Accurate 3D Cell Segmentation Using Deep Features and CRF Refinement

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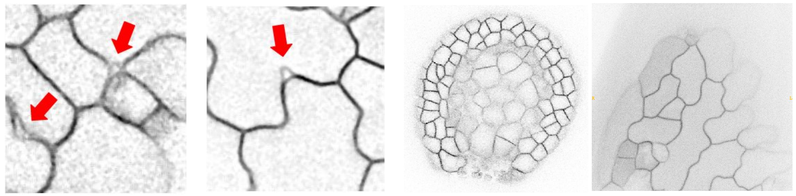
MOTIVATION

Precise identification of cell boundaries, their shapes, and quantifying inter-cellular space leads to a better understanding of cell morphogenesis

CHALLENGE

The current methods are not able to generate closed cell surfaces in the 3D image stack while being able to accurately delineate features of interest such as the inter-cellular spaces and protrusions



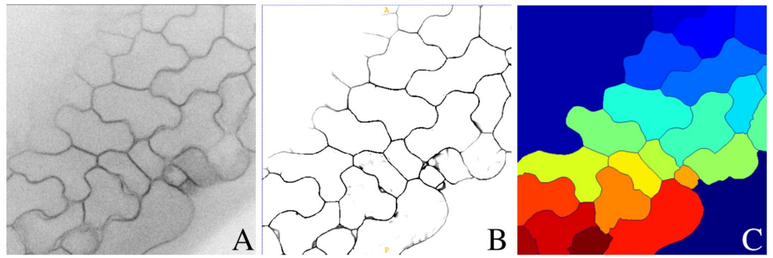
From Left to Right: Inter-cellular space , Protrusion are indicated by red arrows, example images in xy direction from the first and second dataset

DATA

- Two 3D confocal image stack datasets of fluorescent-tagged plasma-membrane cells
- The first dataset contains 3 layers of cells in the shoot apical meristem of 6 Arabidopsis thaliana
- The second dataset consists of a long-term time-lapse from A. thaliana's leaf epidermal tissue that spans over a 12 hour period

METHOD

- A 3D U-Net based neural network is used to generate a probability map of each voxel being the membrane
- A 3D watershed algorithm whose seeds are generated automatically is applied to this probability map, and outputs the initial cell segmentation result



(A) Inverted raw image in xy orientation, (B) inverted probability map from the 3D U-Net, (C) initial segmentation result from 3D watershed.

- Finally, a CRF is used to refine the boundaries of this initial cell segmentation

(A) Inverted probability map from the 3D U-Net, (B) initial segmentation without CRF refinement, (C) final segmentation result with CRF refinement.

EXPERIMENTAL RESULTS

Table 1. 3D Segmentation Performance on L1

Algorithm	Precision	Recall	F-Score
ACME	0.805	**0.966**	0.878
MARS	0.910	0.889	0.899
Supervoxel method	**0.962**	0.932	0.947
Result before CRF	0.944	0.930	0.937
our method	0.953	0.973	**0.963**

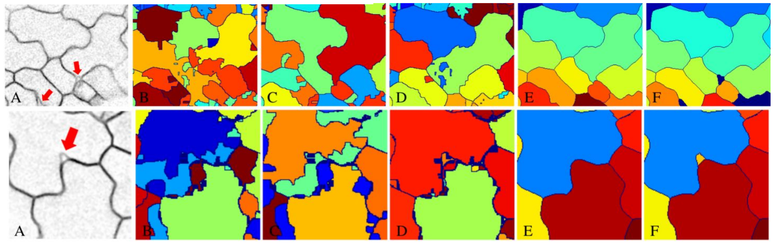
Table 2. 3D Segmentation Performance on L2

Algorithm	Precision	Recall	F-Score
ACME	0.775	**0.980**	0.866
MARS	0.921	0.879	0.900
Supervoxel method	0.910	0.932	0.921
Result before CRF	0.924	0.920	0.922
our method	**0.943**	0.973	**0.953**

Table 3. 3D Segmentation Performance on L3

Algorithm	Precision	Recall	F-Score
ACME	0.745	**0.976**	0.845
MARS	0.909	0.879	0.894
Supervoxel method	**0.982**	0.881	0.929
Result before CRF	0.933	0.888	0.910
our method	0.943	0.932	**0.937**

Table 1 to 3 show the comparison of the final result using our proposed method and other methods including ACME [1], MARS [2], and a supervoxel-based algorithm [3] on 3 layers of cells respectively



The top row shows the segmentation results of the cell image with inter-cellular spaces indicated by red arrows and the bottom row shows the segmentation results of the cell image with a protrusion pointed by a red arrow. (A) Inverted raw image in xy orientation, (B) MARS [1], (C) ACME [2], (D) supervoxel-based method [3], (E) proposed method without CRF, (F) proposed method

CONCLUSION

We present a probability map based 3D cell segmentation method which requires very few parameters for membrane tagged images. The experimental results show that our method achieves better segmentation performance compared to other current methods with much less computation time.

ACKNOWLEDGEMENT

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REFERENCE

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[2] Fernandez, Romain, et al. "Imaging plant growth in 4D: robust tissue reconstruction and lineaging at cell resolution." *Nature methods* 7.7 (2010): 547.
[3] Stegmaier, Johannes, et al. "Cell segmentation in 3D confocal images using supervoxel merge-forests with CNN-based hypothesis selection." *2018 IEEE 15th International Symposium on Biomedical Imaging (ISBI 2018)*. IEEE, 2018.