Glioblastoma Segmentation Via Convolutional Neural Networks

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I. Introduction

Glioblastoma multiforme is the most dangerous form of brain cancer, due to the virulence of its cells. Once detected, the median patient survival time is 18 months [1]. GBM is hard to detect early due to multiple kinds of complications: GBM could arise on its own, or it could the result of the evolution of a more generic tumor [2].

GBM can be identified in CT and MRI scans. However, it is extremely time consuming for radiologists to manually segment the glioma core, the ring of necrotic tissue around the tumor, and the shape and size of the peritumoral edema as they analyze FLAIR, T1, post-contrast weighted T1, and T2 MRI images from patients. All of this information is then used by surgeons to do a resection [3].

Recently, the use of CNNs has been shown to have effectiveness in applications for medical segmentation. Thus, we built an application involving a Convolutional Neural Network (CNN) to aid in the process of automatic and efficient GBM segmentation. In the following sections, we describe our Methods, Results, and a Discussion of the Results with next possible steps.

II. Methods

For this project, we designed a Convolutional Neural Network to produce a segmentation of the brain tumor. This CNN operates by taking as input a 33x33 patch (or series of patches) of a 2D MRI image slice from a 3D MRI image. Each patch has 4 channels, one for each of T1, T2, FLAIR, and T1 post-contrast weighted MRIs. This input is then passed through multiple layers. Our CNN's architecture includes 2 convolutional layers, 2 max pooling layers, and a fully connected layer at the end. A full diagram of our network can be seen in Figure 1 in the Appendix.

Our model is trained and validated using the BraTS 2018 dataset. BraTS is a multimodal brain tumor segmentation challenge that provides MRI data from patients with gliomas [4]. From this dataset, we are using data from 220 patients with High Grade Gliomas. 190 of these patients' data are used to train the model, and the remaining 30 are used to validate and evaluate the model. Each patient has data from the 4 different MRI pulse sequences mentioned in the previous paragraph. This data is provided pre-processed, meaning it is skull-stripped and set onto the same coordinate system. In addition, ground truth data is provided. This dataset recognizes 4 different classes in its ground truth: healthy tissue/background, Gadolinium-enhancing tumor, the peritumoral edema and the non-enhancing tumor core. The non-enhancing tumor core is the center mass of the tumor. The Gadolinium-enhancing tumor is a section that increases in intensity in an MRI after a gadolinium-based material is injected [5]. Finally, the peritumoral edema is an accumulation of fluid that is radially centered around a tumor [6].

To train the model, we randomly sample 33x33 patches surrounding pixels of each class. We ensure that we have a roughly equal amount of data from each class in order to properly train the model. In total, over 50,000 patches of data were used to train our model.

Once we train the model, we can pass in 33x33 patches to it so that it can guess the class of the center pixel. We can use this process to guess the class of every single pixel in a brain image in order to produce a segmentation of the tumor. Once we have this segmentation data, we can generate a PNG image with each tumor class highlighted a certain color.

III. Results

We had to iteratively implement different CNN architectures to derive our present results and each CNN along the way yielded different kinds of segmentations with differing quirks (refer to Figure 3 of the Appendix to see some previous segmentations). For example, some CNN models featured segmentation outside of brain tissue, or even segmented the edge of the brain as a tumor mass due to the contrast between the background and the edge of the brain.

Our current model has a lot of false positives, but specifically for what it regards as part of the peritumoral edema. This could be due to the fact that the peritumoral edema is not a mass, like the tumor, but rather an accumulation of fluid that has varying shape over successive z slices of the brain and is thus harder to segment.

The current model achieves a validation accuracy of 58%, using trained data that is composed of a balanced distribution of classes (tumor, GD-enhancing, peritumoral edema, healthy tissue). In a more practical segmentation, the class types would not be equally distributed, and we could thus achieve an accuracy of near 90%. This discrepancy in accuracies stems from that fact that most of the image is healthy tissue

or background, which the model classifies well. Another factor that contributes to the lower validation accuracy is that the model often misclassifies certain components of the tumor as another class of the tumor. This especially happens on boundaries between sections. For example, the result images in Figure 2 of the Appendix show that the section segmented as gadolinium-enhancing tumor encroaches into what the ground truth defines as the territory of the tumor core. This distinction between tumor classes and their boundaries is important, but not as critical as the distinction between the tumor and healthy tissue.

IV. Discussion

Our model does a decent job of segmenting the non-enhancing tumor core and the gadolinium-enhancing tumor. While our model can generally discern the location of a high grade glioma in the brain, the model is nowhere near perfect when it comes to segmentation boundaries and false positives, as shown in the Results section. In a high-stakes field such as medicine, inaccuracy could add avoidable difficulty to resection. Therefore, our model is not ready to be used as a replacement to manual segmentation.

There are many methods that could be used to improve the accuracy of our model. First, a more deep, complex network would be able to determine more precise features of each class. Examples of such networks include the U-Net network [7] and a cascaded 2-pathway network [8]. Each of these architectures are able to utilize both local and global features of the data and are specifically tailored to segmentation. One flaw in our implementation is that we guess the class of each pixel in an image independently of the other pixels. By considering the classes of pixels nearby, as well as global features in the image, the accuracy of the model would increase. If the model does not know whether a pixel is a part of the peritumoral edema, for example, it would be much more likely if the nearby pixels were already classified as peritumoral edema, or as part of the main tumor. In addition, the model is less likely to produce false positives in a section of the brain that is not near the tumor.

Other possibilities include using a larger dataset. The more types of data the network is able to see, the more accurately it would be able to generally segment a new brain image in the future. These steps will require a lot of iterative development, research, computational resources, and data. However, refining this project in such ways could allow automatic brain segmentation with convolutional neural networks to replace manual segmentation in the future, thus freeing up time and resources for doctors and allowing for more effective treatment.

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Additional Refereneces

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APPENDIX

Link to GitHub Repository: https://github.com/JordanTinker/CS168Project

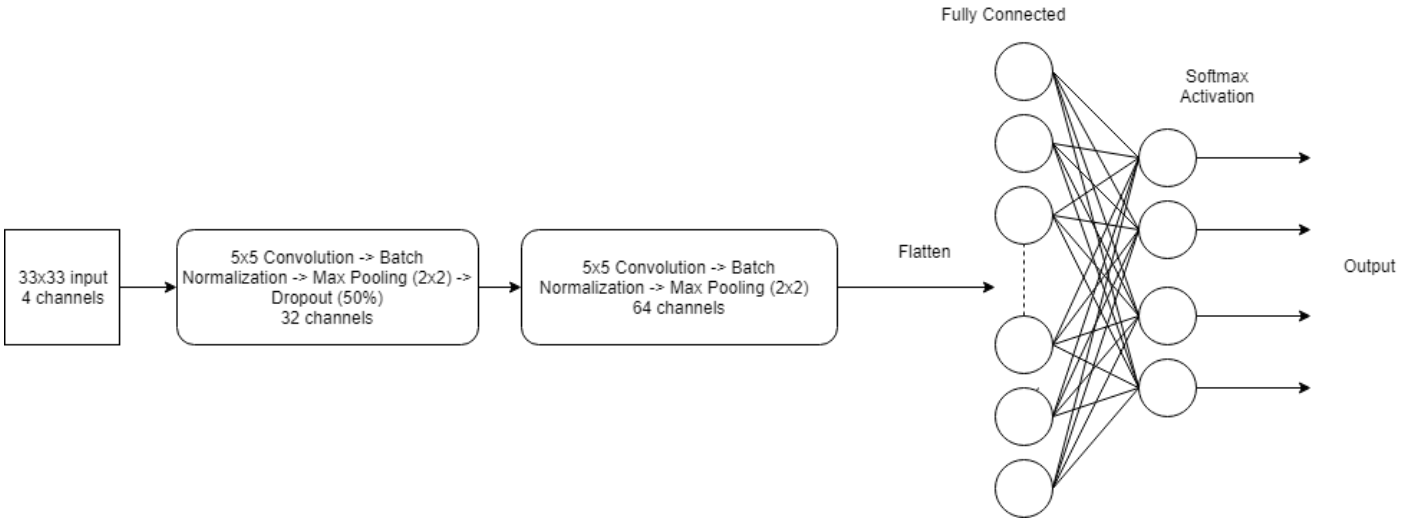

Figure 1. Diagram of our Convolutional Neural Network Architecture

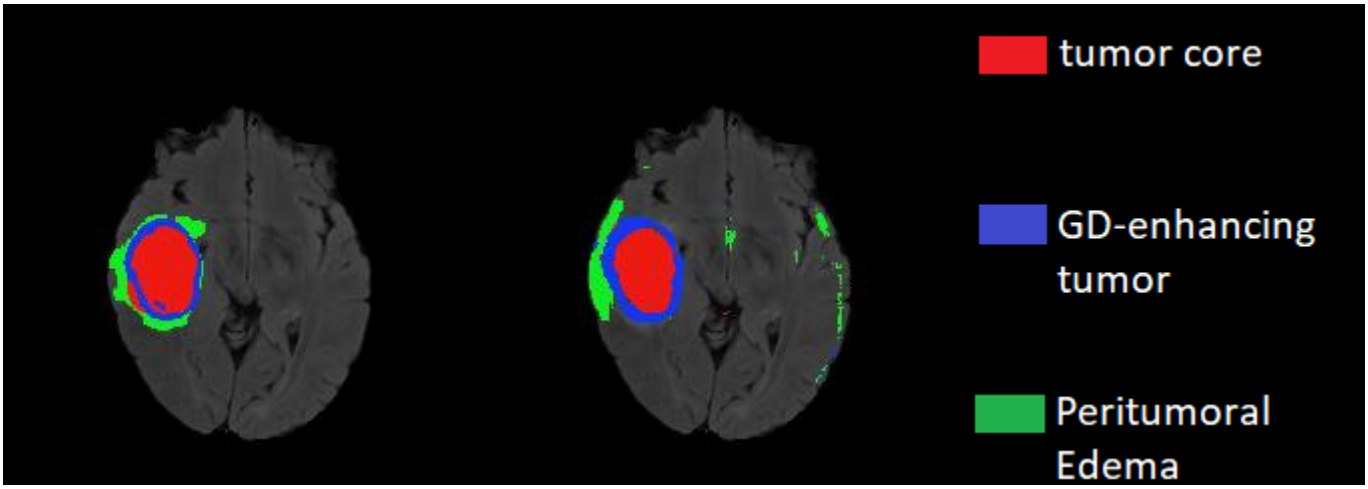

Figure 2. Result images for the project. Professional Segmentation (left) vs our project's prediction (right). For a 3D rendering of the entire segmented brain, refer to our GitHub repository (link above).

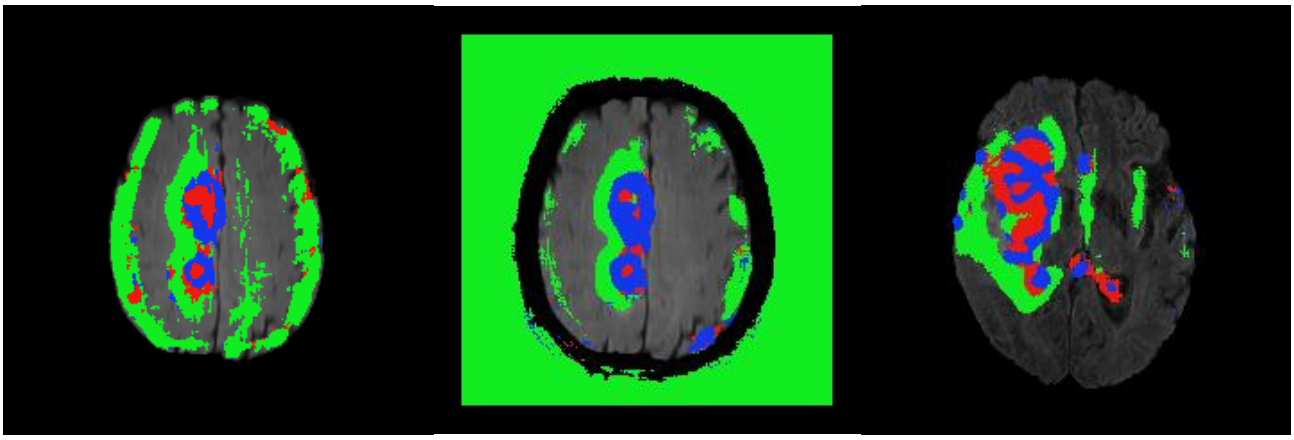

Figure 3. Iterative development results using earlier models. The left image shows the results of a simple neural network with a single fully connected layer. The middle shows a model that incorrectly classifies the background as Peritumoral Edema. The right image shows a later design closer to the final model.