Automated Glioblastoma Segmentation relying on a shorter imaging protocol

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Abstract

INTRODUCTION: Glioblastomas (GBM) are the most common and aggressive primary brain tumours, with a two-year life expectancy of only 20%[1]. Image segmentation is essential for precise therapy planning and progression monitoring. The current gold standard is manual segmentation performed by expert neuroradiologists, but this is a time-consuming task that suffers from inter-observer variability[2]. Thus, reliable automated methods can greatly increase the quality and efficiency of patient care. Most proposed supervised learning segmentation methods have been trained using four modalities - T1, T2, T2 FLAIR and T1CE scans; this may be unfeasible in clinical practice as it requires high-performance computing facilities and affects the minimum duration of the imaging protocol. This work aimed to evaluate the feasibility of reducing the number of input modalities to only two - FLAIR and T1CE - to train a semantic segmentation method capable of generating a classification with comparable accuracy to models trained with the four modalities.

METHODS: The BraTS 2021 challenge dataset was divided into subsets of 60%, 20% and 20% for training, validation and testing, respectively. We tested the performance of two network architectures for brain tumour segmentation implemented in MONAI[3]: 1) a ResNet-based architecture[4]; 2) Swin UNEt TRansfomers[5] (Swin UNETR). The model was trained using: i) all four modalities; and ii) only FLAIR and T1CE. In both cases, three nested subregions were considered: Tumour Core (TC), Enhancing Tumour (ET) and the Whole Tumour (WT), including edema. We considered an ensemble model that combines the WT and TC grading from the ResNet architecture and the ET classification from the Swin UNETR, due to the higher accuracy of the Swin transformers in classifying smaller regions[6] – Figure 1a. Model accuracy was assessed using Dice coefficients of each region with the manual segmentation labels in the BraTS dataset.

RESULTS & DISCUSSION: The segmentation accuracy when training with FLAIR and T1CE images was consistent with the performance when training with four modalities. The manual segmentation can be visually compared to the two outputs obtained for a representative subject in Figure 1b. This suggests that the excluded images and the consequent longer training time did not contribute significantly to the accuracy of the model, strongly implying that this training approach may be beneficial for clinical applications, as it would result in reduced costs due to shorter scanner times, lower computational requirements and increased patient throughput, without compromising segmentation accuracy.

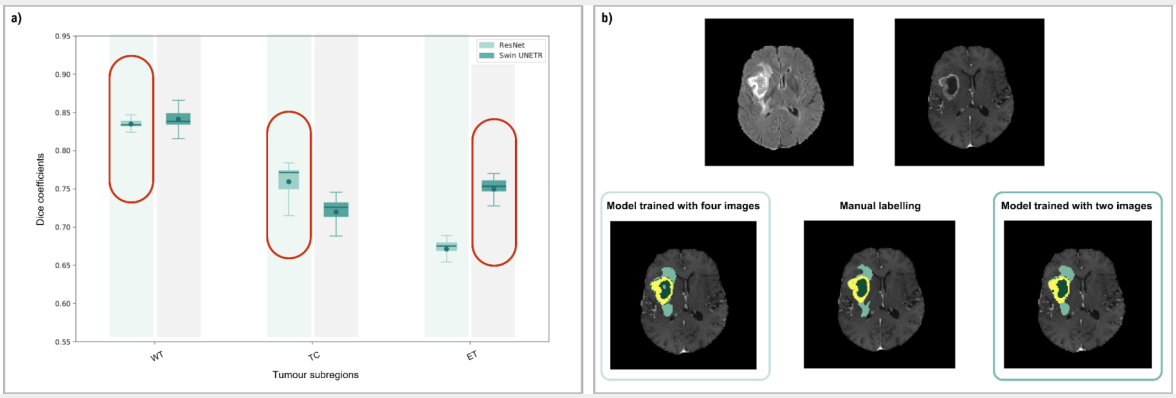

Figure 1: a) Dice score distributions across the test dataset for each architecture and tissue label.; b) Representative slice from the original (left) FLAIR and (right) T1CE scans of a subject, and comparison between the outputs from the two ensemble models and the respective manual segmentation included in the BraTS2021 dataset. The lighter green, yellow and darker green colours correspond to the WT, ET and TC regions, respectively.

References

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