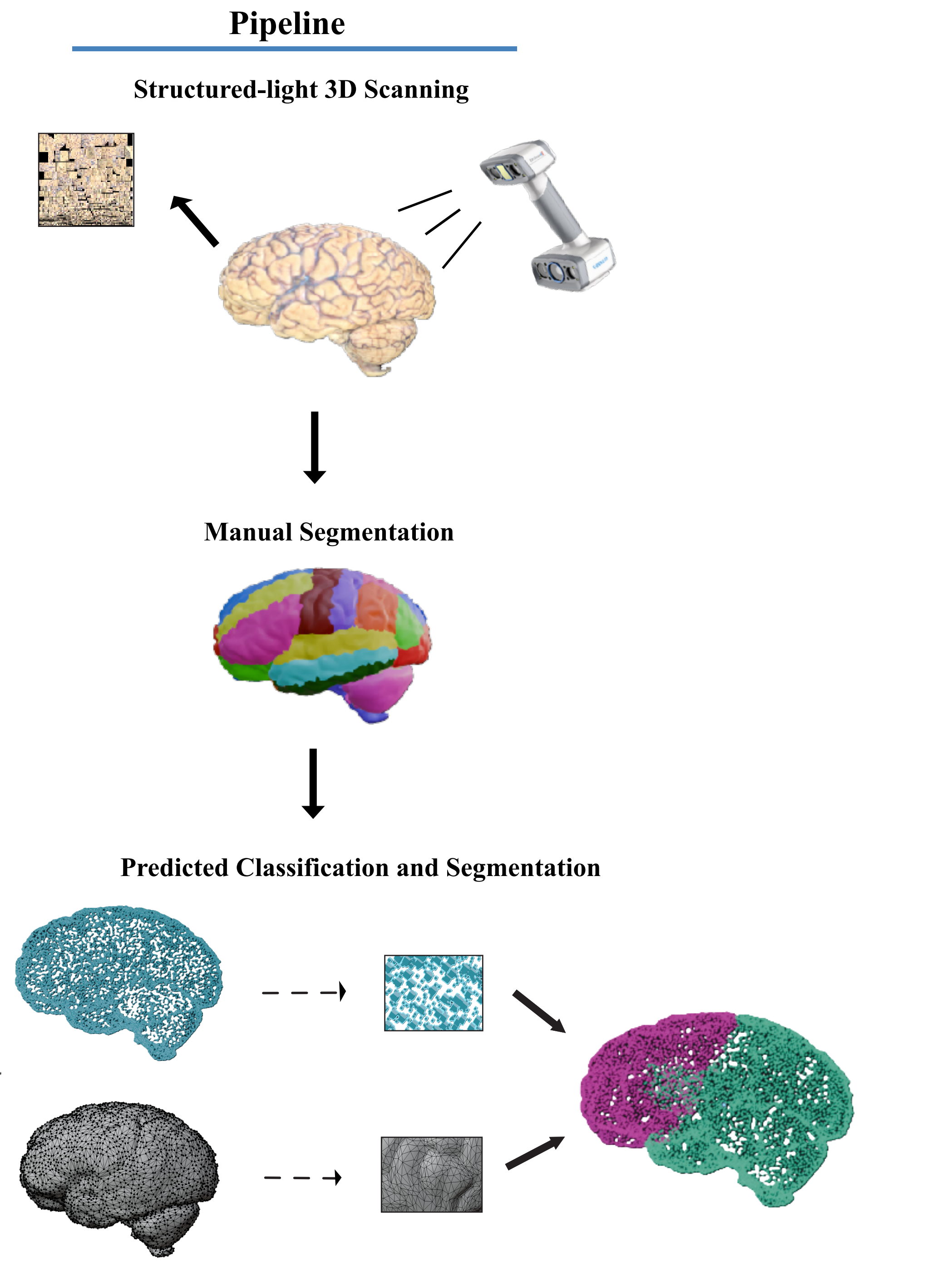


Background

- Pathology and cell loss in neurodegenerative diseases causes cortical atrophy of specific neuroanatomical structures.
- Magnetic resonance imaging (MRI) is the gold standard for quantifying cortical atrophy, however, this technology can be expensive and inaccessible outside of a clinical setting.
- Deep learning is well-established for detecting unseen patterns in complex datasets, demonstrating its applicability in neuroimaging.
- By utilizing Python and the Blender application, we aim to apply three-dimensional (3D) model segmentation to permit quantitative analysis of cortical atrophy.



Classification

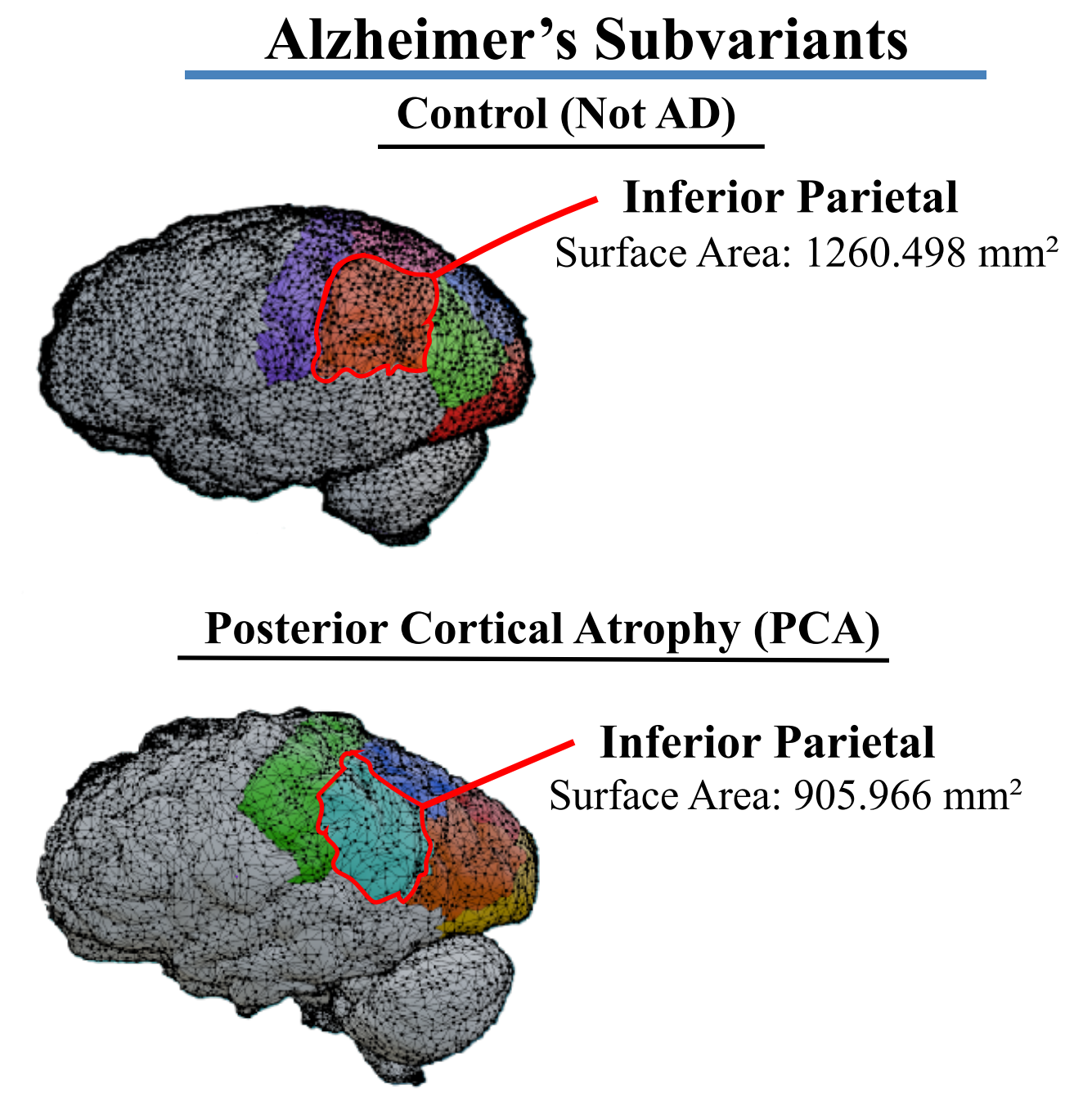
7-output							
Model	System	Accuracy	Precision	Loss	F1-Score	Recall	TP
LR	SL	0.3379	0.5515	0.1084	0.3153	0.2447	119
MLP	SL	0.6805	0.7680	0.0685	0.7212	0.6921	2407
RFC	SL	0.7292	0.7713	0.0674	0.7184	0.6853	1634758
DTC	SL	0.7020	0.6817	0.0841	0.6702	0.6651	19841
VFS-Net	TF	0.7388	0.7820	0.1536	0.7503	0.7286	113159
GCN	PyT	0.6623	0.6593	0.9695	0.6487	0.6623	711
GAT	PyT	0.6977	0.7038	0.8813	0.6934	0.6977	1685
Graph SAGE	PyT	0.6428	0.6434	0.9992	0.6323	0.6428	1351
3D UNet	PyT	0.9714	0.2250	1.0672	0.2086	0.2760	5602727
PointNet	PyT	0.5590	0.6913	1.5961	0.4021	0.4325	835335
19-output							
Model	System	Accuracy	Precision	Loss	F1-Score	Recall	TP
LR	SL	0.0786	0.2782	0.0506	0.0735	0.0465	323
MLP	SL	0.4632	0.6200	0.0390	0.5108	0.4618	3619
RFC	SL	0.5503	0.5998	0.0382	0.5242	0.4735	2857988
DTC	SL	0.5523	0.4907	0.0466	0.4834	0.4840	30309
VFS-Net	TF	0.5697	0.6189	0.0930	0.5812	0.5705	113159
GCN	PyT	0.4902	0.4964	1.5460	0.4781	0.4903	1491
GAT	PyT	0.5290	0.5389	1.4454	0.5266	0.5291	3257
Graph SAGE	PyT	0.4766	0.4833	1.5323	0.4669	0.4766	2889
3D UNet	PyT	0.1852	0.0570	1.1312	0.0318	0.0676	5603123
PointNet	PyT	0.1357	0.1216	0.2195	0.0293	0.0538	838419

Table 1: Classification performance of VFS-Net on AD brains (Gyral). Logistic Regression = LR, Multi-layer Perceptron = MLP, Random Forest Classifier = RFC, Decision Tree Classifier = DCT; Tensorflow = TF, Trainable parameters = TP, SL = Scikit-learn, and PyT = PyTorch.

Segmentation

7-output					
Model	mIoU	pIoU	bIoU	DCF	CD
LR	0.2173	Per region	0.4531	Per region	2.3350
MLP	0.5669	Per region	0.8788	Per region	2.3024
RFC	0.5674	Per region	0.9308	Per region	2.3015
DTC	0.5083	Per region	0.9927	Per region	2.3010
VFS-Net	0.6050	Per region	0.9965	Per region	2.3010
GCN	0.4336	Per region	0.6282	Per region	8.3604
GAT	0.4900	Per region	0.6882	Per region	7.2143
Graph SAGE	0.4169	Per region	0.6224	Per region	5.6289
3D UNet	0.1899	Per region	0.1708	Per region	0.3566
PointNet	0.2763	Per region	0.0555	Per region	0.1016
19-output					
Model	mIoU	pIoU	bIoU	DCF	CD
LR	0.0429	Per region	0.1201	Per region	2.8668
MLP	0.3463	Per region	0.6940	Per region	2.3053
RFC	0.3665	Per region	0.8278	Per region	2.3031
DTC	0.3289	Per region	0.9933	Per region	2.3010
VFS-Net	0.4178	Per region	0.9965	Per region	2.3010
GCN	0.2631	Per region	0.4744	Per region	11.4397
GAT	0.2994	Per region	0.4951	Per region	12.5381
Graph SAGE	0.2598	Per region	0.4544	Per region	10.3009
3D UNet	0.0195	Per region	0.0199	Per region	8.9478
PointNet	0.0199	Per region	0.0019	Per region	1.3174

Table 2: Segmentation performance of VFS-Net on AD brains (Gyral). Logistic Regression = LR, Multi-layer Perceptron = MLP, Random Forest Classifier = RFC, Decision Tree Classifier = DCT; Tensorflow = TF, Trainable parameters = TP; mIoU = mean intersection over union, pIoU = per class intersection over union, bIoU = boundary intersection over union, DCF = Dice coefficient, and CD = Chamfer distance.



Conclusions

- VFS-Net demonstrates that a dual vertex- and face-based deep learning approach can effectively classify and segment dynamic 3D anatomical models while preserving both local and global geometric features.
- Despite limitations, such as class imbalances, small sample sizes, and anatomical similarity between fine structures, the pipeline establishes a scalable baseline for hierarchical segmentation of complex anatomical regions.
- Future work will focus on validating VFS-Net against MRI-based approaches, such as FreeSurfer, by integrating multimodal data to create a fully automated pipeline for postmortem (Figure 2).

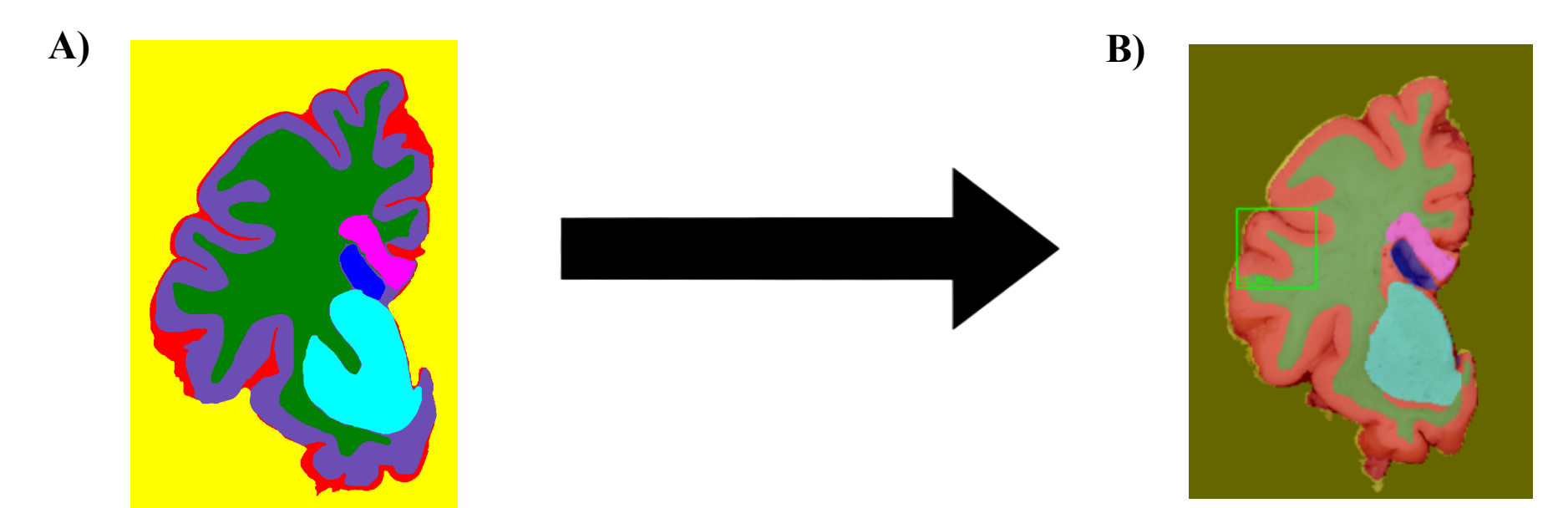


Figure 2: Representative examples of: A) manually segmented 2D brain slices and B) model-predicted segmentation outputs generated from corresponding 2D slices.

References and Contact

<https://doi.org/10.1080/20961790.2017.1330738>
<https://doi.org/10.1016/j.xpro.2024.103246>
<https://doi.org/10.1038/s41598-020-69163>
<https://doi.org/10.36227/techrxiv.177273711.10008818/v1>



Funding Disclosure: This work is supported by funding from the National Institute on Aging (P30-AG066546; R01-AG070214), Texas Alzheimer’s Research & Care Consortium, Zachry Endowment for Alzheimer Research, Reed Precision Medicine Center, and the J.M.R. Barker Foundation.

Figure 1: Schematic overview of preprocessing, manual segmentation, and predictive modeling workflow to generate classification and segmentation outputs from postmortem human brain models.