Applying Deep Learning Methods for Estimating the Volume of Pathological Regions in AD Brain Tissue

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Introduction

Brain substructure volumes are valuable biomarkers for tracking Alzheimer's Disease (AD) progression and aiding diagnosis. Traditional manual MRI annotation is slow and inconsistent. AI-based semantic segmentation offers improved accuracy, speed, and reliability for structural analysis and volumetric assessment. However, current models are limited by the number of structures they can identify, and lesion volume data for AD patients is scarce. In this study, we attempt to develop a deep learning model to segment all gray matter structures on T1-weighted MRIs of AD patients, calculate the volumes of all brain regions, and compare the data between AD patients and age-matched healthy controls.

Hypothesis

We hypothesize that Umamba can be utilized for AI model development to segment all brain regions and identify potential features in T1-weighted MRIs.

Methods

A pre-trained model developed by the research group was applied for this study (figure 1). The proposed AI model, Umamba-Bot, has been shown to achieve superior performance compared to other popular models. From the ADNI database, 134 age-matched elderly Cognitively Normal(CN) and 112 AD patients were selected. Using the trained model, the volumes of all 122 brain regions were calculated and analyzed statistically.

Results

The workflow and a representative 3D reconstructed segmentation mask are shown in Figure 1. Brain sub-structure volume calculations were performed, and the resultant volumes of normal controls and AD patients were compared. The volumes and volume changes of sixteen brain substructures were shown in Table 1, all of them consistent with those reported in existing literature, reinforcing the reliability of the segmentation outputs.

Conclusion

We successfully segmented gray matter regions and accurately calculated the volumes of all brain substructures. Comparisons with age-matched normal controls identified abnormal brain regions in AD patients, consistent with findings in the existing literature. This demonstrates the potential of the proposed approach for clinical applications, including feature extraction, morphological analysis, and as a foundation for downstream diagnostic tools.

Figure(s)

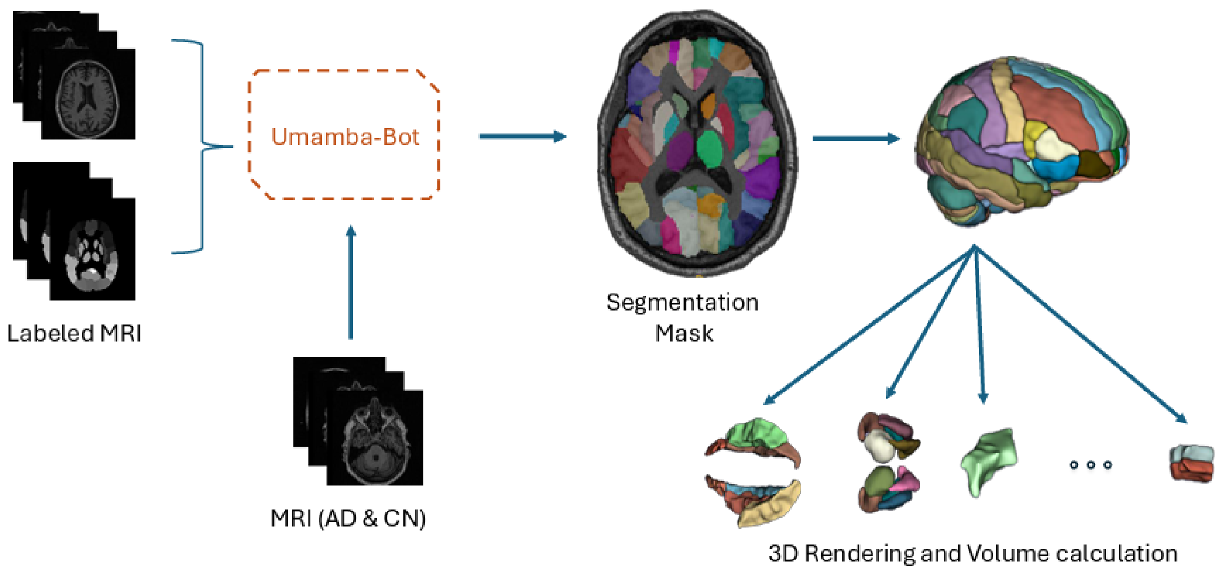

Figure 1. Workflow of the Umamba-Bot model for brain MRI segmentation and analysis. Labeled MRI data and MRI scans from AD and control groups are input into the trained Umamba-Bot deep learning model. The model generates segmentation masks for gray matter regions, which are subsequently used for 3D rendering and volumetric calculations. The outputs include detailed 3D reconstructions of brain substructures and volume estimations, enabling structural analysis.

Brain Volumes (ml)-1

Group	Olfactory_L	Amygdala_L	Amygdala_R	Angular_L	Angular_R	Caudate_L	Caudate_R	Temporal_Mid_L
AD	1.51 ± 0.35	0.98 ± 0.24	1.14 ± 0.27	7.61 ± 1.94	10.01 ± 2.22	4.07 ± 1.04	4.28 ± 1.04	20.50 ± 4.65
CN	1.41 ± 0.33	1.11 ± 0.23	1.26 ± 0.26	8.24 ± 2.06	10.61 ± 2.50	3.73 ± 0.86	3.97 ± 0.89	22.23 ± 4.73
P-Value	0.0337	0.0001	0.0005	0.0141	0.0475	0.0069	0.0144	0.0042

Brain Volumes (ml)-2

Group	Temporal_Mid_R	Temporal_Pole_Mid_L	Temporal_Pole_Mid_R	Temporal_IL	Temporal_Inf_R	Cerebellum_Crus1_L	Cerebellum_Crus1_R	ParaHippocampal_L
AD	22.80 ± 5.04	4.22 ± 1.26	5.49 ± 1.44	13.98 ± 3.23	16.26 ± 3.73	2.42 ± 0.61	2.41 ± 0.61	2.85 ± 0.60
CN	24.21 ± 5.10	4.61 ± 1.15	6.06 ± 1.37	15.00 ± 3.12	17.29 ± 3.49	2.65 ± 0.59	2.65 ± 0.60	3.03 ± 0.62
P-Value	0.0299	0.0133	0.0019	0.0132	0.0273	0.0021	0.0024	0.0246

Table 1. Comparison of brain volumes (ml) between Alzheimer's Disease (AD) patients and cognitively normal (CN) controls. P-values<0.05(Welch's t-test) indicate the significance of volume differences between the two groups.

Keywords

Applications; Artificial Intelligence/Machine Learning; Imaging Research