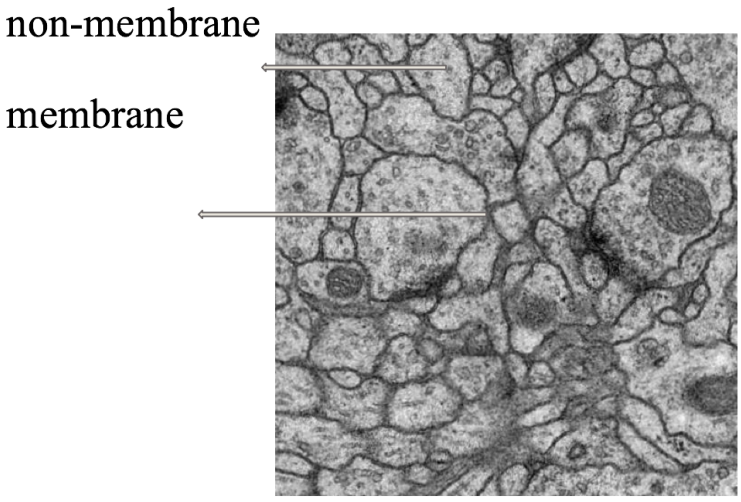


Figure 3: Membrane - Non membrane classification

A DNN architecture

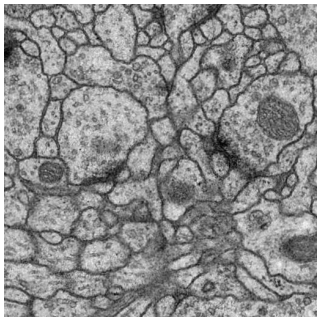
The following table shows the different layers in our ConvNet [1]. The input to the ConvNet is a 65x65 window of pixel intensity values. This is followed by a series of convolutional and maxpooling layers that intoduce increasing levels of abstraction. Towards the end, we have fully connected layers. The ConvNet output is a Softmax layer that gives us the probability of each class (membrane/ non-membrane).

Layer	Type	Maps and neurons	Kernel size
0	Input	65 x 65 x 1	
Layer 1	Convolutional	62 x 62 x 48	4 x 4
Layer 2	Max Pooling	31 x 31 x 48	2 x 2
Layer 3	Convolutional	28 x 28 x 48	4 x 4
Layer 4	Max Pooling	14 x 14 x 48	2 x 2
Layer 5	Convolutional	10 x 10 x 48	5 x 5
Layer 6	Max Pooling	5 x 5 x 48	2 x 2
Layer 7	Fully Connected	200	1 x 1
Layer 8	Fully Connected - Softmax	2	

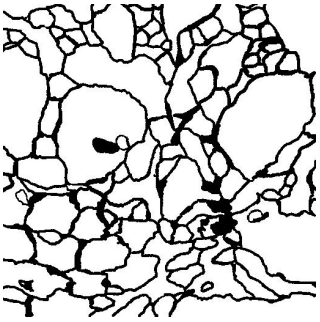
Figure 4: Architecture of the ConvNet

B Training

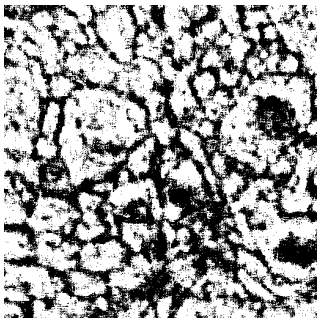
The training data comprises of a stack of 30 512x512 tiff images. We split this into a training set of 20 images, a validation set of 5 images and a test set of 5 images. The training data is highly biased to the nonmembrane class. To counter this, we chose all the membrane pixels from each training image and an equal number of a random selection of nonmembrane



(a) A training image



(b) Corresponding label



(c) Segmented result

Figure 5: Sample result

pixels. Artificially equalizing the number of samples from the two classes helped us to avoid any bias towards the non-membrane class.

The training was done using a Stochastic Gradient Descent Optimizer. We used standard features like momentum upgrade and exponential decay of the learning rate in our training.

C Post processing

The ConvNet outputs the probability of each pixel being a non-membrane. This result has to be further postprocessed to get a good segmentation map. We are currently using a [2 2] median filter to remove outliers and clean up the image but more sophisticated methods are required to fill the holes along the borders and get a good segmentation result.

5 Results

Postprocessing would allow us to perform well on segmentation metrics like Rand Score and Information Theoritic Score [2]. For now, we report pixel accuracies on the training dataset of 30 images which we partitioned into a training, validation and test dataset.

Training Accuracy: 77.45

Validation Accuracy: 72.78

Test Accuracy: 69.32

6 Future Work

We are currently working on procedures to get a good segmentation map by post-processing the ConvNet output.

In case of TEM images, it is known that the appearance of structures is not affected by their orientation. This property can be used to synthetically augment the dataset. Such data augmentation might lead to better results.

In this project, we have attempted the most basic problem in connectomics as it was our first work in this area. Having gained some experience and learnt some valuable lessons, we would now like to attack more complex problems like 3D segmentation, synapse detection and connectivity.

References

[1] Dan C. Ciresan,Luca M. Gambardella, Alessandro Giusti Jurgen Schmidhuber,*Deep Neural Networks Segment Neuronal Membranes in Electron Microscopy Images*

[2] Ignacio Arganda-Carreras, Srinivas C. Turaga, Daniel R. Berger, Dan Ciresan, Alessandro Giusti, Luca M. Gambardella, JuÌĺrgen Schmidhuber, Dmtry Laptev, Sarversh Dwivedi, Joachim M. Buhmann, Ting Liu, Mojtaba Seyedhosseini, Tolga Tasdizen, Lee Kamentsky, Radim Burget, Vaclav Uher, Xiao Tan, Chanming Sun, Tuan D. Pham, Eran Bas, Mustafa G. Uzunbas, Albert Cardona, Johannes Schindelin, and H. Sebastian Seung. *Crowdsourcing the creation of image segmentation algorithms for connectomics. Frontiers in Neuroanatomy, vol. 9, no. 142, 2015.*

[3] Albert Cardona, Stephan Saalfeld, Stephan Preibisch, Benjamin Schmid, Anchi Cheng, Jim Pulokas, Pavel Tomancak and Volker Hartenstein (10, 2010), *An Integrated Micro- and Macroarchitectural Analysis of the Drosophila Brain by Computer-Assisted Serial Section Electron Microscopy, PLoS Biol (Public Library of Science) 8 (10): e1000502, doi:10.1371/journal.pbio.1000502*

[4] MICCAI Challenge on circuit reconstruction from Electron Microscopy images. `http://cremi.org/`

[5] Stanford course : Convolutional Neural Networks for Visual Recognition,`http://cs231n.stanford.edu/`