

Towards automatic and fast segmentation in SBFSEM image stacks

Daniel R. Berger¹

¹Max Planck Institute for Biological Cybernetics, Tübingen, Germany

Recent methodological advances (SBFSEM, see [1]) have made it possible for the first time to scan large volumes of nervous tissue rapidly and automatically at electron microscopic level. If individual neurons could be segmented in these image stacks, neuronal circuits with all synapses could be reconstructed. Due to the huge amount of image data it is not practical to do the segmentation by hand, and methods for fast and automated segmentation are needed.

Contrary to previous work [2], we approach the segmentation problem as one of finding local edge probabilities in the 3-dimensional image block. First, 3-dimensional Fourier transforms are computed on local blocks of 4x4x4 voxels. Next, an unsupervised clustering algorithm (K-Means) is used to group the Fourier blocks into typical image features. This reduces the computational cost, as further computations can be performed on the smaller set of image features rather than on the original data. It also helps to reduce image noise. Then, we fit generated ground-truth data, which contain edges of known position and orientation, to the image features. For each voxel we can then compute an edge probability from the blocks overlapping it. A flood-filling algorithm can then rapidly segment the image into its components.

This method could be easily extended to incorporate further constraints, such as edge continuity. The method is quite fast, since much of the computation can be done once for a certain type of images and then stored and applied to new images; for example the clustering into features and association of edge probability patterns to these features. This probabilistic framework offers great potential for automated, efficient and robust segmentation of neurons in electron-microscopic image stacks.

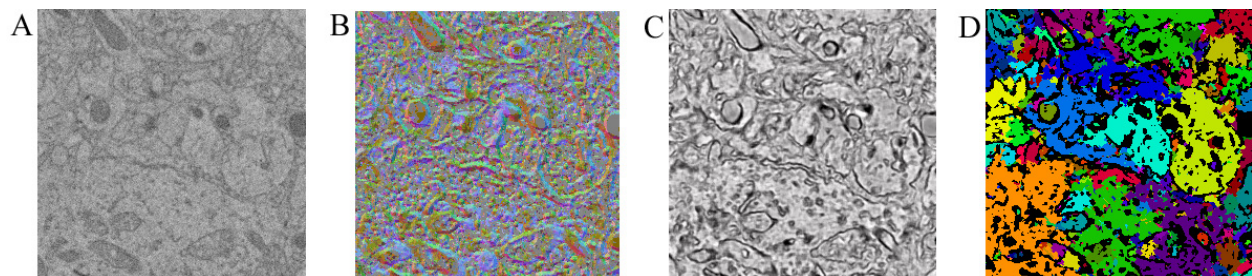


Figure 1: A: Original SBFSEM slice image (see supplementary material in [1]). B: Fitted local edges in 3D (direction is color-coded). C: Resulting edge probability map. D: Segmentation attempt, using flood-filling with edge threshold and connectivity probability propagation.

Acknowledgments

Thanks to J. Butler for helpful discussions. This work was supported by the Max Planck Society.

References

- [1] Serial block-face scanning electron microscopy to reconstruct three-dimensional tissue nanostructure. W. Denk and H. Horstmann, *PLoS Biology*, 2(11):1900-1909 (e329), November 2004.
- [2] Axon tracking in serial block-face scanning electron microscopy. E. Jurrus et al., *Workshop on microscopic image analysis with applications in biology*, Copenhagen, Denmark, October 2006.