The Design and Implementation of An Adaptive Segmentation Technique to Detect Brain Tumors Using 2D Unet

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Abstract— **The UNet is one of the most well-known convolutional neural network (CNN) architectures used for biomedical image segmentation. The 2D variant is typically discouraged for volumetric brain tumor segmentation due to slices being correlated with one another. Thus, 3D-Unets have become prevalent in the annual Multimodal Brain tumor Segmentation Challenge (BRaTS) hosted by the Perelman School of Medicine of University of Pennsylvania (UPenn). However, with unique data preprocessing and generator techniques, 2D-Unets may achieve competitive accuracy and performance with 3D-Unets. Moreover, the addition of residual blocks (R) and squeeze-and-excitation (SE) blocks in the upsampling portion of 2D-Unets may further speed up performance and minimize computational costs without sacrificing f1 or Jaccard's similarity score. This reveals that 2D-UNets for 3D biomedical image segmentation are still valuable. This paper involves the detailed comparison between 2D-Unets and 2D-SE-RUNets for the purposes of segmenting a whole high-grade glioma (HGG) using the metrics of Jaccard's similarity, recall, specificity, and precision**

Index terms: brain tumor, segmentation, Unet, convolutional neural network

I. INTRODUCTION

Semantic segmentation is a technique of classifying and labeling each pixel within an image [1]. Deep learning techniques have become immensely popular for this task. Deep learning models use artificial neural networks to automatically learn useful representations of the data and save physicians time and provide further analysis [1]. Supervised learning algorithms are the most promising compared to unsupervised techniques such as clustering. Supervised learning involves training a model on labeled data in order to adequately predict unseen samples whereas unsupervised learning uses unlabeled data. Semantic segmentation has many applications in biomedical sciences from skin cancer to brain tumors

One very widely used method are UNets, which is an improvement of the fully convolutional neural network (FCN) architecture [2]. It was developed by Olaf Ronneberger et al. in 2015 [3]. A UNet has an encoder and decoder path [3]. In the encoder path, spatial information is reduced whereas feature information increases, but in the decoder path, image size is increased back to its original size with feature channels decreasing. In the decoder path, pooling operations are changed to transposed convolutions, which transform the shrunken feature maps to larger ones. The UNet is symmetric and has skip connections between the encoder and decoder paths, which help concatenate high-level features for localization and learning representations. In brief, one can say that in encoder path, the model learns the "what" but loses the "where", and in decoding the "where" is recovered. Output ends with number of channels corresponding to number of classes via a 1x1 convolutional layer. If the segmentation task has multiple labels, a softmax activation is typically used, but for binary labels, sigmoid activation is used. The softmax and sigmoid activations turn the fine-tuning of weights into probabilities. The final output layer has a large receptive field that corresponds to the height and width of the image. A UNet, much like the traditional FCN, is size invariant, meaning input size does not have to be fixed since output becomes the same size. UNets also have the benefit of requiring one forward-pass to segment an entire image unlike a traditional patch-based method. The UNet has no fully connected or dense layers.

The addition of residual blocks greatly improves the performance of UNets. Residual blocks refer to skipping the training of a few layers, which helps learn residual functions and propagate larger gradients for deeper networks.

II. RESEARCH PROBLEM

In the case of brain tumor segmentation, 3D variants of UNets such as VNets have been more valuable [5]. A VNet uses 3D convolutions and 3D max pooling unlike traditional 2D ones. This is because MRI scans of the brain are volumetric, which means each MRI channel is correlated with the other. MRI is a biomedical imaging technology that uses magnetic fields and gradient along with radiofrequency pulse to take scans of the macroscopic structure the brain at different layers. These scans are taken at different times after the radiofrequency pulse, and they can show various structures better relative to others. For example, FLAIR scans can reveal whole tumors better than T1 scans [13].

Does this mean the 2D-RUnet is definitively inferior for competitive accuracy of brain tumor segmentation? Recently, a new study was published revealing how the use of Squeeze-and-Excitation (SE) blocks in the up-sampling path of 2D-UNets can help correlation of channels be better maintained. Mehrdad Noori modified a traditional 2D UNet with SE and residual blocks for this purpose in his paper "Attention-Guided Version of 2D UNet for Automatic Brain tumor Segmentation" published in 2019 [6].

The authors are interested in seeing these improvements first-hand. They constructed and trained two UNets, one with

residual connections and SE blocks and the other without any modifications, for segmentation of a whole tumor from the BRaTS'19 dataset [7-11].

III. PURPOSE OF THE STUDY

The goal of this project is to classify and segment whole high-grade glioblastomas (HGG) in multi-channel magnetic resonance imaging (MRI) scans using deep learning techniques. Nearly 80% of tumors originate from glia [12]. Tumors originated in glia cells are called "glioma". Glioma are classified as either low-grade or high-grade. Low-grade glioma (LGG) have slower growth rate, meaning treatment can help, whereas high-grade glioma (HGG) are more aggressive, which require radiotherapy and surgery; some forms of LGG can lead to HGG, which has poor survival prognosis. The BRATS'19 labeled dataset had folders for both HGG and LGG. For the purposes of this study, only HGG was focused on.

There are 259 folders in the HGG directory. Each of these folders contain 5 NIfTI-1 data format files, which is used for neuroimaging scans. These include T1, T1ce, T2, FLAIR, and the Ground Truth segment scans or channels. They are each in the dimensions of 240x240x155. The depth of 155 can be interpreted as constituting "slices". T2 and FLAIR are popular MRI sequences for highlighting the whole tumor boundaries [13]. Therefore, both T2 and FLAIR channels were used as input channels in both variants of the UNet for additional information.

The goal is to see if the addition of residual connections and SE-blocks prior to the transposed convolutions in the up-sampling path increases segmentation speed or accuracy for evaluating the test set. Accuracy is primarily assessed with the use of the dice coefficient while segmentation speed is calculated based on total training time.

IV. AUDIENCE

Researchers interested in biomedical image segmentation, UNet architecture, and BRaTS' annual competition may benefit in reading this paper. There are many modifications for UNets [14]. These can include the additions of recurrent convolutions, 3D convolutions, and attention modules [14]. However, the implementation of a SE-block is recent. It also helps in thinking of old problems in new ways, such as how modified 2D-Unets may still be useful for volumetric images. Considering the formulation and addition of various blocks in novel ways may help future researchers in improving their own models. Moreover, our own UNets could be used transfer learning and applied for different health issues such as skin cancer.

V. CONTRIBUTION

This paper's main contribution lies in showing how additional blocks, such as the residual and SE blocks, may improve upon the original 2D UNet as previously described. Moreover, with the use of various techniques like using tables and horizontal and vertical flipping, performance and accuracy can be improved [6].

VI. MOTIVATION

Initially, we constructed and trained a 2D-UNet. They were considering to give up on this endeavour and adopt a 3D-UNet to benefit from 3D contextual information instead. However, after finding Noori's 2D-SE-RUNet, they became interested in seeing if it adequately improved training and testing dice scores or training time. It is a novel way to fix the limitation of the basic 2D-Unet. Moreover, performance time is substantially less than 3D-UNets, which have higher computational complexity due to more parameters [3].

VII. PAPER GOAL AND ORGANIZATIONS

One goal is to see if the 2D-SE-RUNet has higher training and test dice scores, also known as f1, compared to the basic 2D UNet. The dice score or f1 is a measure of overlap between prediction for each class and target class [15]. It is basically multiplying 2 with the number of predicted pixels overlapping with the ground truth segment divided by the total number of pixels:

$$2\frac{|y_{true} \cap y_{pred}|}{y_{true}+y_{pred}} \quad (1)$$

The models will be trained for 20 epochs based on a 60/20/20 training, validation, and testing split of HGG. There are 259 HGG glioma files and two channels, FLAIR and T2, each constituting one brain. Each of the 259 brains is cut into 155 slices. This means there are a total of 40145 2D slices. 24025 are indexed and reserved for training, 8060 for validation, and 8060 for testing. Much of this data is saved into tables to facilitate training.

The loss function used is dice loss:

$$1 - \frac{2\sum_{pixels} y_{true} y_{pred}}{\sum_{pixels} y_{true} + \sum_{pixels} y_{pred}} \quad (2)$$

VIII. RELATED WORKS

Both Olaf Ronneberger et al.'s original 2D-UNet [3] and Mehrdad Noori's 2D-SE-RUnet [6] were taken as inspirations and starting point for this study. The former was initially constructed for transmitted light microscopy images whereas the latter was tweaked for brain tumor segmentation. Noori's model utilized two main additions to the traditional UNet: multi-view fusion and SE blocks. The multi-view fusion of the axial and coronal views of the brain helps gain 3D contextual information, and the SE blocks weighs each channel adaptively to prevent confusion for the model. The SE blocks help weigh multilevel features before the transposed convolutions in the upsampling path. What distinguishes Noori's SE-RUnet model are SE blocks in red and the residual connections between the blue convolutional blocks. Squeeze-and-excitation blocks concatenate multilevel features. They prevent confusion from MRI channels. Noori's model is shallower than Ronneberger's standard 2D-UNet [3].

For pre-processing the data, Noori used the N4ITK algorithm, which helps to correct inhomogeneities of the MRI images. To reduce overfitting, vertical and horizontal flipping of the images is applied in the data generator.

Noori's validation results were competitive with the BRATS'18 top two competition winners, Myronenko and Isensee et. al [17-18]. Myronenko used an assymetric FCN with an added variational autoencoder (VAE) at encoder

endpoint for training and regularization, and the encoder part also had residual blocks. VAEs map the input image into the latent space as a statistical distribution of mean and variance. They have a decoder-encoder structure whereby the decoder takes one point that's randomly sampled from the distribution and reconstructs it. It is good for regularization and speeding up supervised learning. Isensee et al. used a traditional 3D-UNet with minor modifications. It is important to note that since Noori's model is 2D, it was able to train faster too with less memory consumption than his competitors

Surprisingly, Noori's SE-RUNet had the lowest and best shape similarity between prediction for the whole tumor and ground truth compared to the 3D models! Hausdorff distance measures the distance between the ground truth segment and predicted segment. It was this fact which inspired the authors to explore the nature of this model more thoroughly in comparison to the basic UNet.

The BRATS competition involves labelling three parts of the tumor: whole, enhancing tumor, and tumor core. The whole tumor includes necrosis, edema, and enhancing parts of the tumor. Edema refers to the collection of fluid or water, necrosis is accumulation of dead cells, enhancing tumor means blood-brain barrier has broken, and non-enhancing are regions that are none of these [12]. The tumor core includes necrosis and enhancing tumor, and the enhancing tumor is just the enhancing portion. For the purposes of this paper, only the whole tumor is considered.

IX. TECHNIQUES IN THE STUDY

Keras API was primarily used for this project with channels set to first. Keras API was designed Francois Chollet in order to provide classes to facilitate the construction of deep learning modes [19]. Setting channels to first help the authors better visualize the UNet architecture. They used Tensorflow as a backend.

For data preprocessing, a function was created utilizing glob package to match the pathnames in order to read the brain and store it as numpy arrays. Normalization was done by subtracting and dividing by standard deviation for T2, FLAIR, and ground-truth scans. Another function was created to save the brain into table files. Moreover, during saving the table, they were sliced with a for-loop and indexed based on training, validation, and testing split of 60/20/20. T2 and FLAIR scans were then plotted, alongside the ground truth (GT), to ensure table forms worked correctly (Fig. 1).

Afterwards, the model definition was written. The functions for dice coefficient and dice loss were defined alongside a smooth factor, which can help prevent division by zero and avoid overfitting [20]. For the first program, a basic and traditional 2D-UNet is used. The second program defines the 2D SE-RUNet. Since only the whole tumor is being segmented, the model ends with a sigmoid function. The sigmoid function helps crunch the number between 0 and 1 for predicted probability of segment whereby close to 1 means high probability of whole tumor.

Next, a custom data generator from Keras sequence class was used. This data generator speeds up training, further helps with normalization, and vertically plus horizontally flips the scans to gather more information. The data generator is what feeds data for training. Since the data generator consumed a lot of RAM, crashing the kernels in both Floydhub and Google Colab, a more basic one was used for validation and testing.

For both the traditional 2D-UNet and 2D-SE-RUnet, there were 11 training epochs with the same size for training (number of slices =24025) and validation slices (number of slices =8060). A learning graph for 10 epochs is created showing how dice coefficients change across epochs for training and validation. The training weights were saved and used for evaluation of the unseen testing set (number of slices =8060) via this function:

X. PROPOSED METHOD

Much of the proposed method has already been covered in preceding sections. A traditional 2D UNet's (Fig. 2) training speed and testing dice score is compared to a SE-RUNet architecture (Fig. 3) for the purposes of segmenting a whole tumor. They are both trained for 20 epochs. We initially predicted the SE-RUNet will surpass the 2D-UNet.

The SE-RUNet was made to be much shallower. This means it will save more computation time. The SE-RUNet has 7,724,257 trainable parameters and 5,984 non-trainable parameters. The traditional 2D-UNet has 31,043,297 trainable parameters and 12,128 non-trainable parameters.

The optimizer used to minimize dice loss is ADAM for both the standard 2D-UNet and 2D-SE-RUNet. The learning rate is set to 1e-4. The smooth factor was set to 0.01. The metrics to be evaluated for training, validation, and testing are f1 (same as dice score), Jaccard's similarity (also known as IoU), precision, specificity, and recall.

$$Precision = \frac{TP}{TP+FP} \tag{3}$$

$$Recall = \frac{TP}{TP+FN} \tag{4}$$

$$IoU = \frac{target \cap prediction}{target \cup prediction} \tag{5}$$

$$Specificity = \frac{TN}{TN+FP} = \frac{TN}{N} \tag{6}$$

TP refers to true positive, which is number of pixels of correctly predicted whole tumors, which corresponds to ground segment. TN is true negative, and number of pixels correctly identified as not belonging to the whole tumor ground segment. FP is false positive is number of predictions that did not have whole tumor pixel ground truth correspondence. Finally, FN is false negative and the number of tumors, corresponding to ground segment, which weren't predicted.

IoU metric measures the number of pixels for the brain tumor in common between the ground segment and prediction divided by the total number of pixels present in both. Precision describes how many positive predictions of the brain tumor segment were predicted. Precision describes how many of the whole tumors predicted had a matching ground truth segment. Specificity is the correct number of non-tumor predictions divided by the total number of non-tumor pixels.

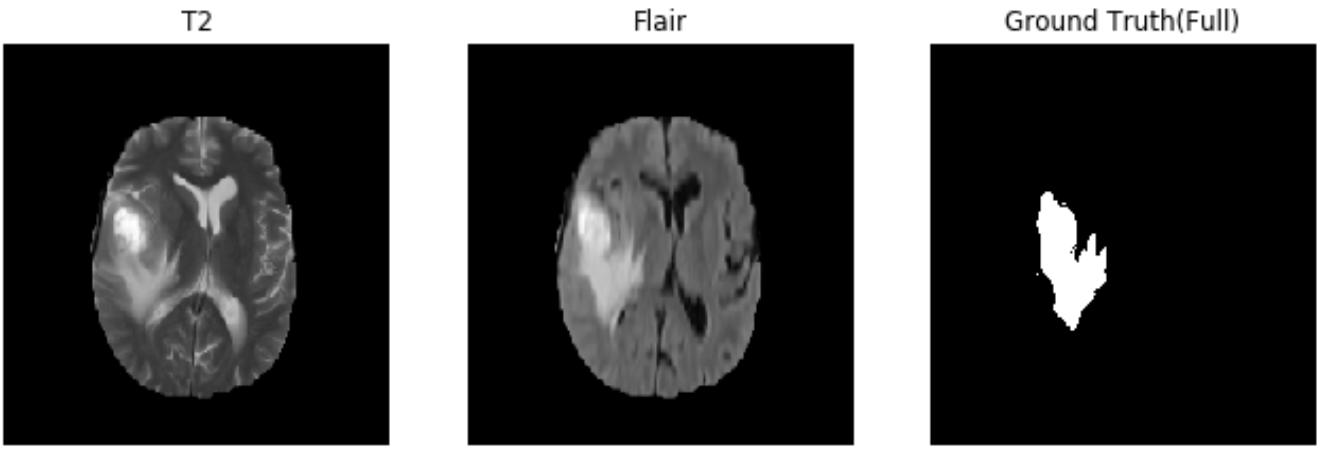

Fig. 1: Slice number 80 chosen from a random brain.

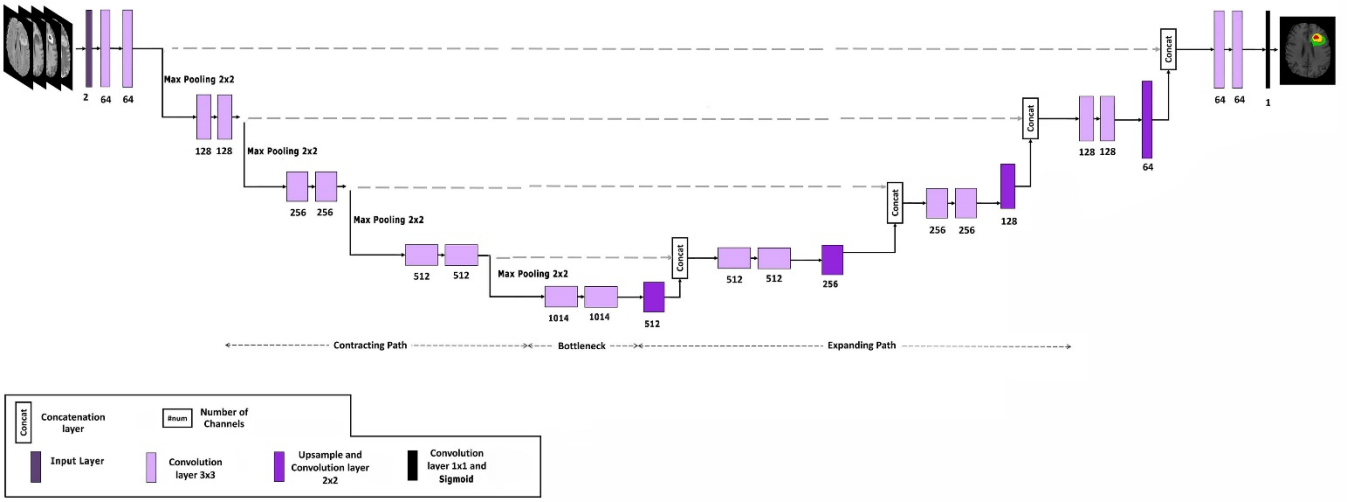

Fig. 2: The traditional 2D-UNet architecture used.

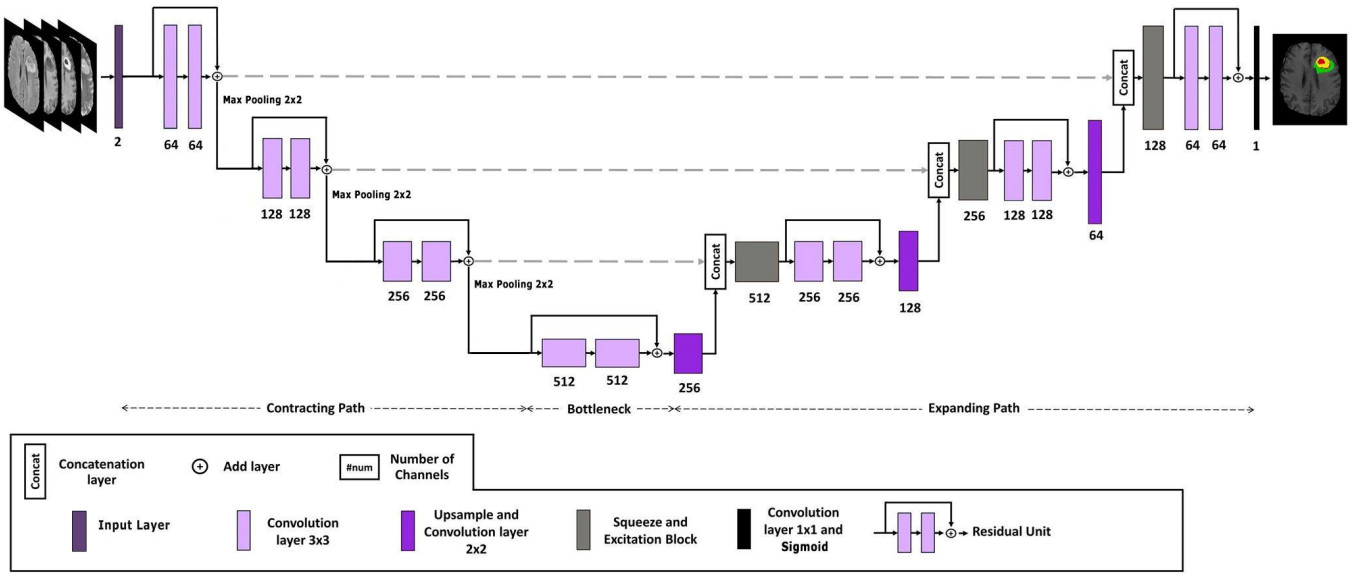

Fig. 3: The modified 2D-SE-UNet architecture improvement.

XI. EXPERIMENTS AND RESULTS

A. First Model

Training Set (Basic UNet)	Scores
Number of Epochs	20
Slices per Epoch	24025
Loss Function	dice loss
f1 score	0.79
Jaccard's Score	0.78
specificity	1
precision	0.82
recall	0.79

Table 1: Training Set of Basic UNet

Validation Set (Basic UNet)	Scores
Number of Epochs	20
Slices per Epoch	8060
Loss Function	dice loss
f1 score	0.37
Jaccard's Score	0.79
specificity	1
precision	0.41
recall	0.36

Table 2: Validation Set of Basic UNet

Test Set (Basic UNet)	Scores
Number of Epochs	20
Slices per Epoch	8060
Loss Function	dice loss
f1 score	0.37
Jaccard's Score	0.79
specificity	1
precision	0.41
recall	0.36

Table 3: Test Set of Basic UNet

The first model total training time took approximately 10 hours. It was trained for 20 epochs with the best validation loss saved.

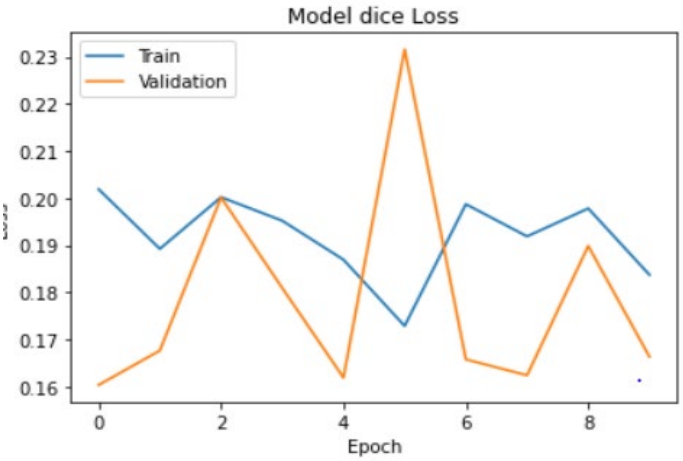

Fig 4: Loss Curve for the last 10 epochs of Training Basic UNet

B. Second Model

Training Set (SE-RUNet)	Scores
Number of Epochs	20
Slices per Epoch	24025
Loss Function	dice loss
f1 score	0.81
Jaccard's Score	0.79
specificity	1
precision	0.82
recall	0.80

Table 4: Training Set of SE-RUNet

Validation Set (SE-RUNet)	Scores
Number of Epochs	20
Slices per Epoch	8060
Loss Function	dice loss
f1 score	0.37
Jaccard's Score	0.80
specificity	1
precision	0.41
recall	0.36

Table 5: Validation Set of SE-RUNet

Test Set (SE-RUNet)	Scores
Number of Epochs	20
Slices per Epoch	8060
Loss Function	dice loss
f1 score	0.37
Jaccard's Score	0.80
specificity	1
precision	0.40
recall	0.37

Table 6: Test Set of SE-RUNet

The second model total training time took approximately 8 hours. This is significantly less time than the first model.

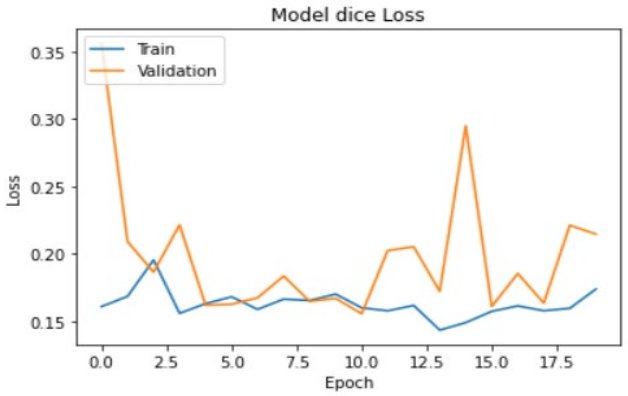

Fig 5: SE-RUNet loss curve

XII. Conclusion and Future Works

When we used the table and index it for both training and validation Keras custom generator and try to train it with model.fit, we get reading array or RAM error. Noori's base code didn't have issues on Google Colab before, but it could be due to incompatibility issues in library or new updates, which we found very difficult to pinpoint. The Keras custom generator normalizes slice values between [0, 1] for MRI, but the authors' generator doesn't. However, when we try to fit the superior Keras custom generator for both training and validation, we get that annoying error. Consequently, the table was used only for training on Keras Custom Generator whereas the author's own generators were used for validation and testing, hence discrepancy between results. Also, the issue may have been that the brain volumes were not cropped when put into the table, which was due to believing it as non-essential.

In conclusion, the 2D-SE-RUNet is superior to the traditional 2D-UNet for biomedical image segmentation of 3D images largely due to efficiency. The 2D-SE-RUNet may be opted by those who wish to save time or minimize computational costs. The addition of modifcatory blocks, such as SE and residual in the case of our example, and the significant reduction of parameters can help fix certain limitations. The authors predict with an additional hour of training, the 2D-SE-RUNet would either reach or surpass the testing dice score of the basic 2D-UNet. The 2D-SE-RUNets would also be interesting to train for the task of skin lesions or cancer, which does not benefit from 3D contextual information.

In the future, it will be interesting to see if SE blocks can likewise apply to the various channels of 3D-UNets in order to minimize parameters. How does a 2D-SE-RUNet compare to a 3D-SE-RUnet? Liu et al.'s 2020 study used 3D SE blocks for brain tumor segmentation [23].

XIII. Acknowledgments and Reflection

We would like to give thanks Mehrdad Noori for giving special consultations over Skype. Initially, the project was done in an 80/10/10 split, but this led to unrepresentative validation dataset [22]. Mehrdad Noori also helped fix some issues with the data generators, which led to array read issues or overuse of RAM in both Floydhub and Google Colab Pro. Therefore, two different data generators were used to minimize RAM usage.

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