

A Soma Segmentation Benchmark in Full Adult Fly Brain

Xiaoyu Liu¹ Bo Hu¹ Mingxing Li¹ Wei Huang¹ Yueyi Zhang^{1,2} Zhiwei Xiong^{1,2,*}

¹University of Science and Technology of China

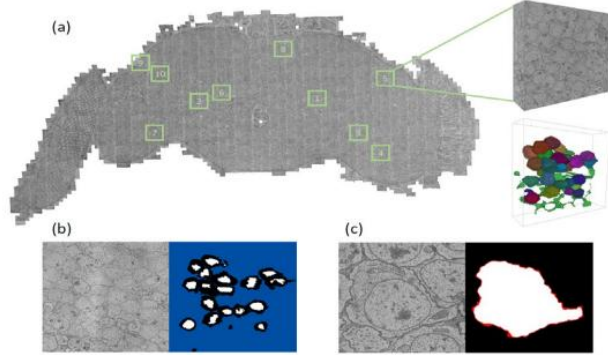
²Institute of Artificial Intelligence, Hefei Comprehensive National Science Center

{liuxyu, hubosist, mxli, weih527}@mail.ustc.edu.cn, {zhyuey, zwxiong}@ustc.edu.cn

Summary

Introduction

EM adult drosophila soma (EMADS) dataset



- Ten EM blocks from the FAFB full brain dataset.
- 204 somas with different sizes and morphologies.
- 8×10^9 annotated voxels.

Contribution

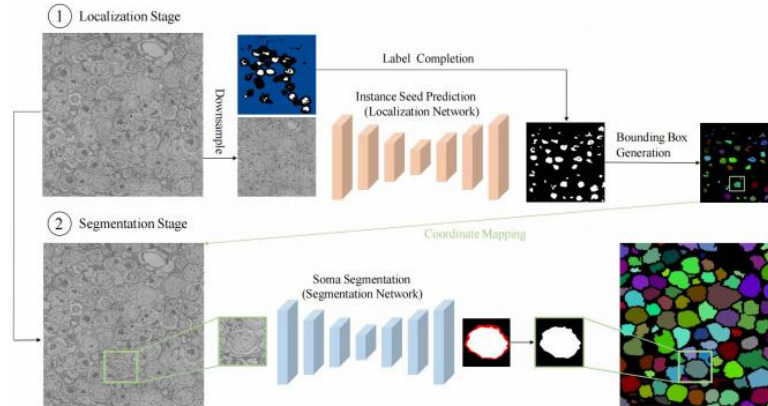
- We mask a high-resolution EM soma dataset with fine-grained 3D manual annotations.
- We propose an efficient, two-stage deep learning algorithm for soma instance segmentation.
- We deploy a parallelized, high-throughput data processing pipeline for executing our algorithm on the full brain, on a 90-GPU cluster within 4 days.
- We provide quantitative and qualitative results for evaluating the accuracy and efficiency of the proposed method, along with preliminary statistics of the reconstructed somas.

Method

Existing Methods

- Recent works of neuron reconstruction in EM images are generally time-consuming when dealing with extremely large-scale EM data.
- 2D nuclei segmentation lacks the utilization of 3D structural information and is difficult to apply to densely distributed somas with complex shapes.

Overall Pipeline



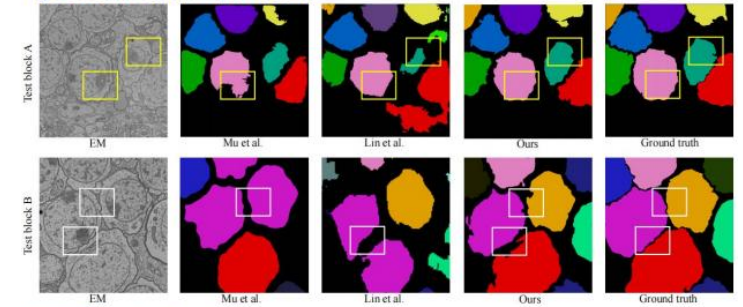
- The localization stage aims to localize somas by predicting instance seeds and generating bounding boxes for them in a given EM block.
- The segmentation stage aims to segment somas from the predicted bounding boxes.

Evaluation

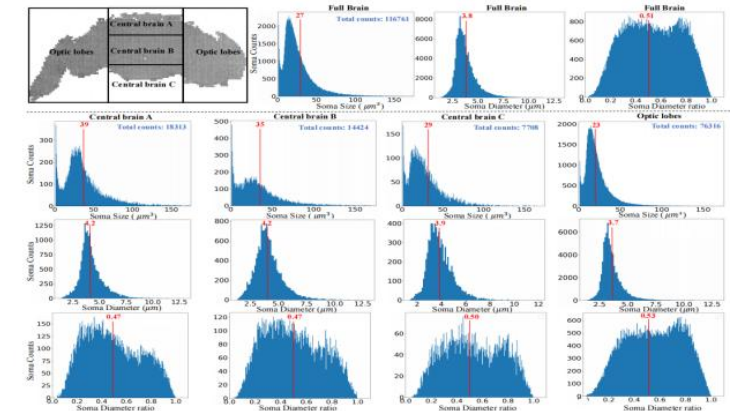
Quantitative comparisons

Method	Test block A			Test block B			Average			
	mAP	mAP ₅₀	Jacc.	mAP	mAP ₅₀	Jacc.	mAP	mAP ₅₀	Jacc.	time
Mu et al.	0.045	0.212	0.579	0.072	0.219	0.578	0.059	0.216	0.579	63s
Lin et al.	0.017	0.096	0.420	0.020	0.093	0.397	0.019	0.095	0.409	32s
Baseline 1	0.213	0.699	0.587	0.179	0.680	0.524	0.196	0.690	0.556	960s
Baseline 2	0.226	0.695	0.592	0.242	0.709	0.558	0.234	0.702	0.575	1142s
Ours-UNet	0.301	0.713	0.638	0.302	0.721	0.590	0.301	0.717	0.614	178s
Ours-Swin	0.420	0.853	0.650	0.303	0.614	0.474	0.362	0.734	0.562	158s

Qualitative comparisons



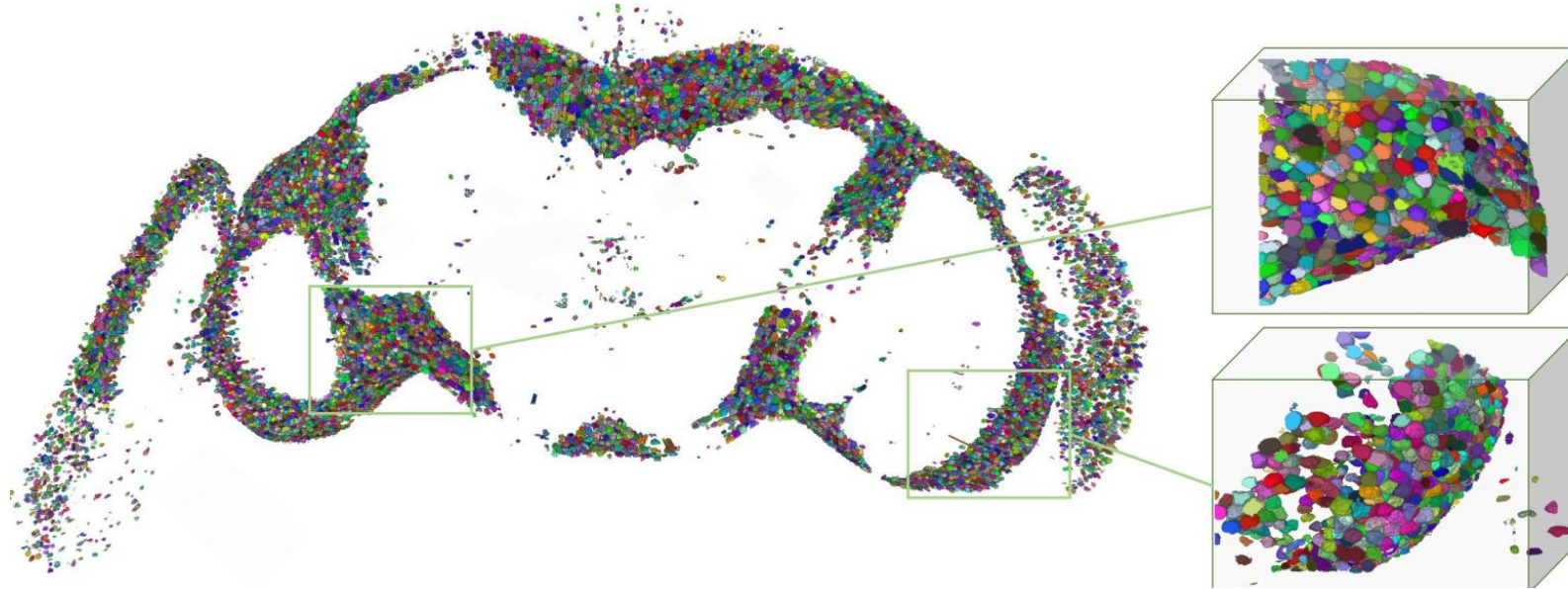
Full Brain Statistic



Introduction

➤ Soma Reconstruction

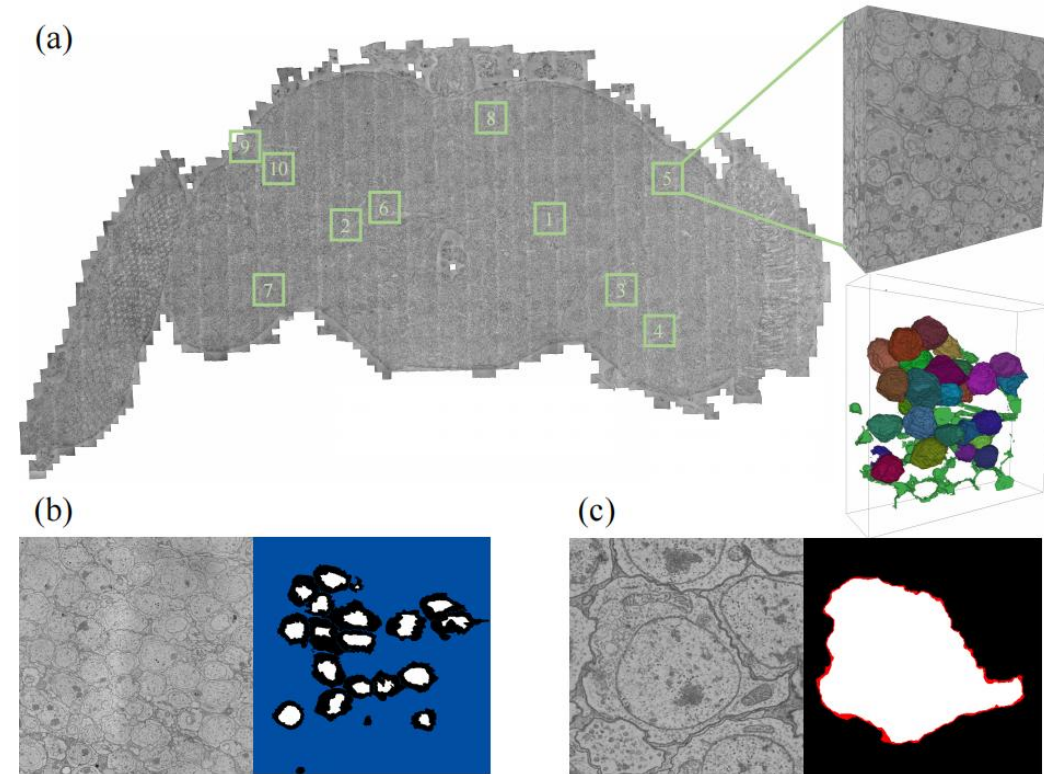
- Great biological significance to investigate soma reconstruction in the full brain of model organisms such as drosophila.
- Full adult fly brain (FAFB) dataset imaged from a complete drosophila brain can be regarded as a representative. Due to the lack of high-resolution EM datasets specifically annotated for somas, existing works cannot directly provide accurate soma distribution and morphology information.



Dataset

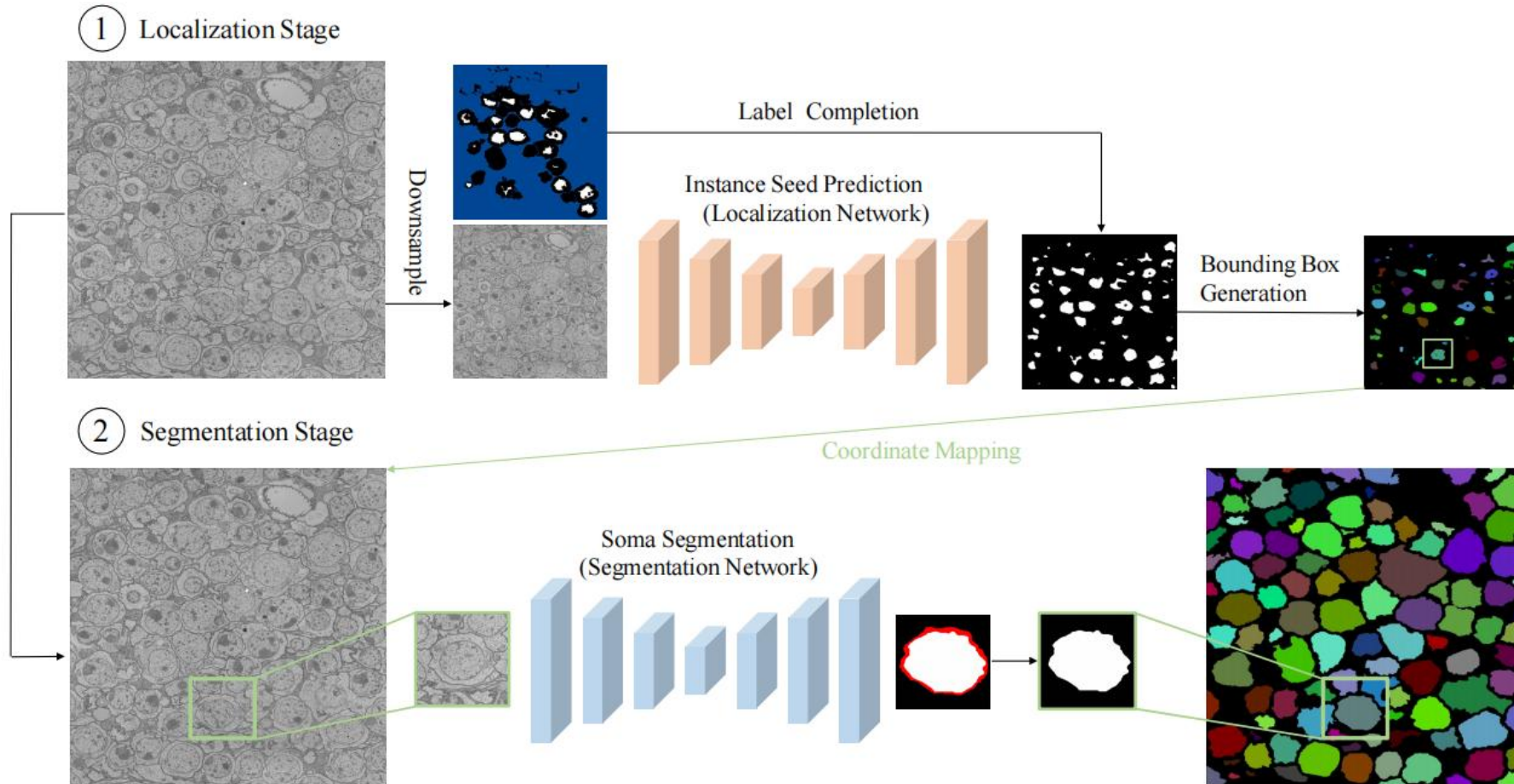
➤ Soma Reconstruction

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Method

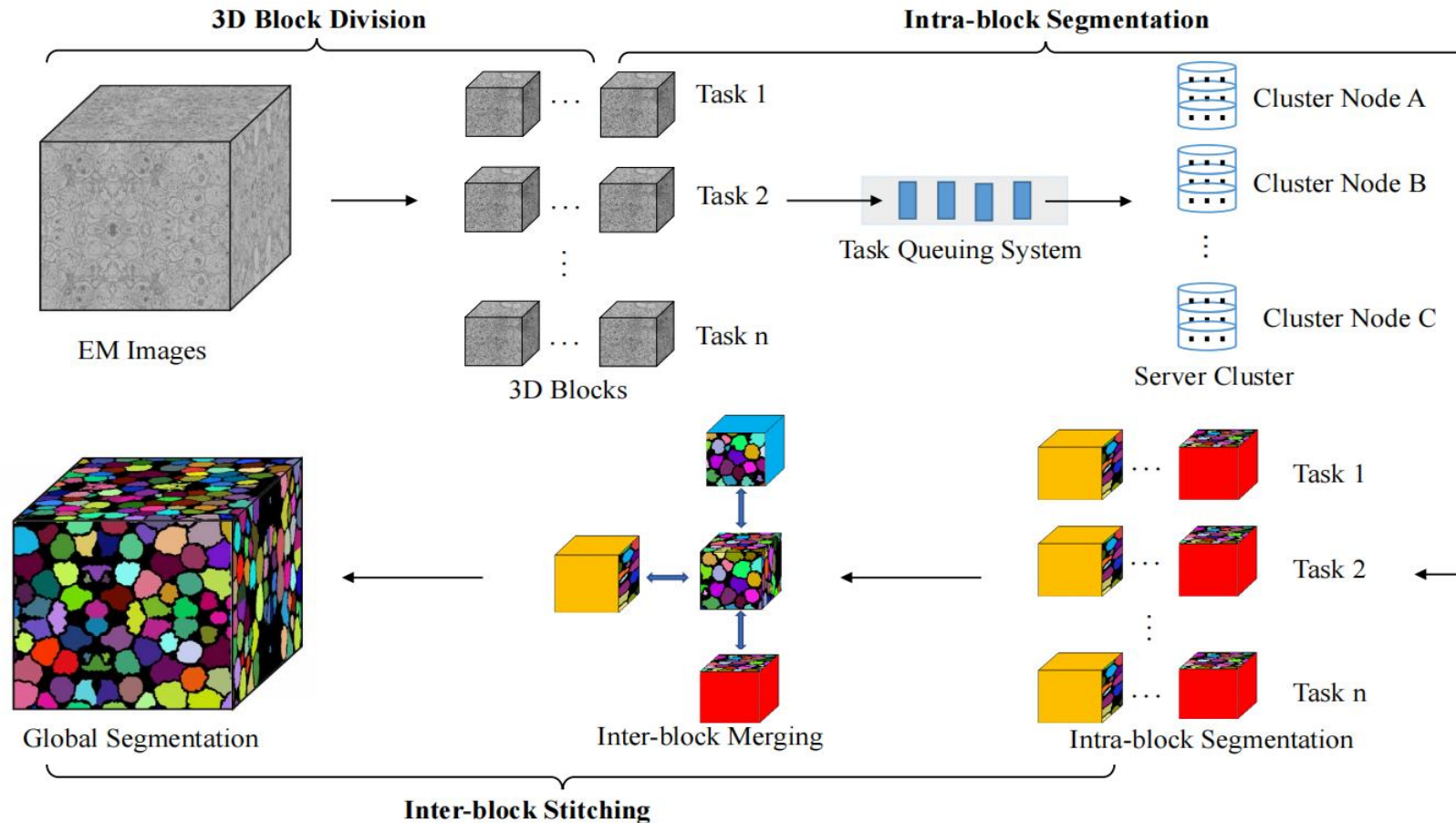
➤ Workflow of our method



Deployment



➤ Parallelized Large-scale Data Processing

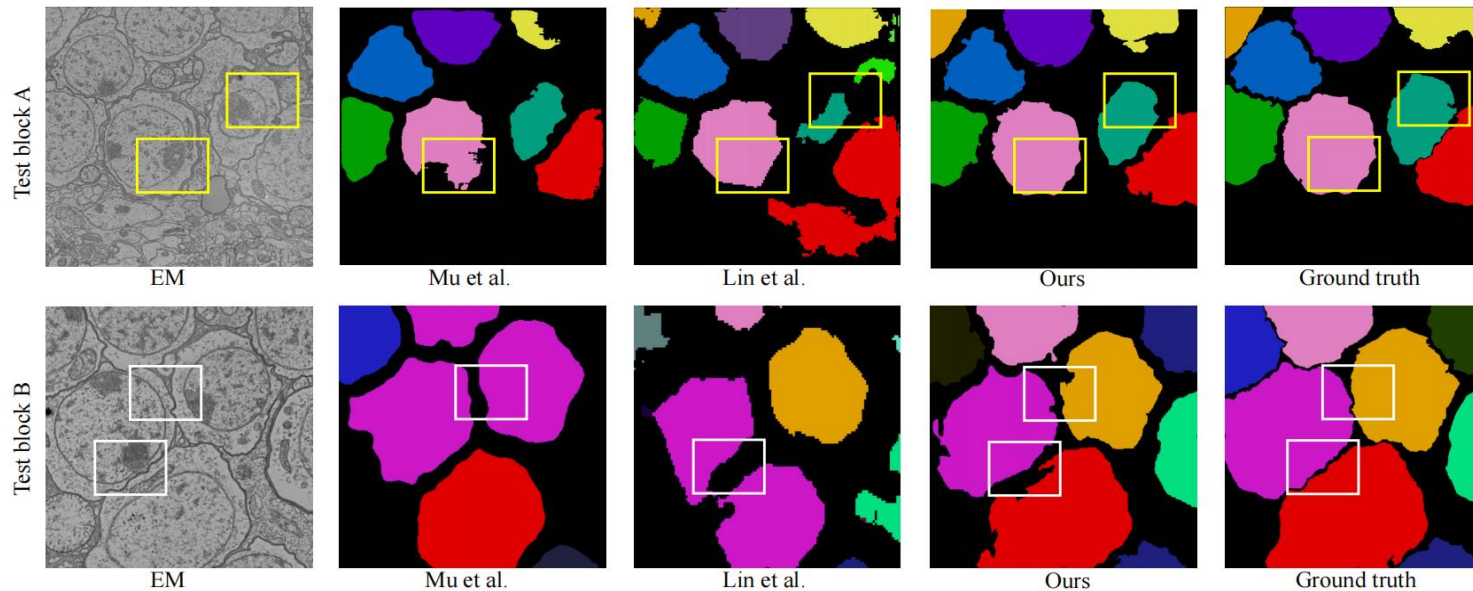


Experiments

➤ Quantitative and qualitative evaluation for our methods

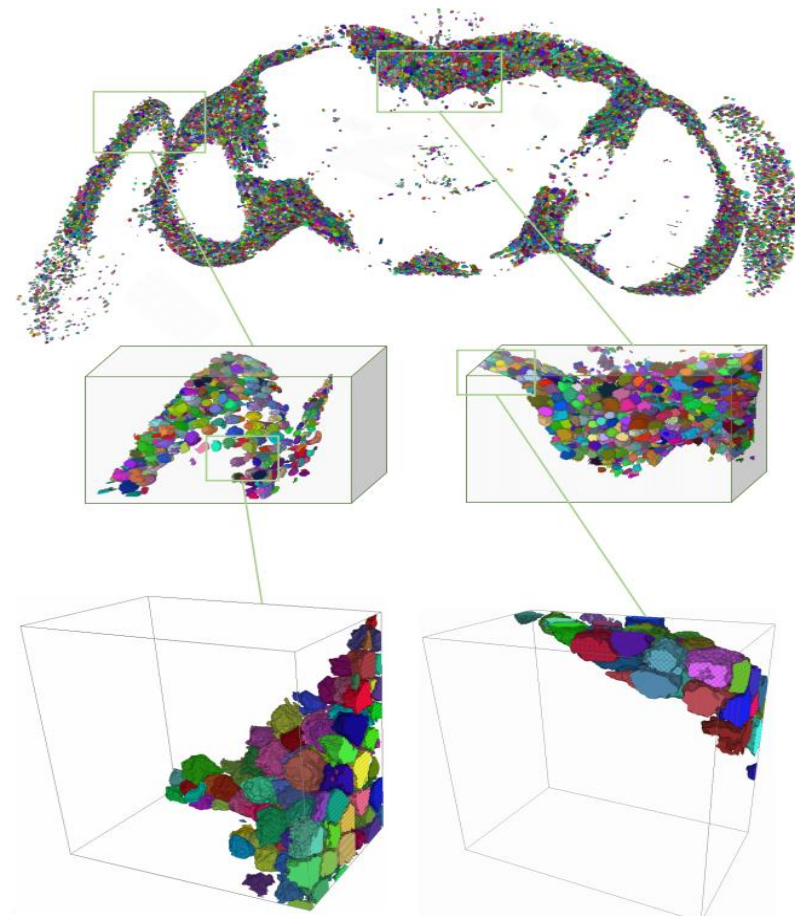
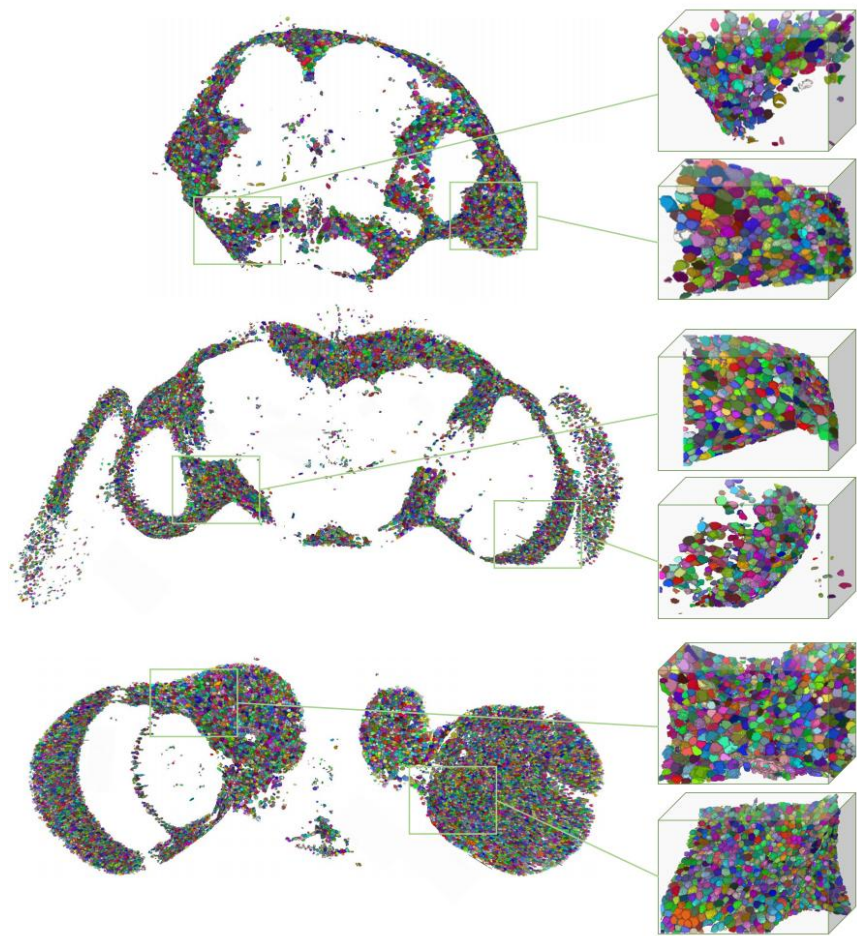


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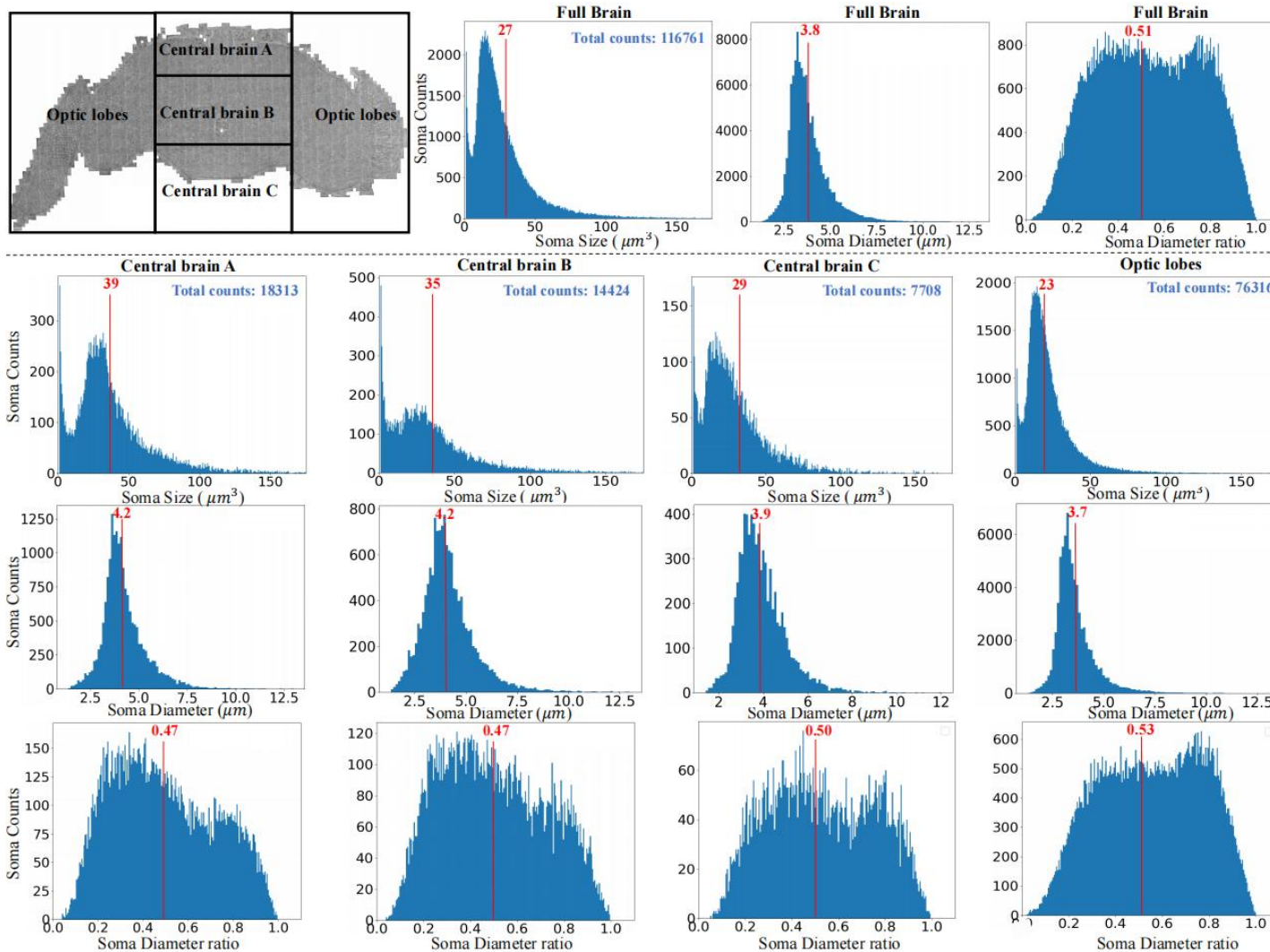
Experiments

➤ Full Brain Visualization



Experiments

➤ Full Brain Statistic



Conclusion

- We make a high-resolution EM soma dataset with fine-grained 3D manual annotations.
- We propose an efficient, two-stage deep learning algorithm for soma instance segmentation.
- We deploy a parallelized, high-throughput data processing pipeline for executing our algorithm on the full brain, on a 90-GPU cluster within 4 days.
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Thanks for your listening!

