



Keywords: Biomedical image processing; Membrane segmentation; Feature learning; Convolutional neural network; Random forest

Introduction

Neuroanatomists face the tough task of reconstructing neuronal structure with synaptic resolution in order to gain insights into the functional connectivity of brain. Currently, EM is the main imaging tool which can provide sufficient resolution for studying connections at the neuron level. This imaging device produces amounts of image data. In order to understand the patterns, the image data should be segmented according to structural and functional modules. For human neuroanatomist, segmentation of neuro-images is a trivial task but, unfortunately, it is very time consuming [1]. Therefore, accurate algorithms for automatic neuronal segmentation are indispensable for large scale geometric reconstruction of densely interconnected neuronal tissue. These neuron images have the characteristics of medical image imaging and they have its own characteristics with respect to general medical image as well. Nevertheless, its structure is complex, such as intricate topology, various cell interference inside, and noisy textures. In addition, the poor quality of the imaging tools causes the border lack of precision in segmentation. Notwithstanding, the use of convolutional neural networks (CNNs) has shown promising results in medical image segmentation [2]. CNNs are deep learning models that can automatically learn features from input data without manual feature extraction. They have been successfully applied to various medical image segmentation tasks, such as brain tumor segmentation [3], liver segmentation [4], and heart segmentation [5].

Structure of the hybrid CNN–RF method.

resolutions. Each neuron on a feature map connects with its previous layers, and they are defined by the 5 by 5 convolutional filtering kernel (known as the “receptive field”). All the neurons in one feature map share the same kernel and connecting weights (known as the “sharing weights”). With a kernel size of 5, and a subsampling ratio of 3, each feature map layer reduces the feature size from the previous feature size. And the CNN learning rate was set to 1. Considering the time cost, the training procedure was stopped after 150 epochs, the consuming time is about one week.

Segmentation based on random forest: Once the feature extractor is trained based on the CNN, the fully connected layer of CNN was replaced by a Random Forest classifier to predict labels of the input patterns. 108 values from the trained CNN network were used to predict the labels of the input patterns. The output of the CNN is a 315 × 6 matrix, which contains 108 values for each input pattern. The output of the Random Forest classifier is a 315 × 1 vector, which contains the predicted labels for each input pattern.

biomedicalimaging.org/2012/index.php). The data set consists of training data and testing data of the Drosophila first instar larva ventral nerve cord, which is provided in the form of EM stack. The training data which was labeled by an expert human neuroanatomist is a set of 30 sections from a serial section Transmission Electron Microscopy (ssTEM) data set. The test data (ground truth unknown to the authors) is another volume from the same Drosophila first instar larva ventral nerve cord as the training dataset.

Evaluation metrics

Segmentation result is evaluated through an automated online system; the system computes three error metrics in relation to the hidden ground truth: pixel error, warping error and the Rand error.

- Pixel error: defined as 1 - the maximal F-score of pixel similarity or squared Euclidean distance between the original and the result labels [19].

- Warping error: The warping error is segmentation metric that tolerates disagreements over boundary location, penalizes topological disagreements, and can be used directly as a cost function for learning boundary detection [19].

- Rand error: The Rand error metric is based on the Rand index, defined as 1 - the maximal F-score of Rand index, a measure of similarity between two clusters or segmentations. It has a more intuitive interpretation, but completely disregards non-letely disregradaE.euuar9>BDC 6t6(e)4(l)7ion, penalizem(t)2irC /Span T5(e eren)19l913(4E.euu)-3(

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Unique features:

‡ 8 V H W L H Q G O \ Z I H H E D W L I E B H R W H D X S U G S B W E I Z R O J O G I - D / G I D Q Q U X D J H V
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Special features:

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