Watershed Merge Tree Classification for Electron Microscopy Image Segmentation

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Introduction

- Electron microscopy (EM) generates images with sufficient resolution in nanoscale for reconstruction of connectome, i.e. neural circuit map. Terabyte-scale data \bullet makes manual analysis infeasible. Automated image analysis is needed.
- Challenging due to intricate intra-cellular structures, large shape variations and high data anisotropy (10 nm in x-y plane, 50 nm in z direction).
- 2D segmentation pipeline: supervised pixel-wise membrane detection + hierarchical segmentation. \bullet

Watershed Merge Tree and Boundary Classifier

- Pixel-wise membrane detection: multi-scale context + serial ANNs [Seyedhosseini et al., 2011]. \bullet
- Watershed transform generates initial over-segmentations and region merging hierarchy. \bullet
- Watershed merge tree: representation of region merging order. \bullet
- Boundary classifier:
 - Predict about each merge/split.

 - Random forest classifier with 141 features (geometry/intensity/texture/merge saliency). lacksquare



Fig. 1: Example of (a) original EM image, (b) membrane detection, (c) initial watershed over-segmentation, (d) region merging with water level rising and (e) watershed merge tree.

bin 2

0.2749

0.1529

Resolving Merge Tree

Consistency constraint:



- Any pixel should be labeled only once. ullet
- Once a node is selected, its ancestors and descendants must be removed. \bullet
- Node potential: \bullet
 - Probability that a node does not merge with its sibling and its children merge.

Thresholding

Merge tree

- In Fig. 2 (b), $P_6 = (1 P_{6.8})P_{1.2}$. ullet
- Resolving merge tree via greedy optimization: \bullet
 - Pick the most potential node;
 - Remove its ancestors and descendants;
 - Repeat until no nodes are left. lacksquare

Fig. 2: Illustration of how (a) final segmentation is acquired by (b) resolving a merge tree.

bin 5

0.2717

0.1595

avg.

0.2500

0.1316

Table 1: Segmentation Rand errors.

bin4

0.2115

0.1029

bin 3

0.2419

0.1113

Results

- Data: 700 x 700 x 70 \bullet SBFSEM mouse neuropil images (10 x 10 x 50 nm resolution).
- Use Rand error as measurement.
- Cross validation.

Original	Membrane detection	Over-segmentation	Final segmentation

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Fig. 3: Segmentation results of two image regions (zoomed in).