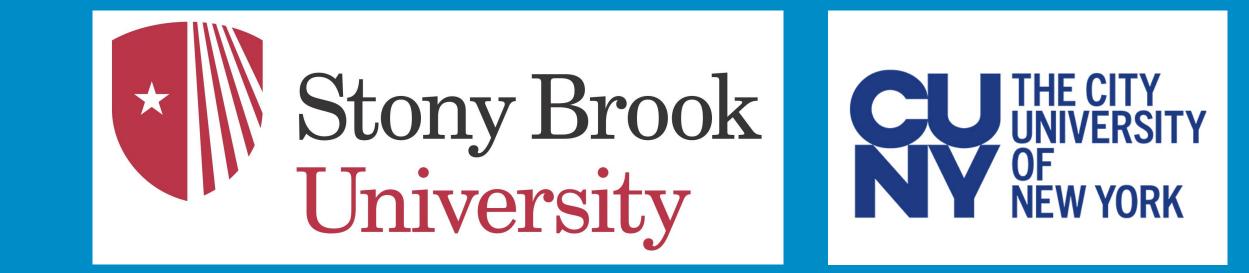


3D Topology-Preserving Segmentation with Compound Multi-Slice Representation

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ABSTRACT

We propose a new topology-preserving method for 3D image segmentation. We treat the image as a stack of 2D images so that the topological computation can be carried only within 2D in order to achieve computational efficiency. To enforce the continuity between slices, we propose a compound multi-slice representation and a compound multi-slice topological loss that incorporates rich topological information from adjacent slices. The quantitative and qualitative results show that our proposed method outperforms various strong baselines, especially for structure-related evaluation metrics.

INTRODUCTION

In biomedical image analysis and accurate segmentation, most existing algorithms are prone to structural errors. However, the topology of structures carries significant semantic/functional information.

We propose a novel method to enforce better topological accuracy. The main contributions:

- Compound multi-slice representation that incorporates information from adjacent slices
- Compound multi-slice topological loss for training the network to incorporate topological information.
- Better performance in topological accuracy.

METHOD

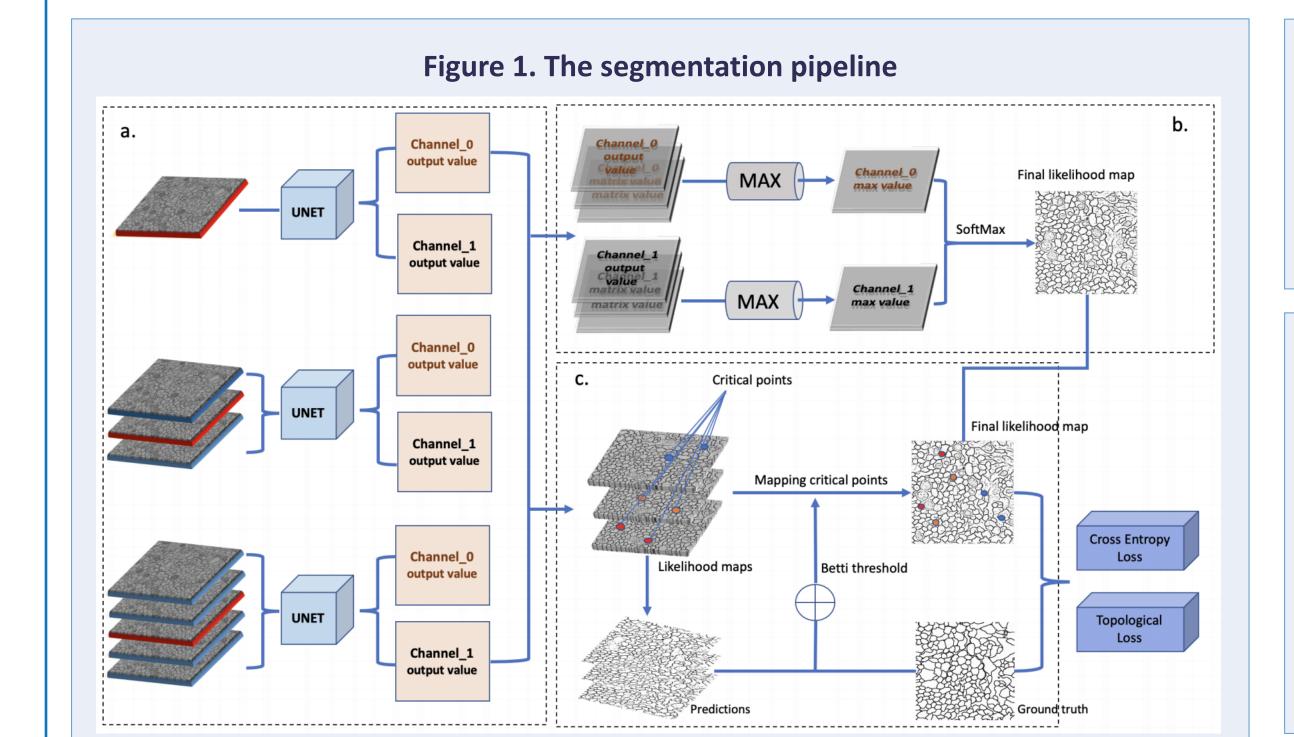
Our method treats a 3D image as 2D slices stacked along the Z-dimension.

Compound Multi-Slice Representations:

- · Figure 1(a): learning feature representation of the targeting slice (middle) with compound networks, passing different collections of nearby slices (1-slice, 3-slices, 5-slices) to sub-networks.
- Figure 1(b): applying the max-projection over the foreground and background likelihood maps, from Figure 1(a).
- · Final likelihood map (\hat{y}_i) is obtained by SoftMax on likelihood maps after max-projection.
- · The module avoids false negative detection in both foreground and background, and being either over-confident or underconfident.

Compound Multi-Slice Topological Loss:

- Figure 1(c): enforcing the final prediction \hat{y}_i to obtain the topology.
- We identify multiple sets of critical points from different multi-slice model(sub-networks)
- Compound multi-slice topological loss as: $L_{mr_topo}(\widehat{y}_i, y_i) = \sum_{c \in C_{1s} \cup C_{2s} \cup C_{5s}} (\widehat{y}_i(c) y_i(c))^2$, where C_{1s}, C_{3s}, C_{5s} are critical point sets from sub-networks, and y_i is the ground truth mask.

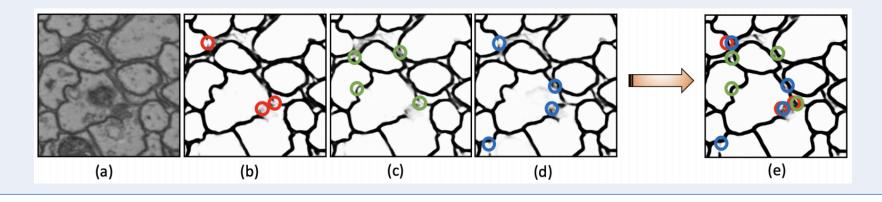


Note that we sample patches over the whole image to improve efficiency, By comparing the Betti error of the prediction and the ground truth mask. Finally, our overall loss is:

$$L_{total} = LCE + \lambda L_{mr_topo}$$

Where λ is the weight of topological loss.

Figure 2. Combination of critical points from multiple predicted likelihood maps. (a) the original image, (b), (c), and (d) are likelihood maps predicted by Different sub networks and their corresponding critical points identified by TopoLoss, (e) the final likelihood map with combining critical points. These critical points from compound models are complementary to each other.



RESULTS

Datasets. 3D Electro Microscopic Images datasets: ISBI13 and CREMI.

Evaluation: The pixel accuracy and Betti number error can be found in Table 1. Betti number is directly related to image structure, which is more applicable to biomedical domain tasks.

Baselines: UNet[1s] is only one slice as input (traditional 2D segmentation) to UNet[2s] takes three consecutive slices representation, and UNet[5s] takes five slices as input, respectively. We re-implement the TopoLoss¹ with our UNet backbone. The last row for each dataset is our proposed model.

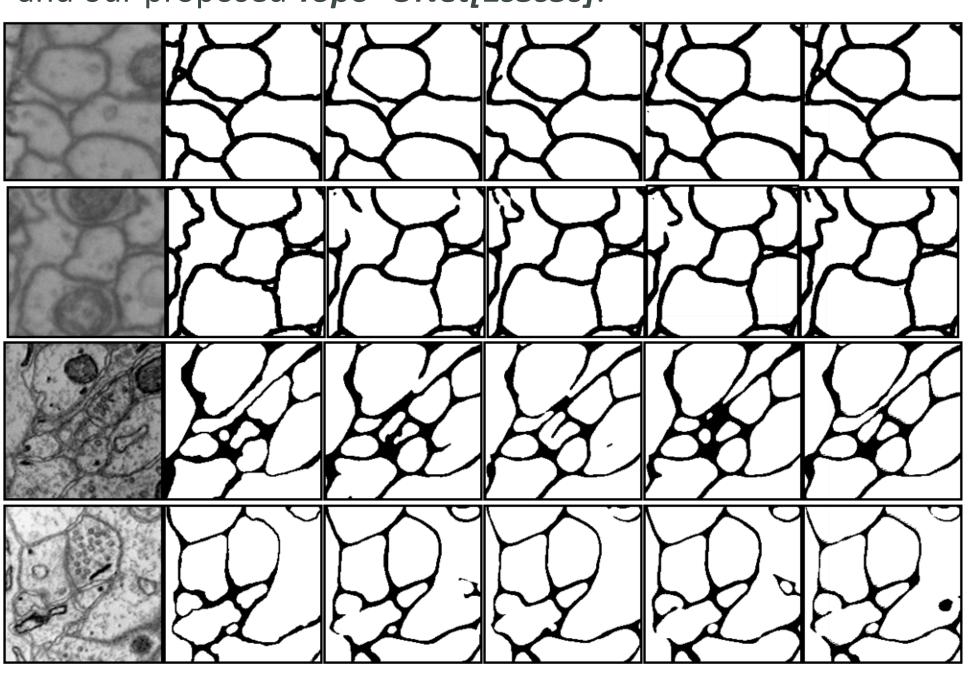
Quantitative Results: In Table 1, the best results are highlighted, most of which generated by our proposed method(Topo-UNet[1s3s5s]). It can also be observed that results of compound multi-slice(UNet[1s3s5s]) are in general better than the results of other configurations

Qualitative Results: In Figure 3, results of Compound multi-slice representation in column 4 are less fragmented. The last column corresponds to the results of our proposed system, compound multislice representation with compound multi-slice topological loss. It demonstrates better connectivity in terms of structures and topology comparing to other network configurations.

Table 1. Experiment results for different models on two popular 3D medical datasets

Models	Accuracy	Betti Error
UNet[1s]	0.9620	2.59
UNet[3s]	0.9601	1.98
UNet[5s]	0.9690	1.85
UNet[1s3s5s]	0.9700	1.67
TopoLoss	0.9664	1.90
Topo-UNet[1s3s5s]	0.9713	1.32
UNet[1s]	0.9123	2.54
UNet[3s]	0.9120	1.88
UNet[5s]	0.9099	1.41
UNet[1s3s5s]	0.9168	1.56
TopoLoss	0.9138	1.67
Topo-UNet [1s3s5s]	0.9156	1.25
	UNet[1s] UNet[3s] UNet[5s] UNet[1s3s5s] TopoLoss Topo-UNet[1s3s5s] UNet[1s] UNet[3s] UNet[5s] UNet[5s] TopoLoss	UNet[1s] 0.9620 UNet[3s] 0.9601 UNet[5s] 0.9690 UNet[1s3s5s] 0.9700 TopoLoss 0.9664 Topo-UNet[1s3s5s] 0.9713 UNet[1s] 0.9123 UNet[3s] 0.9120 UNet[5s] 0.9099 UNet[1s3s5s] 0.9168 TopoLoss 0.9138

Figure 3. Qualitative results of the proposed method compared to other models. From left to right, sample images, ground truth, results for UNet[5s], UNet[1s3s5s], TopoLoss and our proposed *Topo- UNet[1s3s5s]*.



CONCLUSIONS

- A novel method is proposed to extend the topology-preserving training to 3D EM images without much additional computational cost.
- The proposed method leverages adjacent slices' information using a compound multislice representation.
- Topological information of adjacent slices are also used through a compound multislice topological loss to segment with correct topology.

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REFERENCES

- . Xiaoling Hu, Fuxin Li, Dimitris Samaras, and Chao Chen, "Topologypreserving deep image segmentation", in NeurIPS, 2019.
- 2. Ronneberger, Olaf, Philipp Fischer, and Thomas Brox. "U-net: Convolutional networks for biomedical image segmentation," in MICCAI, 2015.

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