

# Supplementary for ShapeMamba-EM: Fine-Tuning Foundation Model with Local Shape Descriptors and Mamba Blocks for 3D EM Image Segmentation

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<b>Dataset</b>	<b>Species</b>	<b>Tissue</b>	<b>Annotations</b>	<b>Image Modality</b>	<b>Resolution</b>
ISBI 2012	Drosophila	Brain-VNC	Cell	SEM	$50 \times 4 \times 4 nm$
SNEMI3D	Mouse	Brain-cortex	Cell	SEM	$30 \times 4 \times 4 nm$
MitoEM-H	Human	Cortex	Mitochondria	mbSEM	$30 \times 8 \times 8 nm$
MitoEM-R	Rat	Cortex	Mitochondria	mbSEM	$30 \times 8 \times 8 nm$
Lucchi++	Mouse	Hippocampus	Mitochondria	FIB-SEM	$5 \times 5 \times 5 nm$
Kasthuri+++	Mouse	Cortex	Mitochondria	ssEM	$30 \times 3 \times 3 nm$
CREMI	Drosophila	Brain	Cell, Synapse	TEM	$40 \times 4 \times 4 nm$
EMR-50	Rat	Cortex	Synapse	mbSEM	$30 \times 8 \times 8 nm$
Gauy	human	Platelet	Axon, Mitochondria	SBF-SEM	$50 \times 10 \times 10 nm$
NucMM-Z	Zebrafish	Brain	Nuclei	SEM	$30 \times 4 \times 4 nm$

**Table 1.** Details of the datasets.

Dataset	Training Set	Testing Set	Patch Size	$\sigma$
ISBI 2012	$24 \times 512 \times 512$	$6 \times 512 \times 512$	$100 \times 256 \times 256$	50
SNEMI3D	$80 \times 1024 \times 1024$	$20 \times 1024 \times 1024$	$100 \times 256 \times 256$	50
MitoEM-H	$400 \times 4096 \times 4096$	$100 \times 4096 \times 4096$	$100 \times 256 \times 256$	5
MitoEM-R	$400 \times 4096 \times 4096$	$100 \times 4096 \times 4096$	$100 \times 256 \times 256$	5
Lucchi++	$165 \times 1024 \times 768$	$165 \times 1024 \times 768$	$100 \times 256 \times 256$	5
Kasthuri++	$85 \times 1643 \times 1613$	$75 \times 1334 \times 1553$	$100 \times 256 \times 256$	5
CREMI	$3 \times 125 \times 1000 \times 1000$	$3 \times 125 \times 1000 \times 1000$	$100 \times 256 \times 256$	50(cell)/5(syn)
EMR-50	$100 \times 700 \times 700$	$99 \times 1000 \times 1000$	$100 \times 256 \times 256$	5
Gauy	$74 \times 800 \times 800$	$121 \times 609 \times 400$	$100 \times 256 \times 256$	15(axon)/5(mito)
NucMM-Z	$18 \times 64 \times 64 \times 64$	$9 \times 64 \times 64 \times 64$	$64 \times 64 \times 64$	2

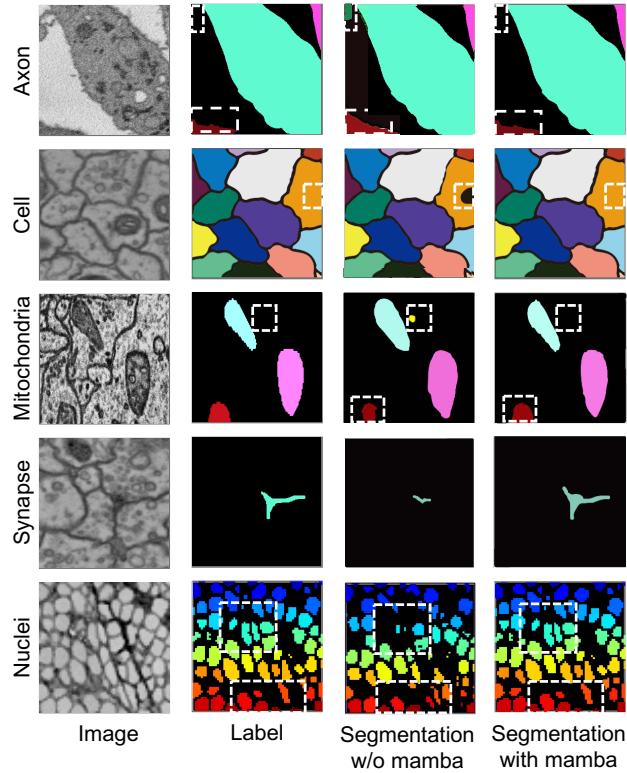
**Table 2.** Parameters of the experiments.

Dataset	Method	Dice		mAP	
		SOTA	Ours	SOTA	Ours
ISBI2012	PS-Net [6]	0.94	0.958	-	0.951
SNEMI3D	DMT [2]	0.971	0.964	-	0.961
CREMI(Synapse)	CleftNet [4]	0.831	0.834	-	0.865
Kasthuri++	HIVE-Net [7]	0.962	0.968	-	0.936
Lucchi++	DualRel [5]	0.934	0.94	-	0.954
MitoEM-H	ATFormer [1]	-	0.847	0.782	0.877
MitoEM-R	ATFormer [1]	-	0.852	0.682	0.93
NucMM-Z	U3D-BCD [3]	0.879	0.915	0.894	0.907

**Table 3.** Comparison with SOTA results. For each of the eight datasets, we choose the SOTA method with the best Dice or mAP performance for comparison. The performance in the original paper of the methods is reported. Since the EM-R50 and Gauy datasets lack corresponding SOTA methods reporting performance with these metrics, no SOTA methods are chosen for these two datasets.

## References

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**Fig. 1.** The segmentation results of the models with and without the 3D Mamba Adapter.

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