
Evaluation of Influence of Physical Layers to Brain Segmentation

Xuan Liu¹, Yu Miao²

Department of Electrical and Computer Engineering¹

Department of Biomedical Engineering²

Duke University

Durham, NC 27705

xuan.liu115@duke.edu, yu.miao148@duke.edu

Abstract

In this project, we used a computer-aided diagnosing system to segments the brain lesion from Magnetic Resonance Imaging (MRI) scanned images with multiple convolutional layers to simulate the effects of physical layers. The dataset is Brain MRI segmentation from Kaggle. This dataset contains brain MR images from 110 patients from 5 institutions with 3930 brain MRI images and 3930 manual FLAIR abnormality segmentation masks. The images were obtained from The Cancer Imaging Archive (TCIA)[1]. The U-net model is adapted from MONAI framework[2]. All images are preprocessed by multiple three-by-three convolutional layers and one one-by-one convolutional layer to simulate the illumination effects. After training, the results are evaluated by pixel accuracy metric and the performance score are calculated. For future work, there are multiple parameters such as adding gaussian kernel and changing gamma value of contrasts could be tunned to test out the performance of the model.

1 Introduction

In recent years, a drastic increase of disease related with abnormal brain anatomical features has been noted. Since the subtle change of brain features could not be easily captured, the demand of computer vision has spiked and more and more sophisticated machine learning tools are applied to address this problem. We propose to segment brain Magnetic Resonance Imaging (MRI) using general deep learning algorithms such as the U-Net. However, due to the artifacts of MRI, it's challenging for doctors to correctly localize the potential lesion in the brain. For example, unstable patients during scanning, low contrasts and low signal intensity[3]. In order to capture the generalized cases, we mimic the varied physical layers to help to address the low signal intensity problem by adding additional convolutional layers to increase signal intensity of the images. The adjusted image will again be trained and validated with fine-tunned U-net model to classify the segmentation of anatomical features in the brain. The network showed huge potential in classification of MRI scans in the presence of artifacts. However, the accuracy of segmentation also needs to be improved to address this problem.

1.1 MONAI U-Net

One of the most widely used Convolutional Neural Network (CNN) architecture is called MONAI framework which is an open-source PyTorch based framework for deep learning in healthcare imaging[2]. This network contains three basic U-Net structures: down-sampling, skip connection, and up-sampling. The number of channels could be specified during function call and the depth of layer could be customized by modifying the sequence of modules.

1.2 Physical layers

Due to the fact that the neural networks could be used to design physical layers, we then simulate the illumination effects by adding layers with kernel=(3,3) or layers with kernel=(1,1) to test out different illumination effects. The resulting output will be improved with properly tuned parameters.

2 Related work

There are several related studies conducted with the same dataset. The goal of their studies are to construct the association between the genomic features and predicted brain tumor shapes and the performance are evaluated by the dice score.

The original study is performed by Mateusz et al[4] with the same dataset. In their study, they used [256, 128, 64, 32, 16] as the number of output channels during the down-sampling process. The goal of their paper is to quantify the tumor imaging characteristics using deep learning-based segmentation and construct the relationship between genomic subtypes with segmentation characteristics[4]. The dice coefficient is 0.82 in their study.

The other study performed by Maciej et al[5] uses the same dataset to assess the association between angular standard deviation(ASD), RNASeq cluster and DNA copy number[5]. In conclusion, it validated the strong connection between genomic subtypes and outcomes in lower-grade glioma based on the tumor shape features from deep learning model[5].

3 Methods

3.1 Preprocess

This dataset contains brain MR images from 110 patients from 5 institutions with 3930 brain MRI images and 3930 manual FLAIR abnormality segmentation masks. Multiple image could belong to one patients due to reconstruction from 3D view to 2D slices. Each patients has features: RNASeqCluster, MethylationCluster, miRNACluster, CNCluster, RPPACluster, OncosignCluster, COCCluster, histologicaltype and neoplasmlhistology. However, we won't use any of these features. Our goal in this project is to use image masks to predict segment lesions.

Each image is converted into 255 x 255 pixels. Each image has corresponding size of lesion with 255 x 255 images. The combined image could be visualized through image overlay as shown in Figure 1.

The image is later changed from RGB into grayscale image to mimic the true MRI slice for model training. The image is shown in Figure 2.

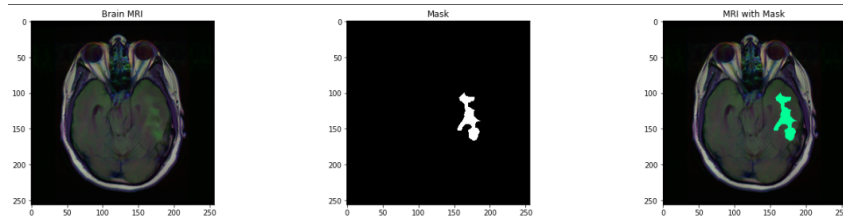


Figure 1: Annotated MRI with lesion mask overlay

The contrast of the image has been adjusted to gamma=3 to increase the difference between bright and dark area which could be useful for later deep learning process.

3.2 Overall architecture

The model structure is based on general U-net model with input size of 256 x 256 pixels. During down-sampling phase, the size of the input image has been halved for four times into 16 x 16 pixels. After down-sampling phase, the feature map starts to increase in size from 16 x 16 pixels to 256 x 256 pixels and this process is called up-sampling phase. Similarly, the up-sampling process has

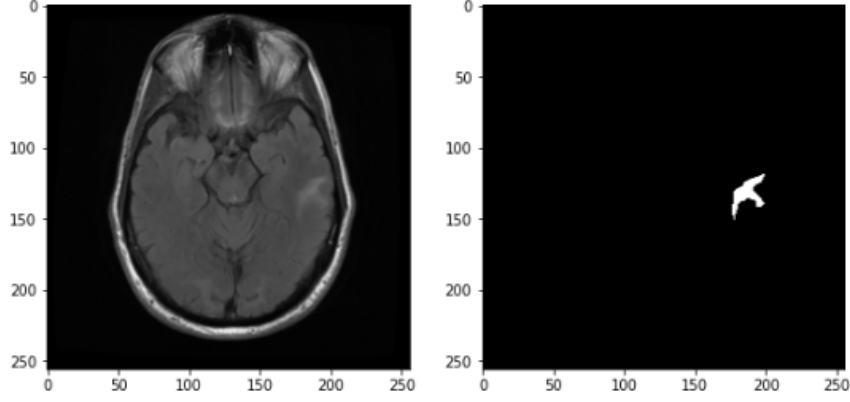


Figure 2: Gray scale MRI with lesion mask

doubled the image size 4 times and each step has concatenated previous same-in-size feature maps for training purposes. At the end of the model, we use sigmoid activation function for the output image. The general architecture is shown in Figure 3.

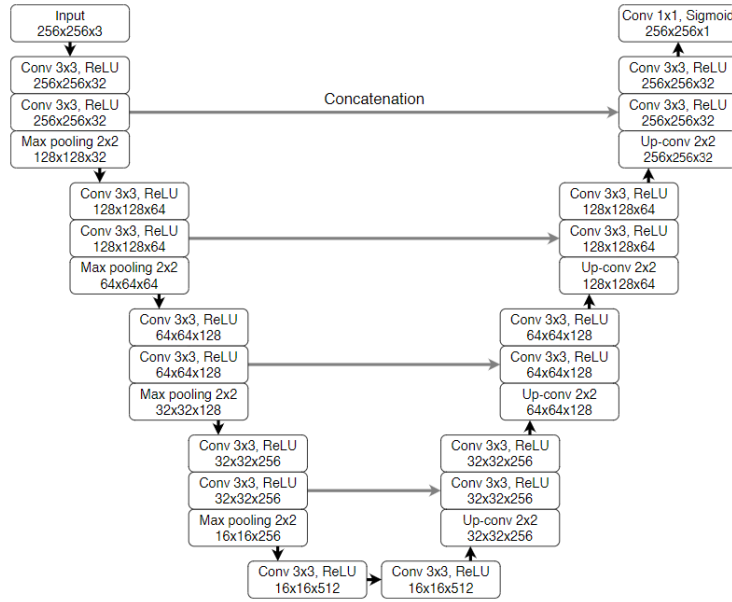


Figure 3: U-net model architecture[5]

From Figure 4, we could see that after our customized kernel in either 3 x 3 or 1 x 1, the processed image could be illuminated with large contrast between the lesion and normal tissues. After the model has been trained, we will modify our illumination kernel accordingly to gain improvement of accuracy based on Pixel Accuracy score.

4 Results

The following evaluation equations are used to measure the performance of the models:

- 1) Pixel Accuracy(PA) measures how many pixels in the images are correctly predicted compared to the mask images. It is calculated as

$$PA = \frac{TP + TN}{TP + TN + FP + FN}$$

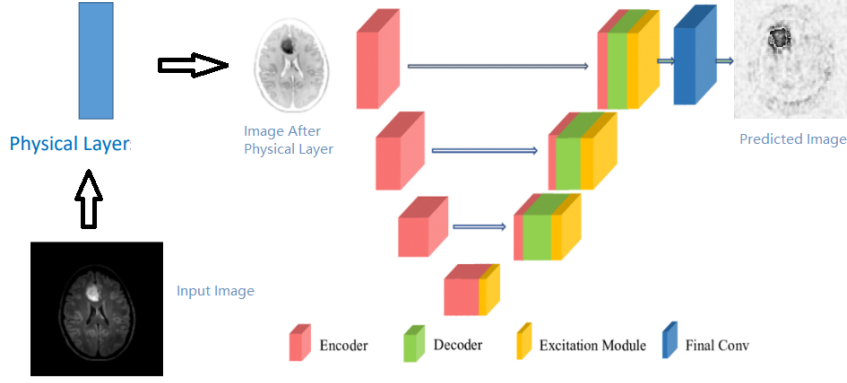


Figure 4: Proposed general pipeline for lesion prediction model

where TP is true positive, TN is true negative, FP is false positive and FN is false negative.

- 2) Pixel Accuracy with weights (PAW) is based on PA but it is multiplied by a weight. We used PAW as one of performance metrics to reduce the impact of pixel number differences in each images. It is represented as

$$PAW = \frac{AMP}{SMP} \times \frac{TP + TN}{TP + TN + FP + FN}$$

where AMP is average number of mask pixels from all images in the test dataset, SMP is the number of mask pixels from single test image.

4.1 Unet with (3,3) kernel convolution layers

We used one and two convolution layers both with (3,3) kernel size and compared their performance with Unet without physical layers. As shows in Figure 5, Unet without physical layers overfits much early and its loss does not decrease significantly after 50 epochs. Validation loss of Unet with two (3,3) kernel convolution layers keeps decreasing even after 200 epochs. Table 1 shows that both PA and PAW of Unet without physical layers achieves the best performance, which is 0.8511 and 0.1469. Figure 5 shows 4 samples of predicted mask on validation images.

4.2 Unet with (1,1) kernel convolution layers

We compared the influence of one and two (1,1) kernel convolution layers and their performance is very similar to the Unet without physical layers. Both of them overfits after nearly 75 epochs.

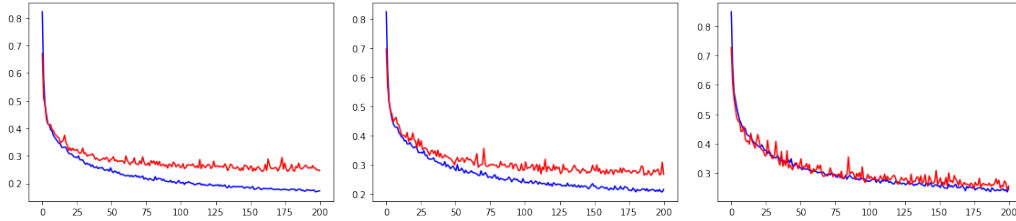


Figure 5: Loss with 200 epochs. Left: Unet without physical layers. Middle: Unet with one 3x3 Conv layer. Right: Unet with two 3x3 Conv layers. Blue line: train loss. Red line: validation loss

5 Discussion

As showed in Table 1, both PA and PAW performance of Unet with physical layers is not as good as Unet without physical layers. Physical layers might blur the original images to some extent and it leads to excessive information loss. However, in Figure 5, the train and validation loss of Unet with

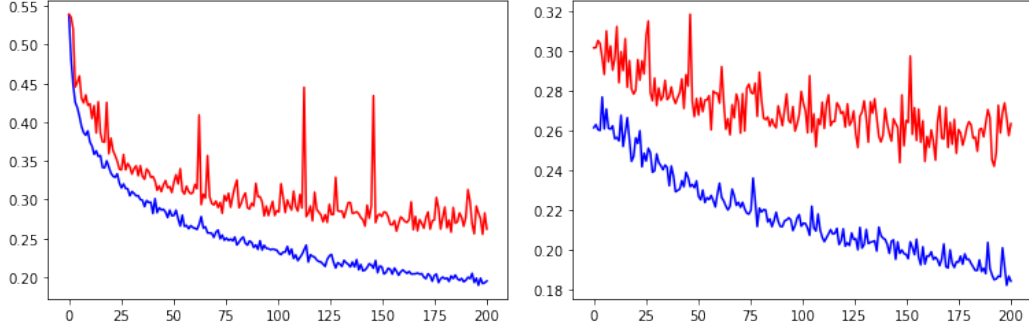


Figure 6: Loss with 200 epochs. Left: Unet with one 1x1 Conv layer. Right: Unet with two 1x1 Conv layers. Blue line: train loss. Red line: validation loss.

Table 1: Evaluation Metrics Table

Unet Structure	PA	PAW
without Conv	0.8511	0.1469
one (1,1) Conv	0.7834	0.0416
two (1,1) Conv	0.6028	0.0962
one (3,3) Conv	0.7885	0.0991
two (3,3) Conv	0.7519	0.0823

two (3,3) convolution layers does not diverge obviously even after 200 epochs, and it means that this model is still not overfitting and it may have better performance after more training epochs. With more combination of both (1,1) and (3,3) convolution layers and some weight restricts, it might have higher performance even better than Unet without physical layers.

References

- [1] Buda, M., *Brain MRI segmentation*, Kaggle Retrieved April 26, 2022, from <https://www.kaggle.com/datasets/mateuszbeda/lgg-mri-segmentation>.
- [2] Jafar, M. (2021, October 28). *MRI artifacts: Radiology* reference article. Radiopaedia Blog RSS. Retrieved April 26, 2022, from <https://radiopaedia.org/articles/mri-artifacts-1?lang=us>
- [3] *MONAI.io* MONAI. (n.d.). Retrieved April 26, 2022, from <https://monai.io/>
- [4] Buda, M., Saha, A., & Mazurowski, M. A. (2019). Association of genomic subtypes of lower-grade gliomas with shape features automatically extracted by a deep learning algorithm. *Computers in Biology and Medicine*, 109, 218–225. <https://doi.org/10.1016/j.compbiomed.2019.05.002>
- [5] Mazurowski, M. A., Clark, K., Czarnek, N. M., Shamsesfandabadi, P., Peters, K. B., & Saha, A. (2017). Radiogenomics of lower-grade glioma: Algorithmically-assessed tumor shape is associated with tumor genomic subtypes and patient outcomes in a multi-institutional study with the cancer genome atlas data. *Journal of Neuro-Oncology*, 133(1), 27–35. <https://doi.org/10.1007/s11060-017-2420-1>

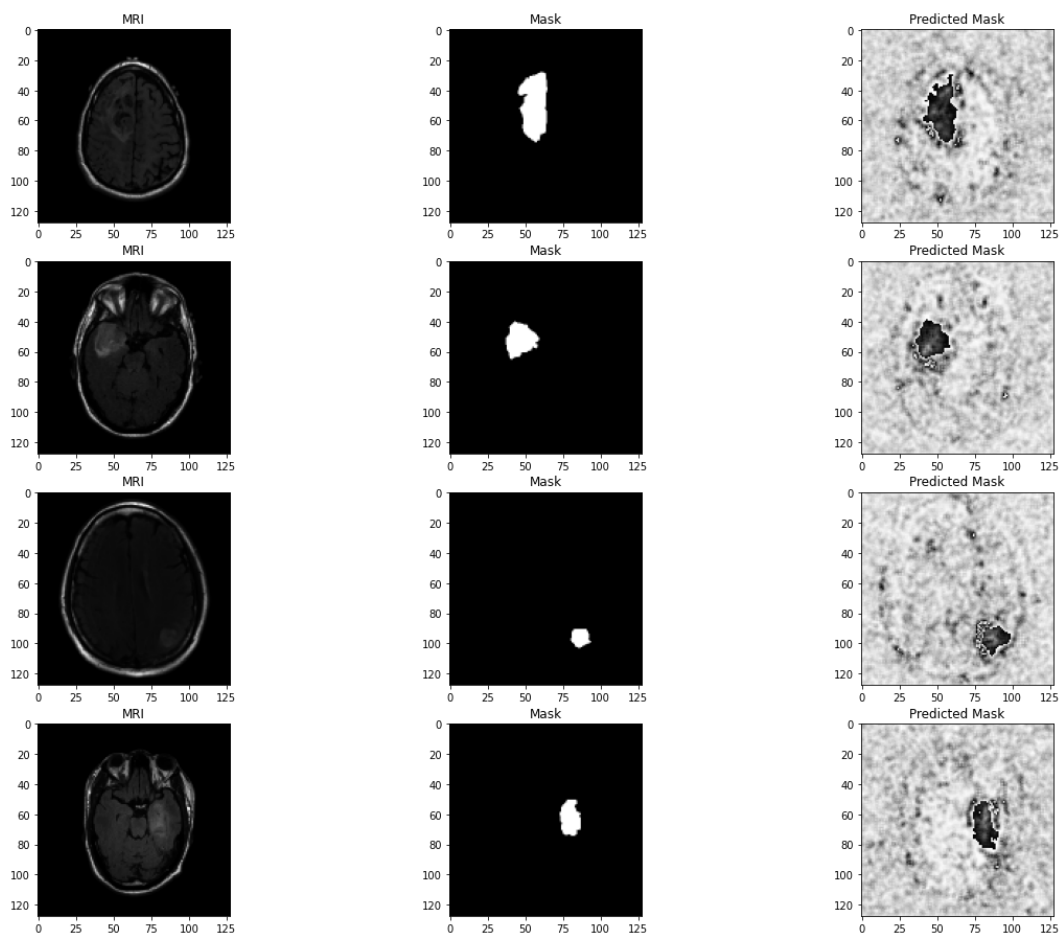


Figure 7: Samples of Predicted Cancer Mask. Left: Original images. Middle: Mask Labels. Right: Predicted Mask.