

Automatic Residual Meningioma Segmentation using Deep Learning: An Exploratory Approach in Artificial Intelligence

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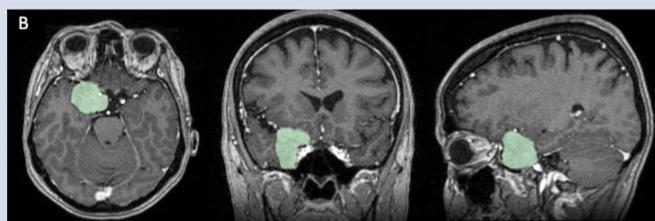
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Introduction

Accurate automated segmentation of residual meningiomas could reduce the burden of postoperative monitoring and provide precise volumetric measurements.

While convolutional neural networks such as nnU-Net can accurately segment large lesions, cases involving small lesions adjacent to iso-intense structures - as is often the case with residual disease - remains a significant challenge.

This study represents the first artificial intelligence based attempt of meningioma remnant segmentation.



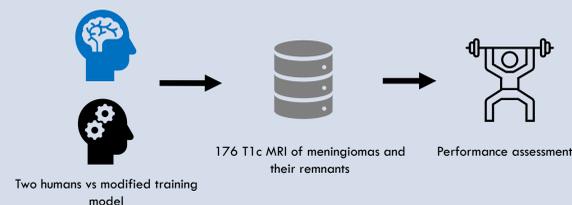
Manual meningioma segmentation.

Materials & Methods

A total of 176 T1 C+ MRIs monitoring meningiomas and their subsequent remnants were segmented by two independent observers and tested against the automated model.

A modified nnU-Net model comprising of an ensemble of a Tversky-modified 2D model, and a baseline 3D model were used. The Tversky-modified 2D component aimed to address any class imbalance and improve recognition of small lesions, while the 3D component aimed to provide volumetric awareness.

Model performance was evaluated against the observers through volumetric error, relative and absolute errors, and the Dice Similarity Coefficient.

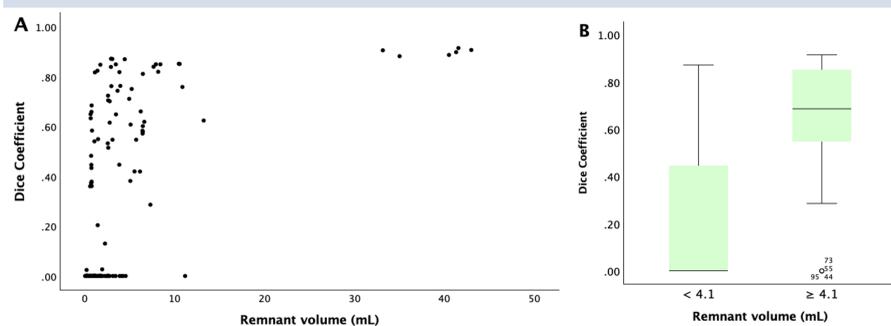


Results

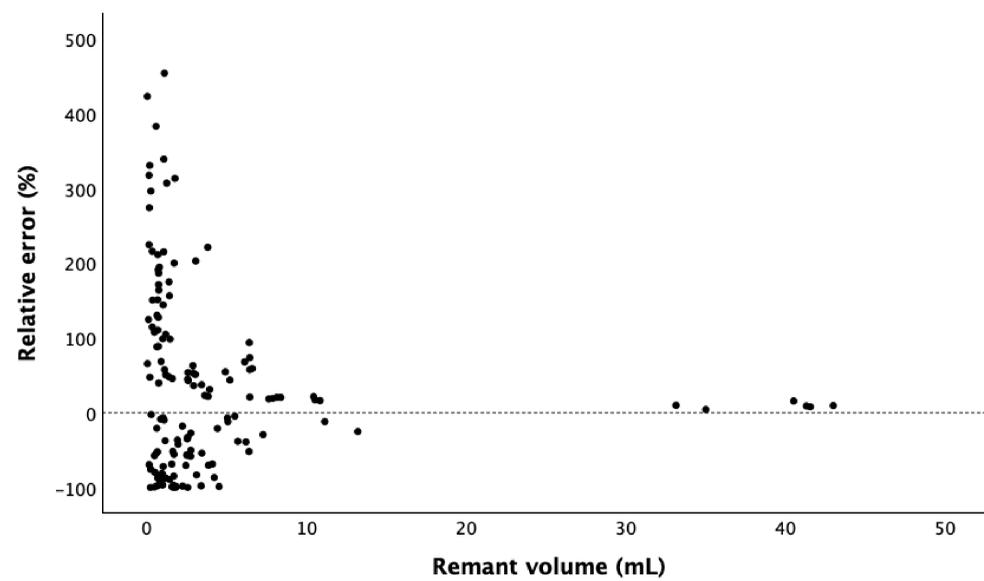
Segmentations were performed on 32 MRI of meningiomas preoperatively and 144 MRI of their respective remnants over time. The model significantly underperformed on residual disease when compared to preoperative tumors.

	Meningiomas	Remnants	p-value
Mean relative error (%)	32.1 ± 65.9	108.4 ± 136.8	0.006
Dice Coefficient	0.73 ± 0.30	0.31 ± 0.35	< 0.001

Relative error on remnants decreased as volume increased. Dice Coefficient was significantly higher in remnants with volumes above the sample mean of 4.1 cm³ (p < 0.001).



Remnants adjacent to iso-intense structures, such as in the sphenoid wing and tuberculum, showed lower Dice Coefficients than falcine or posterior fossa remnants, although no direct effect of location was measured.



Model relative error against mean observer volume

Conclusions

Our novel deep learning model displayed significant underperformance in the segmentation of residual meningiomas

Despite replicating clinically relevant performance in large tumors preoperatively, small and complex residual lesions continue to pose a significant challenge.

Future integration of additional MRI sequences may help mitigate these limitations.

Isensee, F., Jaeger, P. F., Kohl, S. A., Petersen, J., & Maier-Hein, K. H. (2021). nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation. *Nature methods*, 18(2), 203-211.

Yeung, M., Rundo, L., Nan, Y., Sala, E. (2022). Calibrating the Dice Loss to Handle Neural Network Overconfidence for Biomedical Image Segmentation. *Journal of Digital Imaging*.

Abraham, N., & Khan, N. M. (2019). A novel focal Tversky loss function with improved attention U-Net for lesion segmentation. *Proceedings of the IEEE International Symposium on Biomedical Imaging (ISBI)*. arXiv: <https://doi.org/10.48550/arXiv.1810.07842>

Bouget, D., Pedersen, A., Hosainey, S. A. M., Solheim, O., & Reinertsen, I. (2023). Meningioma segmentation in T1-weighted MRI leveraging global context and attention mechanisms. *Frontiers in Radiology*, 3, 1116374. <https://doi.org/10.3389/fradi.2023.1116374>