

Annotation of Microtubule and Membranes in Cell Tomography images.

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Introduction

Electron cryo-tomography(cryo-ET) is a popular tomography technique used by biologists in recent years to determine nanometer resolution 3-D sub-cellular structures. This technique is normally featured with imaging a rotating sample for 120 degrees, generating a series of 2D tilt images that can be combined to produce a 3D volume. The main method researchers use in reconstructing the 3D volume of the sample starts with manually annotating various features such as cytoskeletal filaments, cell wall elements and internal compartments in each 2D image slice. In particular, lots of efforts are devoted in annotating membranes and the microtubules. Considering the large number of slices in each 3D volume, low efficiency becomes the biggest challenge in manual annotation. Although remaining as the most accurate method, the concern of this low efficiency becomes more serious when data collection is speeding up.

Goal

Here I propose an algorithm for microtubule and membrane annotation based on their curvature difference. The goal is to recognize all of the microtubules and membranes in the image and label them in different colors.

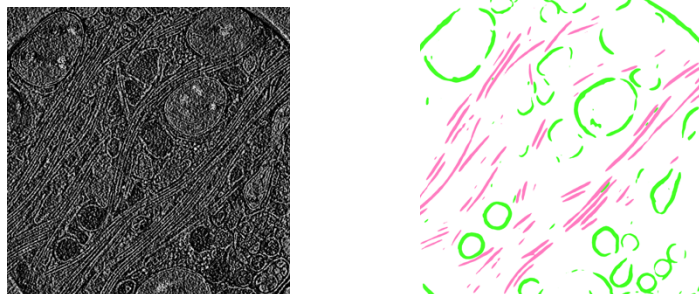


Figure 1. Example image and its corresponding label. Microtubules are shown in pink while membranes are shown in green.

Datasets and strategy

The data is a PC-12 cell tomogram in size of (96, 864, 868) used in Muyuan Chen's paper[1]. This data is acquired at low magnification on cryo-electron microscopy. I will use a few slices from this tomogram for testing the algorithm. I will implement, test and compare different strategies to identify microtubules and membranes. The initial algorithms consists of the following steps.

Data preprocessing two steps. The first step is image binarization using thresholding. Then detect edge followed by small region removal with region labeling and counting.

Since microtubule is more close to line and membrane is with high curvature and most time is a circle. We will try hough transform to detect which class one region belong to. In addition, we will also try to detect the curvature for each region. For each feature, e.g. microtubule, The curvature profile will be taken by its second derivative. And the average curvature profile will be the signature for microtubule.

We will use these strategies to develop an optimal algorithm to identify two features, comparing the annotation accuracy in terms of both features. Upon successful development of our detection strategy, we can then apply our algorithm to new/unpublished datasets such as tomograms of neuron cells.

References

1. Chen, M. et al. Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. *Nat. Methods* 14, 983–985 (2017).
2. Karthik Raghupathy and Thomas W. Parks. Improved curve tracing in images. 10.1109/ICASSP.2004.1326611.
3. B.S.Y.Lam, H.Yan. A curve tracing algorithm using level set based affine transform. <https://doi.org/10.1016/j.patrec.2006.07.001>