

Figure S1 The Loss and Pseudo Dice Curves. The loss curves and Pseudo Dice curves for all models during training. The nnU-Net model recommends using 1000 epochs, and following this recommendation, satisfactory performance was achieved. As shown in the figure, the loss curves for all models tend to converge around 1000 epochs. Pseudo Dice is an approximate metric used during training to evaluate model performance quickly. It calculates a global Dice score by randomly sampling patches from the validation set, assuming that all sampled patches originate from the same overall volume and aggregating true positives, false positives, and false negatives. This metric is used to monitor the training trend of the model. While it provides rapid feedback on the model's state, its results may deviate from the Dice score obtained through complete validation since it is based only on partial data. 2D: Two Dimensional; 3D: Three Dimensional.

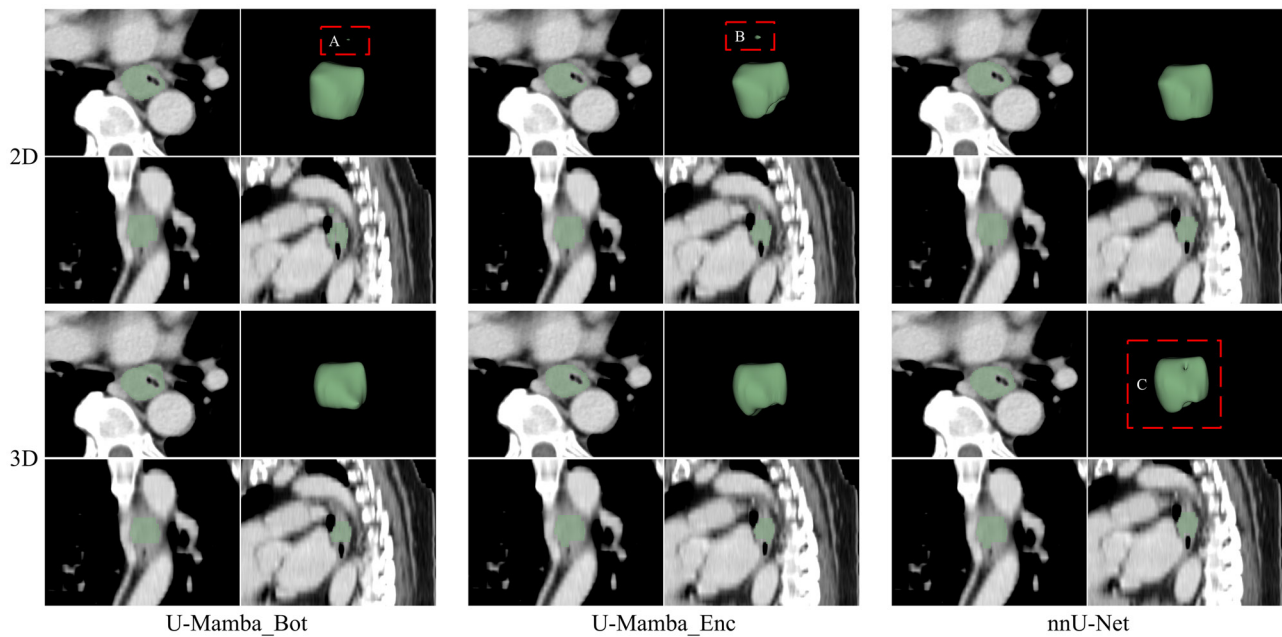


Figure S2 Comparison of Segmentation Results from 2 nnU-Net Models and 4 U-Mamba Models. The figure compares the segmentation results of six models: 2D and 3D versions of nnU-Net and U-Mamba models. A, B: Minor segmentation errors are observed in the U-Mamba 2D models. C: The nnU-Net 3D model demonstrates more detailed segmentation compared to the nnU-Net 2D model. 2D: Two Dimensional; 3D: Three Dimensional

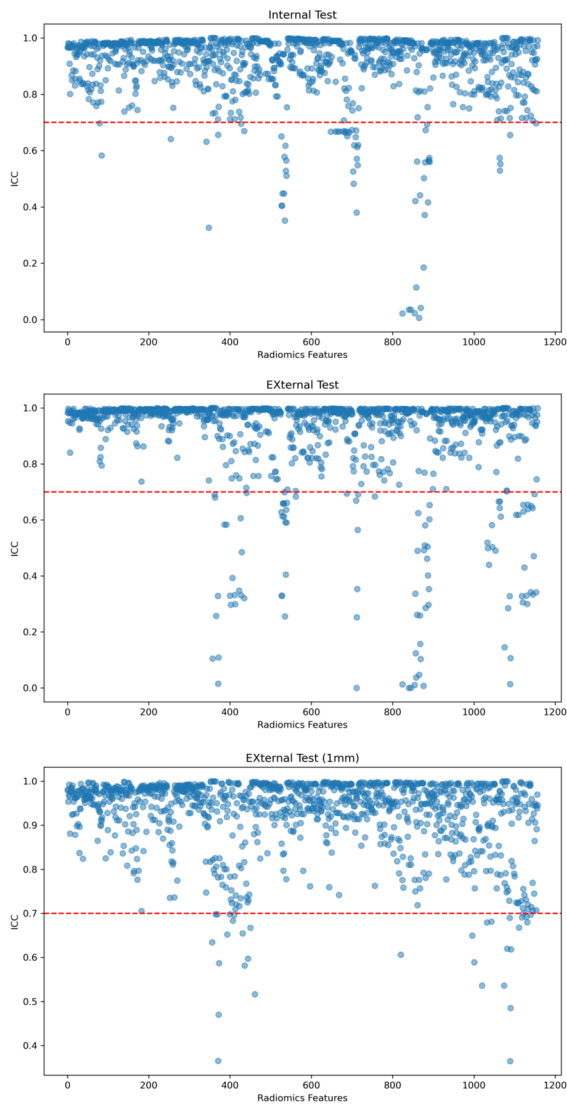


Figure S3 ICC scatter plot of radiomics features extracted based on nnU-Net and U-mamba model segmentation results. The red dotted line represents ICC=0.70. ICC: Intra-class Correlation Coefficient.

Table S1 Detailed parameter settings for radiomic features extracted by PyRadiomics

Parameter	Settings
Image Type	
Original	
LoG	Sigma: [1.0, 2.0, 3.0, 4.0]
Wavelet	
Feature Class	Shape; First-order; GLCM; GLRLM; GLSZM; GLDM
Setting	
Normalize	true
Normalize Scale	100
Resampling	
Interpolator	'sitkBSpline'
Resampled pixel Spacing:	[1, 1, 1]
Image discretization	
Bin width:	5
First order specific settings	
Voxel array shift	200

Blank means the Pyradiomics default parameters are used. LoG: Laplacian of Gaussian filter; GLCM: gray level co-occurrence matrix; GLSZM: gray level size zone matrix; GLRLM: gray level run length matrix; NGTDM: neighborhood gray tone difference matrix (); GLDM: gray level dependence matrix.