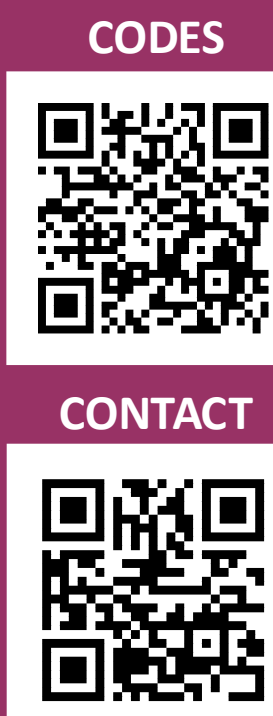




# SegNeuron: 3D Neuron Instance Segmentation in Any EM Volume with a Generalist Model

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## BACKGROUND

Efficient and accurate neuron segmentation from electron microscopy (EM) volumes has become a bottleneck that hinders progress in connectomic analysis [1,2]. SOTA approaches [3,4,5] train models to predict descriptors for neuron boundaries (e.g., affinity maps) and then employ graph-based agglomeration [6,7] for instance segmentation. While effective, learning-based methods suffer from poor model generalization, which requires repetitive annotation, training, inference, and proofreading for new datasets with different voxel resolution and visual appetences (Fig. 1). Such cumbersome workflow could be streamlined and expedited with a generalist model that robustly determines the instance-level belonging of each voxel in any EM volume.

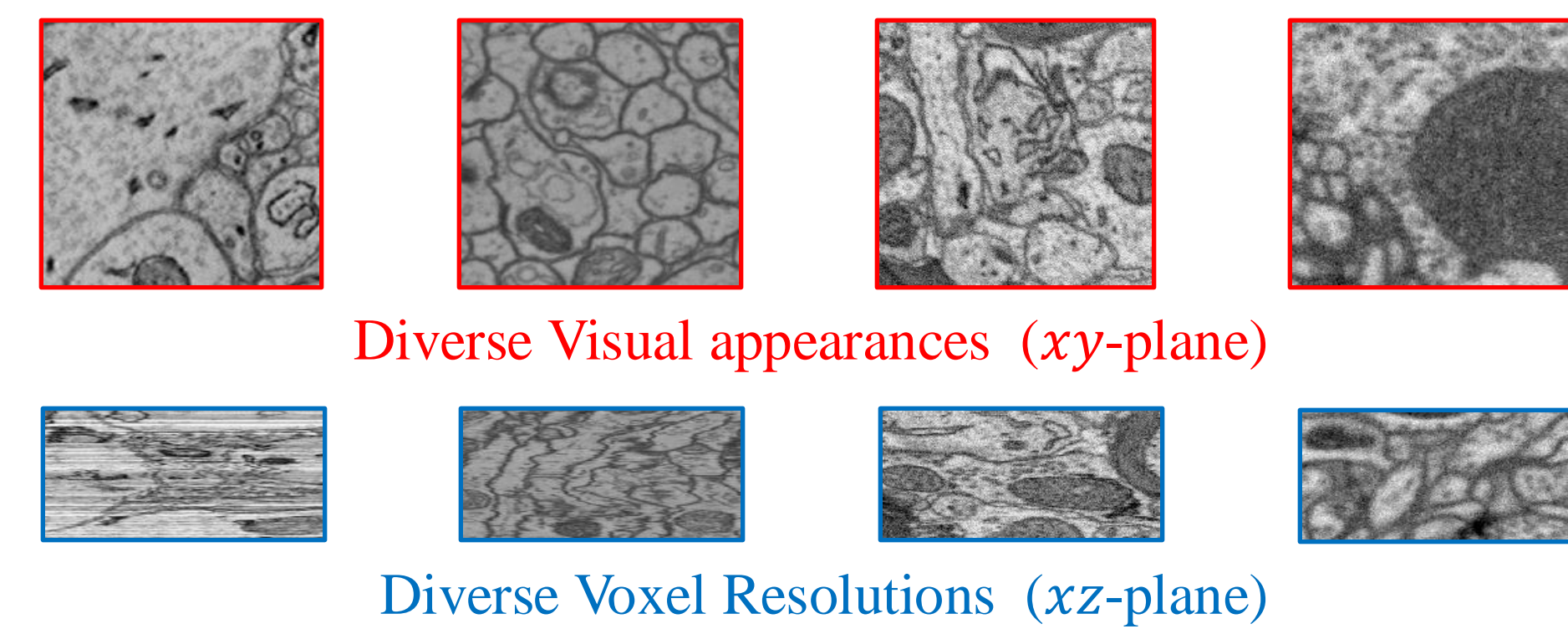


Fig.1 Challenges in generalist model development

## METHOD

In this paper, we introduce **SegNeuron**, a boundary-based neuron segmentation model, generalized across diverse data distributions and spatial resolutions. To this end, we first construct a multi-resolution, multi-modality, and multi-species volume EM database, named **EMNeuron**, consisting of over 22 billion voxels, with over 3 billion densely labeled (Table 1). To avoid ambiguous feature learning caused by inconsistent annotation styles, we conduct comprehensive **data cleaning and transforming**. On this basis, we devise a novel workflow to build the model with customized strategies (Fig. 2), including **pretraining via multi-scale Gaussian mask reconstruction** (avoids global statistics distortion and severe distribution changes in masked inputs), **domain mixing finetuning** (preserves discriminative boundary information while enriching visual appearances and voxel resolutions), and **foreground-restricted instance segmentation** (filters background voxels in the predicted affinity map to mask noise values)

Dataset	Modality	Res.(nm)	Total Labeled voxels	Dataset	Modality	Res.(nm)	Total Labeled voxels
1.ZFinch	SBF-SEM	9,9,20	3635M 131M	9.HBrain	FIB-SEM	8,8,8	3072M 844M
2.ZFish	SBF-SEM	9,9,20	1674M -	10.FIB25	FIB-SEM	8,8,8	312M 312M
3.vEM1	ATUM-SEM	8,8,50	1205M 157M	11.Minnie	ssTEM	8,8,40	2096M -
4.vEM2	ATUM-SEM	8,8,30	1329M 281M	12.Pinky	ssTEM	8,8,40	1165M 117M
5.vEM3	ATUM-SEM	8,8,40	1301M 253M	13.FAFB	ssTEM	8,8,40	2625M 577M
6.MitoEM	ATUM-SEM	8,8,30	1048M -	14.Basil	ssTEM	8,8,40	23M 23M
7.H01	ATUM-SEM	8,8,30	1166M 118M	15.Harris	others	6,6,50	30M 30M
8.Kasthuri	ATUM-SEM	6,6,30	1526M 478M	16.vEM4	others	8,8,20	45M 45M

Table 1. Details of EMNeuron dataset. Underlined items represent in-house datasets.

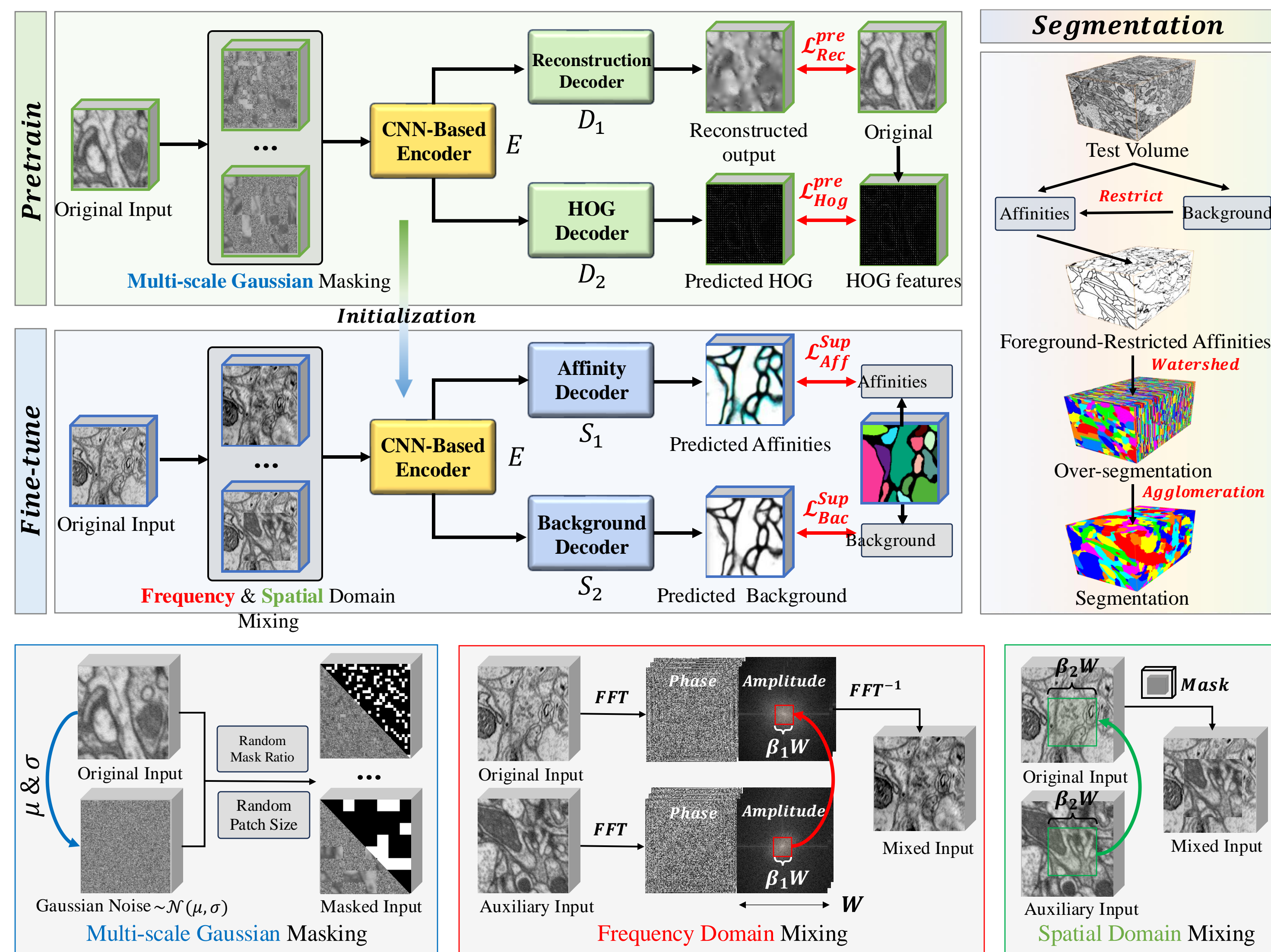


Fig.2. Customized training & inference strategies for SegNeuron.

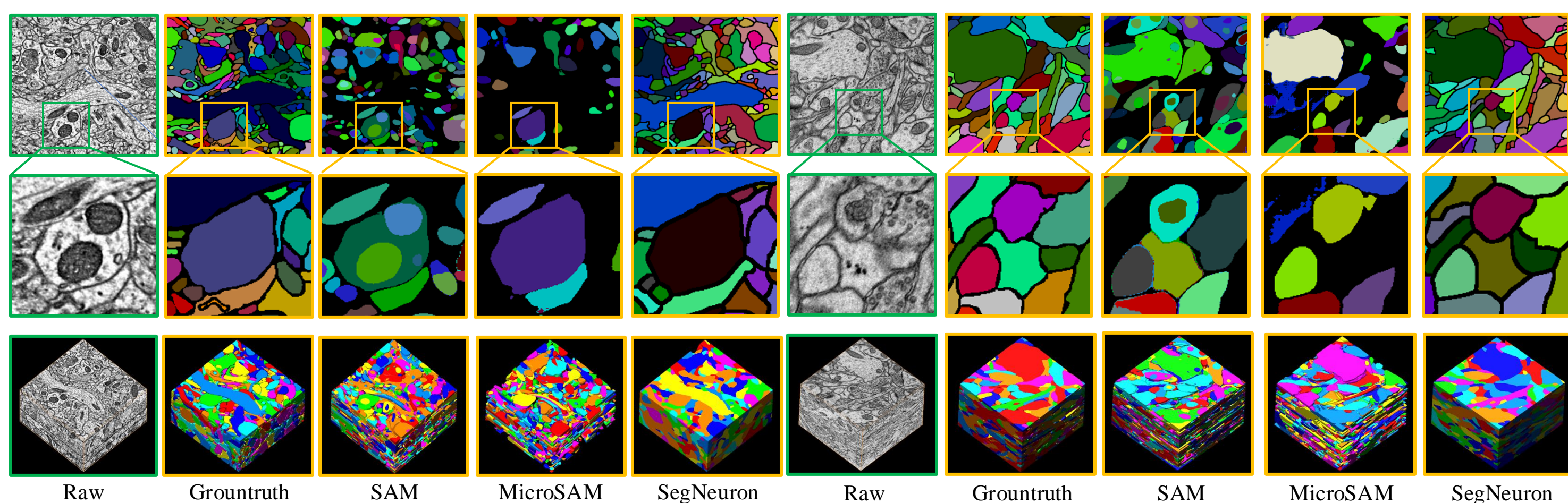
## RESULT

Qualitative and quantitative results illustrate the superior performance and strong generalizability of SegNeuron on both in- and out-of-distribution datasets.

### Comparison with Generalist Models

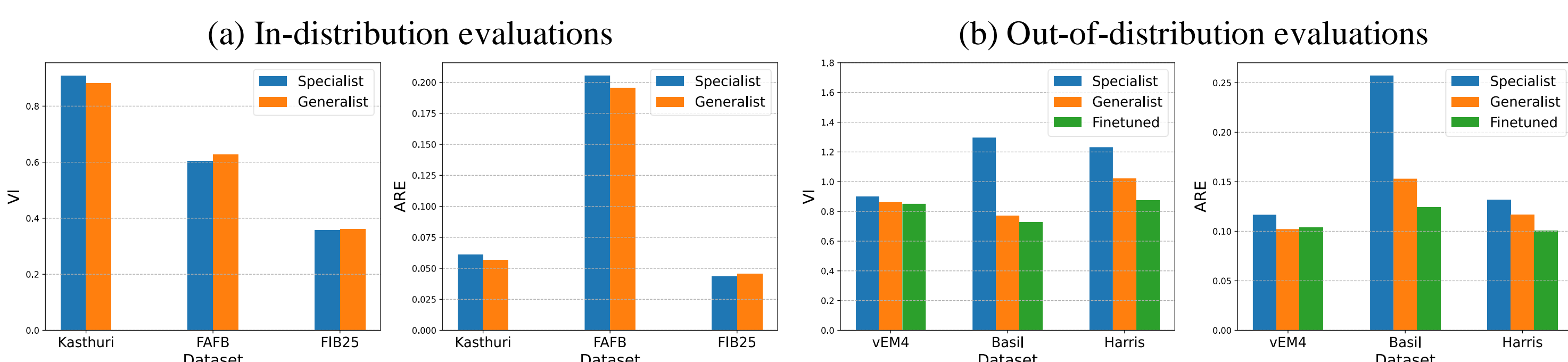
MicroSAM is a finetuned version of SAM on microscopy images. (Lower values indicates better performance.)

Methods	vEM4		Basil		Harris	
	VI ↓	ARE ↓	VI ↓	ARE ↓	VI ↓	ARE ↓
2D						
SAM	2.8579	0.8113	2.3677	0.7881	2.0374	0.5252
MicroSAM	3.9972	0.9310	3.3483	0.8891	2.1904	0.5755
SegNeuron	<b>0.4028</b>	<b>0.0839</b>	<b>0.6749</b>	<b>0.0922</b>	<b>0.5229</b>	<b>0.1063</b>
3D						
SAM	5.5215	0.8985	4.6624	0.9482	5.1034	0.8538
MicroSAM	5.7512	0.9640	4.8111	0.9655	4.4460	0.6566
SegNeuron	<b>0.8655</b>	<b>0.1022</b>	<b>0.7719</b>	<b>0.1531</b>	<b>1.0221</b>	<b>0.1170</b>



### Comparison with Specialist Models

Specialist models are trained and tested on the same datasets. (Lower values indicates better performance.)



### Ablation Study

Network architectures and pretraining schemes. (Lower values indicates better performance.)

Methods		vEM4		Basil		Harris	
Architectures	Params/ FLOPs	VI ↓	ARE ↓	VI ↓	ARE ↓	VI ↓	ARE ↓
UNETR	115M/ 334G	from scratch		1.1190	0.1490	1.8955	0.4489
		SimSiam		1.1059	0.1492	1.8446	0.4161
		MAE		1.0829	0.1391	1.8145	<b>0.4130</b>
		Ours		<b>1.0493</b>	<b>0.1369</b>	<b>1.8002</b>	<b>0.4182</b>
SwinUNETR	62M/ 197G	from scratch		1.0944	0.1679	1.5552	0.3509
		SimSiam		1.0825	<b>0.1624</b>	1.5092	0.3562
		Ours		<b>1.0748</b>	0.1628	<b>1.4662</b>	<b>0.3131</b>
PNI-Net	33M/ 317G	from scratch		0.9984	0.1480	0.9018	0.1782
		SimSiam		0.9804	0.1393	0.8878	0.1765
		Ours		<b>0.9674</b>	<b>0.1295</b>	<b>0.8479</b>	<b>0.1647</b>
MNet	40M/ 471G	from scratch		0.9096	0.1211	0.8437	0.1543
		Ours(SegNeuron)		<b>0.8655</b>	<b>0.1022</b>	<b>0.7719</b>	<b>0.1531</b>

Key components in the customized pipeline. (Lower values indicates better performance.)

Methods		vEM4		Basil		Harris	
Database		VI ↓	ARE ↓	VI ↓	ARE ↓	VI ↓	ARE ↓
Pretraining	-	0.9480	0.1241	0.9929	0.2288	1.2300	0.1298
	w/ preprocessing	<b>0.9338</b>	<b>0.1217</b>	<b>0.9625</b>	<b>0.1805</b>	<b>1.1036</b>	<b>0.1246</b>
	zero mask	0.9338	0.1217	0.9625	0.1805	1.1036	0.1246
	mean mask	0.9377	0.1173	0.8644	0.1854	1.0888	<b>0.1107</b>
	Gaussian mask	0.9191	0.1197	0.9199	0.1921	1.1024	0.1194
	Gaussian mask w/o multi-scale	0.9241	<b>0.1102</b>	<b>0.8213</b>	<b>0.1647</b>	<b>1.0600</b>	0.1141
	Gaussian mask w/o HOG loss	<b>0.9119</b>	0.1168	0.9029	0.1713	1.0940	0.1306
Finetuning	-	0.9341	0.1190	0.8446	0.1651	1.0882	0.1155
	w/ frequency mixing	0.9241	0.1102	0.8213	0.1647	1.0600	0.1142
	w/ spatial mixing	0.9031	0.1112	0.7821	0.1544	1.0563	0.1197
	w/ spatial & frequency mixing	0.9058	0.1133	0.8208	0.1617	<b>0.9935</b>	<b>0.1126</b>
Segmentation	-	<b>0.8655</b>	<b>0.1022</b>	<b>0.7719</b>	<b>0.1531</b>	<b>1.0221</b>	<b>0.1170</b>
	w/o foreground restriction	0.8879	0.1056	0.8069	0.1620	1.0414	0.1182

## Conclusion

This paper proposes SegNeuron, a neuron instance segmentation model trained on large-scale heterogeneous EM datasets with strong zero-shot generalization capabilities. We believe the released model can significantly simplify existing workflows and accelerate the scientific analysis of connectomics.

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