Brain Tumor Anomaly Detection and 3D Segmentation using Multimodal Brain MRI Data

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Introduction

Gliomas are brain tumors arising from glial cells. They can be classified into different histopathological grades based on the World Health Organization (WHO) grading system. Low grade glioma (LGG) and high-grade glioma (HGG) are subtypes of Grade I, II and III and IV tumors, respectively.

The goal of this project is to accelerate the mean time to achieve results from MRI scans, particularly related to brain tumors. In doing so, we help the medical practitioners plan treatments better and in a timely fashion. Lastly, it is our hope that the preliminary MRI insights provided to a radiologist help guide them towards any novel anomalies that may be present.

In our project, we use 2D and 3D MRIs in order to train anomaly detection and tumor segmentation models. When a query MRI is presented, an anomaly score is first generated in order to score the anatomical differences from a normal, healthy brain. Next, if it is found to be anomalous, tumor segmentation is

Methodology

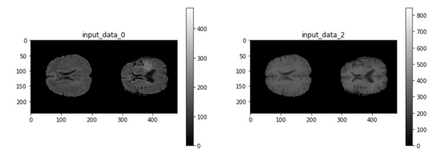
Datasets

- (2D) Brain MRI Images for Tumor Detection
- (3D) OASIS-3
- (3D) Brain Tumor and Segmentation (BraTS)

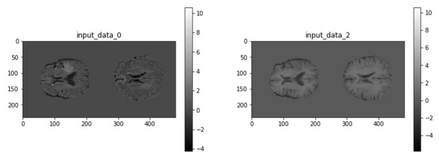
Data Pre-Processing

- 2D
  - Single slice extraction for healthy brain anatomy in 2D
  - Data augmentation including: brightness, contrast, jitter, rotation, and zoom
- 3D
  - Zero Mean Normalization using DeepNeuro library

Raw



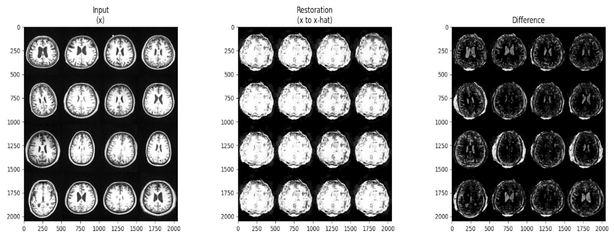
Transformed



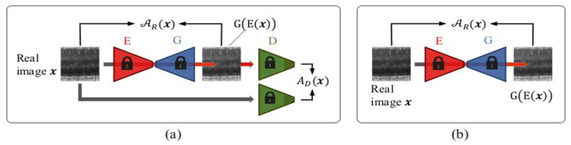
Analysis and Results

Anomaly Detection

We utilize the fast AnoGAN (f-AnoGAN) to build a generative model of healthy training data. The mapping is based on a trained encoder, and anomalies are detected via a combined anomaly score based on the building blocks of trained model.



Encoder training step where an input image (x) is decoded by encoder and serves as input to the generator. The output of generator is shown in the restoration step in the middle frame. The difference between the output of generator and original image is shown on the right.

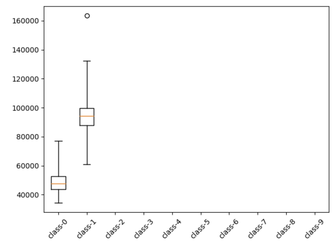


Anomaly Score is calculated based on sum of reconstruction loss and discriminator loss

$$\mathcal{A}(\mathbf{x}) = \mathcal{A}_R(\mathbf{x}) + \kappa \cdot \mathcal{A}_D(\mathbf{x}), \quad (4)$$

where $\mathcal{A}_R(\mathbf{x}) = \frac{1}{n} \cdot \|\mathbf{x} - G(E(\mathbf{x}))\|^2$, $\mathcal{A}_D(\mathbf{x}) = \frac{1}{n_d} \cdot \|f(\mathbf{x}) - f(G(E(\mathbf{x})))\|^2$ and κ again is a weighting factor

Training box plot representing the average anomaly score for normal (class-0) and tumor (class-1) data

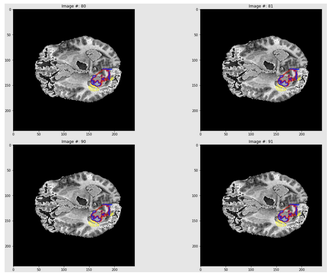


Validation Results

TN (healthy detected healthy)	312/413	75.5%
FN (anomalous detected healthy)	14/100	14%
TP (anomalous detected anomalous)	87/100	87%
FP (healthy detected anomalous)	101/413	24.4%

Tumor Segmentation

We utilize U-Net 3D Architecture to build a segmentation model on top of Anomaly detection model. We use BRATS-2017 multimodal dataset with around 155 frames for each MRI datapoint.

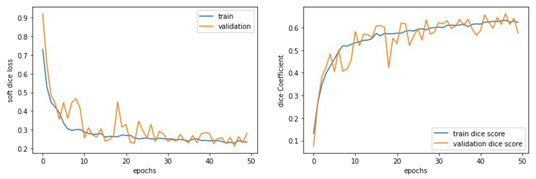


U-Net 3D Training comprises of analysis path and synthesis path. In Analysis path convolution layers are followed by ReLU and then a layer of max pooling. In Synthesis each layer consists of up-convolution of 2 strides followed by convolution layer with ReLU activation.

We measure segmentation results by metrics called dice score or F1 measure. Dice score measures difference between two images for semantic segmentation.

$$DSC = \frac{2|X \cap Y|}{|X| + |Y|}$$

Performance:

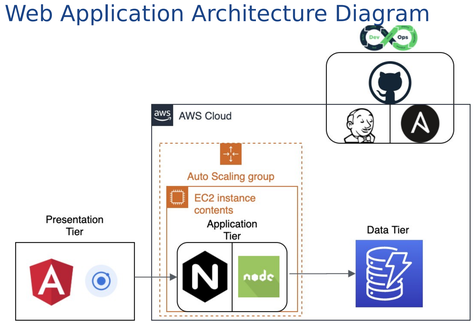


Web Application Key Features

The application has the following features:

1. Provide enhanced experience and reduce the workload of the radiologists
2. Help medical practitioners run anomaly detection algorithm to get anomaly score for the uploaded MRI
3. Generate tumor segmentation image viewer on the basis of score to localize the tumor
4. Get remarks from the radiologist on the pre-classified results from the models
5. Notify patients immediately with their diagnosis results

Web Application Architecture Diagram



Summary/Conclusions

Brain malformation and disease detection using computer vision techniques is a challenging yet fruitful research area to solve difficult problems related to medicine science. There has been a lot of research going on with the medical image data but there has been a lot less adoption from the medicine and healthcare industry in spite of high performance model results because of the complex nature of medical problems.

Key References

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[3] Schlegl, Thomas, et al. "Unsupervised Anomaly Detection with Generative Adversarial Networks to Guide Marker Discovery." ArXiv:1703.05921 [Cs], Mar. 2017. arXiv.org, http://arxiv.org/abs/1703.05921.

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