

BRAIN TUMOUR SEGMENTATION USING MULTIMODAL NEUROIMAGING TECHNIQUES: A DEEP CONVOLUTIONAL NEURAL NETWORK APPROACH

Malvika Ganesh Iyer¹, Ranganayaki Sathyanarayanan¹, Jijoe John Vithayathil², Rimjihim Agrawal¹, Saurabh Jain^{1*}

¹BrainSight Tech Pvt Ltd, Bengaluru, Karnataka,

²Amala Hospital, Thrissur, Kerala.

(* Corresponding Author)



INTRODUCTION

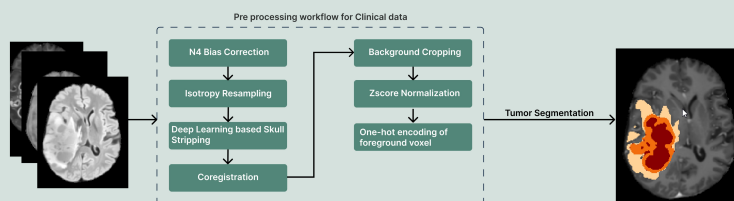
Glioma is the most prevalent malignant primary brain tumour, and more than 50% of these tumours are grade IV glioblastomas. This calls for an early detection and segmentation to decide treatment/therapy. Various techniques for forecasting and segmenting gliomas have been developed, which have following limitations:

- Requirement of specialised assistance
- Lengthy run-time
- Selection of appropriate feature extractor

We propose a convolutional neural network-based method for segmenting gliomas from multimodal structural magnetic resonance data in order to get over these challenges (T1w, FLAIR and Post contrast T1w).

METHODOLOGY

This study made use of the mpMRI Brain Tumour Segmentation (BRATS 2021) dataset. Three classes—Enhancing Tumour, Peritumoral Edematous Tissue, and Necrotic Tumour Core—were included in the scan annotation for each image. In order to create the tumour segmentation masks, our method was created by training deep neural networks utilising just three modalities: T1w, FLAIR, and Post contrast T1w.



RESULTS

Using 1251 mpMRI images for training and validation, we were able to attain a mean dice score coefficient (DSC) of 0.89 in this study. We have validated the model algorithmically by separating data into training and validation sets. Additionally, we have also generated tumor masks manually for data never seen by model and compared the results to those generated by our algorithm. This yielded a mean DSC of 0.88 and a tumour core DSC of 0.92.

Table 1: Validation set results. Predictions made on Brats21 validation set and expert verified manually annotated set of 50 scans

Region	Radiologist Validated Set			Brats21 Validation set		
	Enhancing Tumor(ET)	Tumor Core(TC)	Whole Tumor(WT)	Enhancing Tumor(ET)	Tumor Core(TC)	Whole Tumor(WT)
Dice Score	0.84	0.92	0.9022	0.872	0.9032	0.92
Mean Dice Score	0.8875			0.8987		

Table 2: Average Dice Scores of Enhancing Tumor(ET), Tumor Core(TC) and Whole Tumor(WT) region classes for different models.

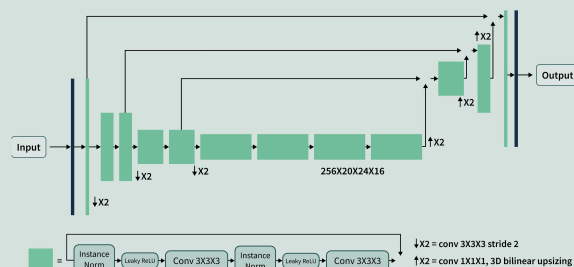
Model	U-net	UNETR	SegResNetVAE	SegResNet_3Modal
Mean Dice	0.913	0.9031	0.9118	0.8987

CONCLUSIONS

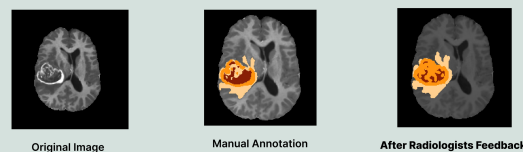
1. Uses only 3 modalities with similar Dice score as achieved using 4 by previous methods.
 2. Reliability: We tested our model on 50 manually annotated datasets, this was not a part of training dataset and we achieved 0.88 dice score.
 3. Reproducibility: We have used data versioning to avoid data leakage, set randomizer seed value during training and containerised the inference code to remove environment dependencies for better reproducibility
- Implication on lower grade: Training data had low grade glioma scans, however extensive testing is not done to understand the implication of LGG.

OBJECTIVE

To develop a deep learning based efficient tumour segmentation model designed for clinical use by reducing the footprint on data economy



Manual Annotation Process



Original Image

Manual Annotation

After Radiologists Feedback

IMPLICATIONS

This study demonstrates that deep convolutional neural networks can accurately and quickly separate distinct subregions of a tumour, which has important therapeutic implications in brain tumour detection, prognosis, therapy, and presurgical planning. Additionally, it can be useful in understanding how tumours affect tractography and network mapping. Better segmentation will give more accurate edema correction, that will aid in more accurate tractography. Similarly, more accurate segmentation of the tumour will result in better classification on tumour tissue and brain tissue, preventing misclassification of tumour tissue as healthy and vice versa. In the long run, this could help in understanding and possibly predicting network shift and possible compensatory effects caused in the brain due to tumour. Utilizing these segmentation masks to account for a general shift in the brain's tissues and improve the precision in capturing functions of the brains, in turn making a better Eloquent cortex mapping.

References

- Isensee, F., Jaeger, P. F., Full, P. M., Vollmuth, P., & Maier-Hein, K. H. (2020). NnU-Net for Brain Tumor Segmentation (arXiv:2011.00848). arXiv. <http://arxiv.org/abs/2011.00848>
- Futrega, M., Milesi, A., Marcinkiewicz, M., & Ribalta, P. (2021). Optimized U-Net for Brain Tumor Segmentation (arXiv:2110.03352). arXiv. <http://arxiv.org/abs/2110.03352>
- NVIDIA DALI Documentation—NVIDIA DALI 1.18.0 documentation. (n.d.). Retrieved October 31, 2022, from <https://docs.nvidia.com/deeplearning/dali/user-guide/docs/>
- Menze, B. H., Jakab, A., Bauer, S., Kalpathy-Cramer, J., Farahani, K., Kirby, J., Burren, Y., Porz, N., Slotboom, J., Wiest, R., Lanczi, L., Gerstner, E., Weber, M.-A., Arbel, T., Avants, B. B., Ayache, N., Buendia, P., Collins, D. L., Cordier, N., ... Van Leemput, K. (2015). The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS). IEEE Transactions on Medical Imaging, 34(10), 1993–2024. <https://doi.org/10.1109/TMI.2014.2377694>
- Official BrATS site: <http://braintumorsegmentation.org/>
- Dataset for training the deep learning model was taken from BrATS21 competition. It can be downloaded from below link -
- <https://www.kaggle.com/datasets/dschettler8845/brats-2021-task1>