**Final Report – IDS 705 – Kyle Bradbury**

**Spring 2022**

**Team 10**

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***GitHub Repository: https://github.com/FR-Schwartz/IDS705\_Team10***

**1940/2500 words**

**Abstract**

*Purpose*

The purpose of our project is to use computer vision algorithms to detect a specific type of brain tumor – glioblastoma multiforme – on clinical 3D MRI data.

*Materials and Methods*

We used a dataset collected and labelled by the Radiological Society of North America (RSNA) Brain Tumor Segmentation (BraTS) Challenge 2021, which included 570 cases in the training and 219 cases. Each case represents a patient with a known glioblastoma multiforme and contains four MRI sequences that each provide different information about the anatomical situation in the brain and the tumor. A fifth dataset for each patient contains the ground truth segmentation from the RSNA.

*Results*

We were able to implement a deep learning algorithm that was successful in segmenting the enhancing tumoral rim and the affected brain tissue (edema zone) but not the necrosis zone. For this we used a …

*Conclusion*

Our computer vision project was a full/partial success in segmenting glioblastoma multiforme from clinical MRI scans.

**Abbreviations**

ASNR: American Society of Neuroradiology

BraTS: Brain Tumor Segmentation

GBM: Glioblastoma Multiforme

i.v.: intra-venous

MICCAI: Medical Image Computing and Computer Assisted Interventions

mpMRI: multi-parametric Magnetic Resonance Imaging

RSNA: Radiological Society of North America

WHO: World Health Organization

**Introduction**

The Radiological Society of North America (RSNA), the American Society of Neuroradiology (ASNR) and the Medical Image Computing and Computer Assisted Interventions (MICCAI) combined forces a few years ago to collect a well annotated and standardized set of MRI images of a specific brain tumor for the purposes of being able to use it for machine learning tasks (1).

As a result, the RSNA-ASNR-MICCAI Brain Tumor Segmentation (BraTS) 2021 Challenge makes publicly available the largest and most diverse retrospective cohort of glioma patients (an initial, smaller dataset was published as a challenge in 2020). Ample manually annotated multi-institutional routine clinically acquired mpMRI scans of glioma are used as the training, validation, and testing data for the BraTS challenge.

Specifically, the datasets used in the 2021 challenge were updated, since BraTS'20, with many more routine clinically acquired mpMRI scans from institutions that have not previously contributed to BraTS, increasing the demographic diversity of the represented patient population.

Ground truth annotations of the tumor sub-regions are created and approved by expert neuroradiologists for every subject included in the training, validation, and testing datasets to quantitatively evaluate the predicted tumor segmentations, so every dataset includes the same type of tumor with features of glioblastoma.

**Background**

Glioblastoma multiforme (GBM) is a World Health Organization (WHO) grade IV (highest/least favorable grade) brain tumor which represents one of the most lethal human cancers, with a 5-year survival rate of only 7.2% (2). The incidence of GBM increases with age and shows the highest incidence in the 75–84-year-old age group in the United States (3). The incidence is higher in men than women, as well as in Caucasians than in other ethnicities (4).

Initial diagnosis is generally made, based on MRI imaging which can depict the contrast enhancing (“active”) tumor, the necrotic tumor center (dead tumor cells, due to rapid growth without sufficient blood supply) and the edema caused by the tumor infiltration of the surrounding healthy tissue (5-7).

To do this, multiple imaging sequences are acquired before and after the patient receives intra-venous gadolinium-based contrast material. These sequences allow for the evaluation of different soft tissue properties. The two basic sequences that are acquired in virtually every MRI performed on patients are the T1- and T2-weighted sequences. T1-sequences are often called the “anatomical” sequences because they show tissues similarly to what the actual anatomy looks like. They show fluids as “black”, while the T2-sequence shows fluid as “white”. In addition, the FLAIR sequence acquired for the imaging of GBM suppresses the signal from cerebrospinal fluid, but not other fluid in the brain (e.g., from edema) and the T1-contrast enhanced sequence shows uptake of gadolinium in tumor tissue, especially when compared to the “native” (i.e. no i.v. contrast) T1-sequence (8).

The first line therapy for GBM is usually surgery, followed by radio-chemotherapy. MRI-guided surgery has been established as the method of choice for years and relies on the ability of the surgeon to distinguish the tumor tissue from healthy brain tissue and is crucial for patient outcomes (9, 10).

We segmented glioblastoma multiforme based on MRI images, which could be helpful for surgical planning, e. g. when trying to determine how close the tumor is to important areas of the motor cortex. There is a gap between imaging specialists (radiologists), who are used to seeing 2-D images in sequence and transforming them into a 3-D image in their head while “reading” a scan and surgeons (neurosurgeons), who are used to seeing and touching the actual tumor tissue but not to translating 2-D image data into the 3-D tumor they are confronted with in the operating room (11, 12).

The planning and surgical approach might benefit from better tumor segmentation, based on the pre-operative MRI scans. In addition, radiotherapy volumes could be planned in a more comprehensive manner and disease progression monitoring could be improved (13-15).

**Data**

*Imaging Data Description*

There are 570 cases in the training and 219 cases in the validation set provided by the BraTS 2021 Challenge (16).

All BraTS multi-parametric magnetic resonance imaging (mpMRI) scans were available as NIfTI files (.nii.gz) and describe a) native (T1 – shows brain anatomy very similar to what an autopsy would look like), b) post-contrast T1-weighted (T1Gd – gadolinium-based contrast is taken up by metabolically active tissue; this sequence is compared directly with the native T1 sequence to find active tumor tissue), c) T2-weighted (T2 – shows fluid in tissues better than T1), and d) T2 Fluid Attenuated Inversion Recovery (T2-FLAIR – used primarily to find the edema zone at the edge of the tumor) volumes (17). They were acquired with different clinical protocols and various scanners from multiple data contributing institutions but cleaned for the competition to all be in the dame format (e.g., slice thickness, image matrix, de-identified).

All the imaging datasets have been annotated manually, by one to four raters, following the same annotation protocol, and their annotations were approved by experienced neuro-radiologists. Annotations comprise the gadolinium-enhancing tumor (ET — **label 4** – active tumor tissue that takes up blood and thus gadolinium-based contrast), the peritumoral edematous/invaded tissue (ED — **label 2** – brain tissue surrounding the tumor that is affected by it), and the necrotic tumor core (NCR — **label 1** – dead tumor cells). The ground truth data were created after their pre-processing, i.e., co-registered to the same anatomical template, interpolated to the same resolution (1 mm3) and skull-stripped.

![Chart

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**Figure 1:** Demonstrates the visualization of our data. The T1 sequence shows anatomical detail and serves as the comparison for the ce (= contrast enhanced) sequence, which is acquired after all the other sequences post i.v. injection of gadolinium-based contrast material. The T2 and Flair sequences are more fluid weighted and show the edema surrounding the tumor well. Our labels (seg) are also shown, with label 4 (enhancing tumor) in yellow, label 2 (edema zone) in turquoise and label 1 (necrosis zone) in dark blue. All healthy brain tissue (label 0) is purple like the background.

**Methods**

We used Deep Learning Methods specialized in the class of problems known as Semantic image Segmentation (18, 19). In semantic segmentation, the goal is to classify each pixel in the input image (20, 21). We will segment each pixel in the MRI scan to be either gadolinium-enhancing tumor (ET — **label 4**), the peritumoral edematous/invaded tissue (ED — **label 2**), the necrotic tumor core (NCR — **label 1**), and any tissue not belonging to the previous three, which is unaffected brain tissue (**label 0**). The architecture of the neural network was a U-Net.

This resembles an encoder-decoder network where the first half of the network is a series of convolutional layers that decrease the size of the image after each layer while increasing the number of channels, culminating into a single dense layer composed of many channels and 1 pixel (22, 23). The second half of the network converts this dense layer back to an image of the dimension as that of the input image, but with the number of channels equal to the number of possible output classes. Thus, the final output represents the probabilities of each pixel belonging to each of the classes. Since we cannot expect the encoder-decoder mechanism to accurately form borders at the pixel-level, we add skip layer connections connecting across the “U” to guide the formation of pixel-level outputs (24-26).

We trained these models on Google-Colab to take advantage of the free GPUs. In addition, we used … . We will took advantage of the well-established deep learning framework Tensorflow (27, 28). We also used self-supervised learning techniques because our validation data did not include the segmentations that the training data had. Thus, we performed a separate split to get test data out of our training data (where we need the ground truth segmentations) and add the validation data to our training data. To accommodate the fact that we had mixed data we used … for our self-supervised learning (29-31).

We evaluated the performance of our model using the same methods as the BraTS challenge applies to the submissions that they receive which are the Dice Similarity Coefficient, and the Hausdorff distance (95%).

The Dice Similarity Coefficient is given by the formula:

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where A is the reference segmentation, Bm is the segmentation for the different models m, ∩ denotes the intersection of two sets and |⋅| is the cardinal of a set. This results in the ratio of how many voxels in Bm are correctly segmented (32).

The Hausdorff distance measures the extent to which each point of a model set (i.e., the ground truth segmentation in our case) lies near some point of an image set and vice versa. This distance can be used to determine the degree of resemblance between two objects that are superimposed on one another (33).

In addition, we submitted our segmentation to the continuing evaluation that BraTS provides and are hoping to be able to add our score from that to our report in the future. The winning entry in the 2021 challenge achieved a Dice score of ~92%, so we set that as our benchmark.

**Results**

We were able to implement a neural network based on … that performed … at segmenting the enhancing tumor tissue, … at segmenting the tumoral necrosis zone and … at segmenting the edema zone. Graphical user interface, application

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**Figure 2**: Demonstrates several slices through the brain from bottom to top of the clinically acquired sequences (T1, T2, T1+contrast and FLAIR) and the ground truth segmentation (seg) as well as four different models we trained to detect the different glioblastoma zones. The bce-argmax model partially detected the contrast enhancing tumor zone (blue) and correctly classified the healthy tissue (purple). Both the bce and the dice\_prob0 models correctly detected the healthy tissue (label 0) but the dice model detected less of the normal anatomy as abnormal. The dice-argmax model performed very well at detecting the enhancing tumor (yellow), the necrosis zone (dark blue) and the edema zone (light blue), as well as the healthy tissue (purple). It very closely matches the ground truth segmentation.

**Conclusions**

Our computer vision project was a full/partial success in segmenting glioblastoma multiforme from clinical MRI scans, achieving a DICE-score of … and a Hausdorff distance of … . This is better/slightly worse/somewhat worse than the benchmark of the competition winner from the German Cancer Research Institute. This reflects the evolution of methods over time. In one of the initial challenges in 2013, the winning team achieved a Dice Score of 0.88 and in 2015 the runner up achieved a score of 0.78 (1).

**Roles**

Tego Chang: preparing power point presentation for video

Jaya Kahn: programming neural network for segmentation of brain tumors

Satvik Kishore: programming neural network for segmentation of brain tumors

Fides Schwartz: accessing the dataset, providing domain knowledge about MRI imaging of glioblastoma multiforme, spot-checking segmentation experiments, writing of final report

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