
MRI Brain Tumor Segmentation with 3D U-Net

Isaac Tuckey

isaactuckey@ucf.edu

UCF Medical Image Computing, Spring 2024

1 Data

The data used for this project is a subset of the 2016 and 2017 Brain Tumour Image Segmentation (BraTS) challenge datasets found here: <https://www.med.upenn.edu/cbica/brats/>. The provided training set is 484 MRI instances each with 4 modalities. The 3D segmentation mask consists of 3 classes (GD-enhancing tumor, peritumorial edema, and necrotic, non-enhancing tumor) . These labels are manually annotated and approved by neuro-radiologists. In Figure 1 are two samples from the dataset captured along with their segmentations in the ITK-SNAP software.

Github Repository: <https://github.com/isaactuckey/brats-segmentation.git>

2 Implementation Details & Results

The dataset loading and preprocessing are done in the same manner as MONAI's tutorial. The dataset is loaded as a cross validation dataset so that it can easily be adjusted to train and evaluate on each of the five folds. The model used is a 3D U-Net with an input channel for each MRI modality and an 3 output channels for each of the three segmentation types. An Adam optimizer and cosine annealing learning rate scheduler are used. MONAI also implements the Dice metric that the model optimizes on and that is used for evaluation.

After training on the first evaluation fold for 10 epochs, the overall dice scores are shown in Table 1. A visual example of the segmentation results are included in the accompanying Python notebook. I had some difficulty calculating the Hausdorff distance over the entire validaion set, but most were in the 110-120mm range.

Such poor results are most likely attributed to the lack of training time. Some existing segementation models are trained for thousands of epochs in order to achieve 70-80% Dice Scores.

Table 1: Dice Scores

Dice	Score (%)
Overall	20.77
TC	17.79
WT	36.97
ET	7.54

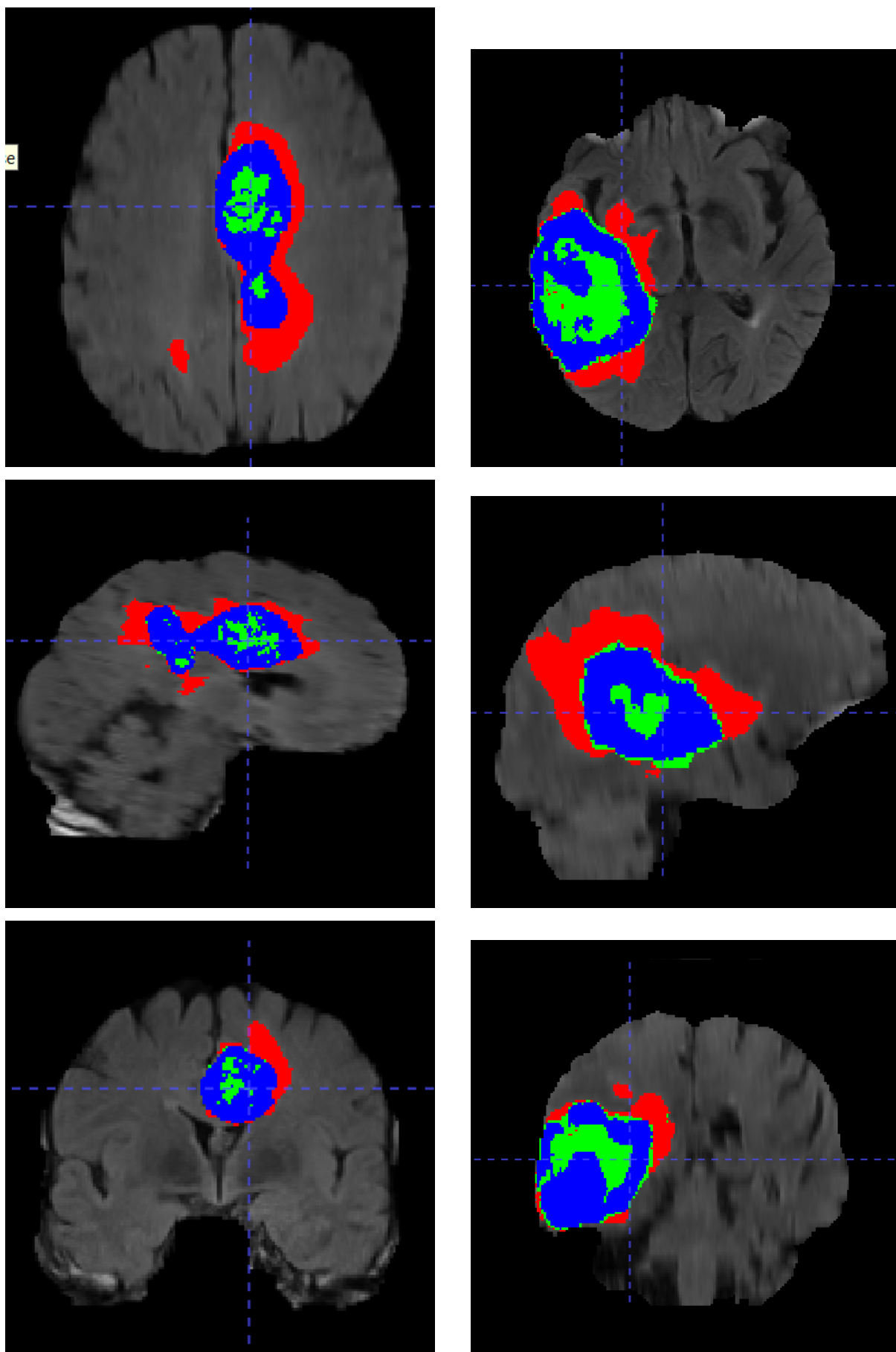


Figure 1: ITK SNAP Visualization