Development and Implementation of an Automated Pipeline for Multi-Compartmental Segmentation and Extraction of Perfusion and Diffusion MRI Parameters in Glioblastomas

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Purpose

- Glioblastomas are aggressive brain tumors with irregular morphology on MRI.
- Detecting changes in tumor sub-compartment volumes, perfusion, and diffusion can reveal tumor biology, predict clinical outcomes, and guide treatment.
- Yet, manual segmentation is labor-intensive and variable, underscoring the need for automated reproducible pipelines.
- We developed and implemented an automated pipeline for multi-compartmental segmentation and quantitative physiologic MRI parameter extraction, enabling longitudinal correlation with clinical outcomes.

Results

- The pipeline outputs coregistered, isotropically resampled anatomic, diffusion, and perfusion sequences (Figure 2). FLAIR and postcontrast T1 images are displayed without and with overlaid segmentation masks and descriptive statistics for sub-compartment volumes. ADC and rCBV maps are also displayed without and with overlaid masks and statistics.

Discussion

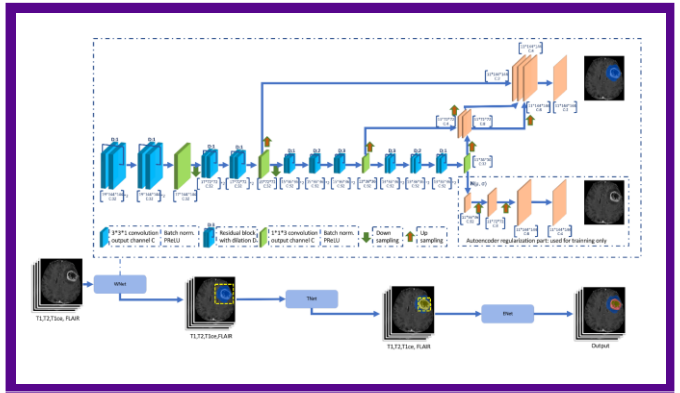
- The proposed automated end-to-end pipeline aims to serve as a proof of concept for integrating deep learning with advanced imaging software to enhance the efficiency and consistency of glioblastoma volumetric segmentation and quantitative parameter extraction on MRI.
- By enabling automated comprehensive analysis of perfusion and diffusion metrics across tumor compartments, utilizing segmented volumes rather than manually sampled regions of interest, this tool has the potential to support the validation of imaging biomarkers and contribute to personalized treatment approaches and prognostic assessments in glioblastoma management.
- Future work will involve validating the pipeline with real-world data and exploring its integration into clinical workflows. Additionally, we plan to extend the pipeline's capabilities to include other advanced imaging modalities and tumor types, thereby broadening its applicability. Ultimately, this pipeline aims to contribute to improved patient outcomes by bridging the gap between advanced neuroimaging research and clinical practice.

References

1. Lotan E, Zhang B, Dogra S, Wang WD, Carbone D, Fatterpekar G, et al. Development and Practical Implementation of a Deep Learning-Based Pipeline for Automated Pre- and Postoperative Glioma Segmentation. AJNR Am J Neuroradiol. 2022;43(1):24-32.
2. Wang G, Li W, Ourselin S, et al. Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks. Lect. Notes Comput. Sci. 2018;10670 LNCS:178-190.
3. Myronenko A. 3D mri brain tumor segmentation using autoencoder regularization. BrainLes. 2019;11384: 254–266.

Methods

- We developed an automated end-to-end pipeline to process preoperative and postoperative MRI scans of glioblastomas.
- The pipeline integrates a deep learning segmentation algorithm based on autoencoder regularization and a cascaded convolutional neural network with Olea Sphere software (Olea Medical, France).
- The previously validated deep learning model segments glioblastomas into enhancing, nonenhancing, and peritumoral T2 signal abnormality/edema sub-compartments (1).
- Olea Sphere processes dynamic susceptibility contrast (DSC) perfusion and diffusion-weighted imaging (DWI) sequences to generate quantitative parameter maps of leakage-corrected relative cerebral blood volume (rCBV) and apparent diffusion coefficient (ADC). Anatomic sequences (pre- and post-contrast T1, T2, and FLAIR) and these quantitative parameter maps are automatically transferred to an image processing server that runs the segmentation algorithm and extracts rCBV and ADC statistics from each sub-compartment. Descriptive statistics include histogram analysis of the perfusion and diffusion parameters.

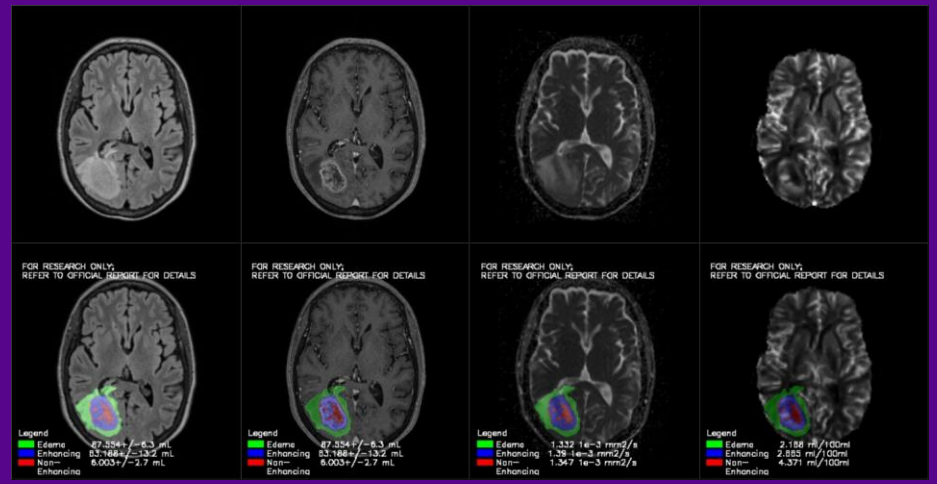


Network architecture with triple cascaded anisotropic convolutional networks (2) and autoencoder regularization (3). Three networks hierarchically segment whole tumor (WNet), tumor core (TNet) and enhancing tumor (ENet). Each network has dilated ResNet-like blocks with GroupNorm normalization, multi-scale fusion, down- and up-sampling. ENet has one down-sampling layer. Segmentation decoder output has 2 channels followed by sigmoid. Autoencoder regularization branch reconstructs the input image into itself and is used only during training to regularize the shared encoder.

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Our automated end-to-end pipeline for glioblastoma segmentation and quantitative MRI parameter extraction sends overlaid images to PACS



Example pipeline output on PACS. FLAIR, postcontrast T1, ADC map, and rCBV map (left to right) without (top row) and with overlaid segmentation masks and calculated statistics of the sub-compartment volumes and their respective averaged ADC and rCBV values (bottom row).