Improving Brain Tumor Segmentation with Data Augmentation Strategies

Radhika Malhotra[1]*, Jasleen Saini[2], Dr. Barjinder Singh Saini[1], Dr. Savita Gupta[2]

[1] Dept of ECE, Dr. B R Ambedkar NIT Jalandhar, Jalandhar, India
[2] Dept of CSE, UIET, Panjab University Chandigarh, India

*Corresponding author

Abstract

In the past decade, there has been a remarkable evolution of convolutional neural networks (CNN) for biomedical image processing. These improvements are inculcated in the basic deep learning-based models for computer-aided detection and prognosis of various ailments. But implementation of these CNN based networks is highly dependent on large data in case of supervised learning processes. This is needed to tackle overfitting issues which is a major concern in supervised techniques. Overfitting refers to the phenomenon when a network starts learning specific patterns of the input such that it fits well on the training data but leads to poor generalization abilities on unseen data. The accessibility of enormous quantity of data limits the field of medical domain research. This paper focuses on utility of data augmentation (DA) techniques, which is a well-recognized solution to the problem of limited data. The experiments were performed on the Brain Tumor Segmentation (BraTS) dataset which is available online. The results signify that different DA approaches have upgraded the accuracies for segmenting brain tumor boundaries using CNN based model.

Keywords: Data Augmentation, Deep Learning, Brain tumor, CNNs

1 Introduction

Thanks to the emergence of convolution neural networks, deep neural networks have been successfully applied to many computer vision applications as well as in medical domain [1]. For medical image analysis, convolutional neural networks (CNNs) consisting of multi-layered structure are utilized to extract a large number of hidden image characteristics [2] [3]. Compared to conventional machine learning algorithms, a major advantage of CNN deep learning algorithms is that there is no need to extract features manually. The CNN model itself computes the important features that are required for a specific task. But the main challenge faced by these models is improving the generalization ability on the test dataset [4]. In deep learning, various strategies have been applied to overcome this overfitting problems that mainly occurs when the size of the training dataset is small for supervised learning methods [5] [6].

- Dropout [7] is the process of randomly deactivating some of the neurons by initializing their weights to zero during training of neural networks. This technique will upgrade the network performance by eliminating overfitting problem by preventing neurons to adapt too well in the learning phase [8].

- Batch Normalization [9] is a simple technique of pre-processing a batch of feature maps by normalizing its mean to zero and standard deviation to one. Normalizing the data prevents the values from any one channel from disproportionately affecting the losses and gradients. This makes the data to be well distributed in a specific range so as to maximize the optimizers performance.

- In Transfer learning [10] [11] technique, a CNN model is firstly trained on huge datasets like ImageNet and then transferred on the smaller datasets by fine-tuning the last few layers. Fine-tuning the high-level portion of the network is beneficial because the first few layers are designed to extract generic information and it is not specific to dataset. Also, it is possible to fine-tune all the layers of

the convolutional network or to keep a few of early layers fixed[12]. This concept has been widely applied in many medical related problems where databases are of limited nature.

Among above all mentioned techniques, data augmentation is the proved to be the most effective method one as it simply increases the amount of training dataset which is the prime requirement of supervised learning methods [13]. It artificially enlarges the dataset by simply performing some operations on the input samples. These operations incorporate flips (horizontal, vertical), shear, adding random noises, rotations (45°,90°,180°), image cropping, scaling, blurring etc. This kind of image manipulations have been extensively applied in medical domain particularly in magnetic resonance images of brain tumor patients and have shown promising results in fields like tumor classification, detection, segmentation and survival prediction [14]. The objective of this work is to examine the effect of augmentation approaches on the BraTS 2018 dataset. Since the training samples in this dataset are limited, so we have the compared the results after applying DA approaches for segmenting the tumor boundaries in FLAIR MRI modality.

2   Materials & Methods

2.1   Dataset for Brain MRI and Patients

The dataset utilized for this study is BraTS 2018 dataset, comprising of 210 high grade glioma (HGG) and 75 low grade glioma (LGG) patients collected from 19 different institutions. Four MRI modalities namely T1 weighted (T1), T1 contrasted enhanced (T1-CE), T2 weighted (T2) and T2 Fluid-attenuated inversion recovery (T2-FLAIR) are available for all of these patients for addressing heterogenous brain tissues in an effective way. All the images are already co-registered into TI-CE modality and image resolution is about 240×240×155. The images are in NIfTI (Neuroimaging Informatics Technology Initiative) format. In our experiments, FLAIR modality is employed for segmenting the tumor boundaries as FLAIR is considered to be the most informative modality of all and it is easier to delineate whole tumor part from this modality [15].
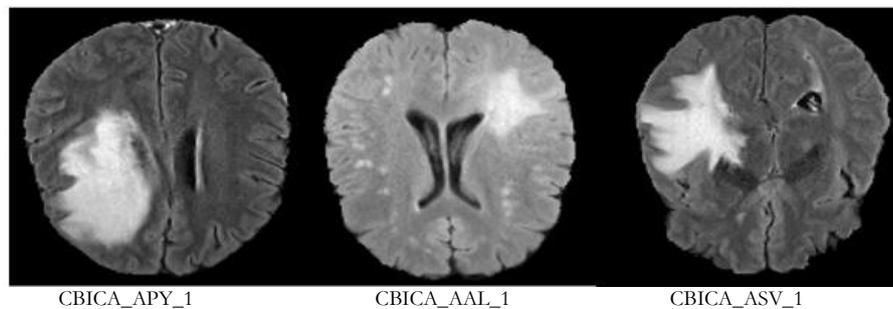

<div align="center">CBICA_APY_1   CBICA_AAL_1   CBICA_ASV_1</div>

Fig 1. T2-FLAIR sequence of brain MRI with respective training IDs

2.2   Encoder-Decoder Based Convolutional Neural Networks

 The network architecture deployed for this study involves encoder-decoder paths which comprise of various convolutional blocks, max-pooling, up-sampling layers etc. as shown in Fig 2. This network resembles the basic U-net architecture with skip connections for enhanced information flow at different levels. This is the type of semantic based segmentation in which both input and output images are of equal resolution. As depicted in the Fig. 2 the input image (240×240×1) is firstly convolved with filters of size 3×3 with different number of feature maps at various levels. This is followed by the non-linear activations namely rectified linear unit (ReLU) and max-pooling layers with 2×2 stride to reduce the input dimensions to half. In between convolutional layers dropout is also provided to overcome overfitting concerns. The decoder path uses up-sampling layers to compensate for decreased feature map size due to max-pooling layers. Here at each block, the output is concatenated with feature maps from encoder side using skip

connections. This basically improves local and global information at up-sampling side [16] [17]. Before introducing the images to the network, these were pre-processed using intensity normalization techniques to achieve zero mean and unit variance. This would help in uniform distribution of the intensities of the image dataset.
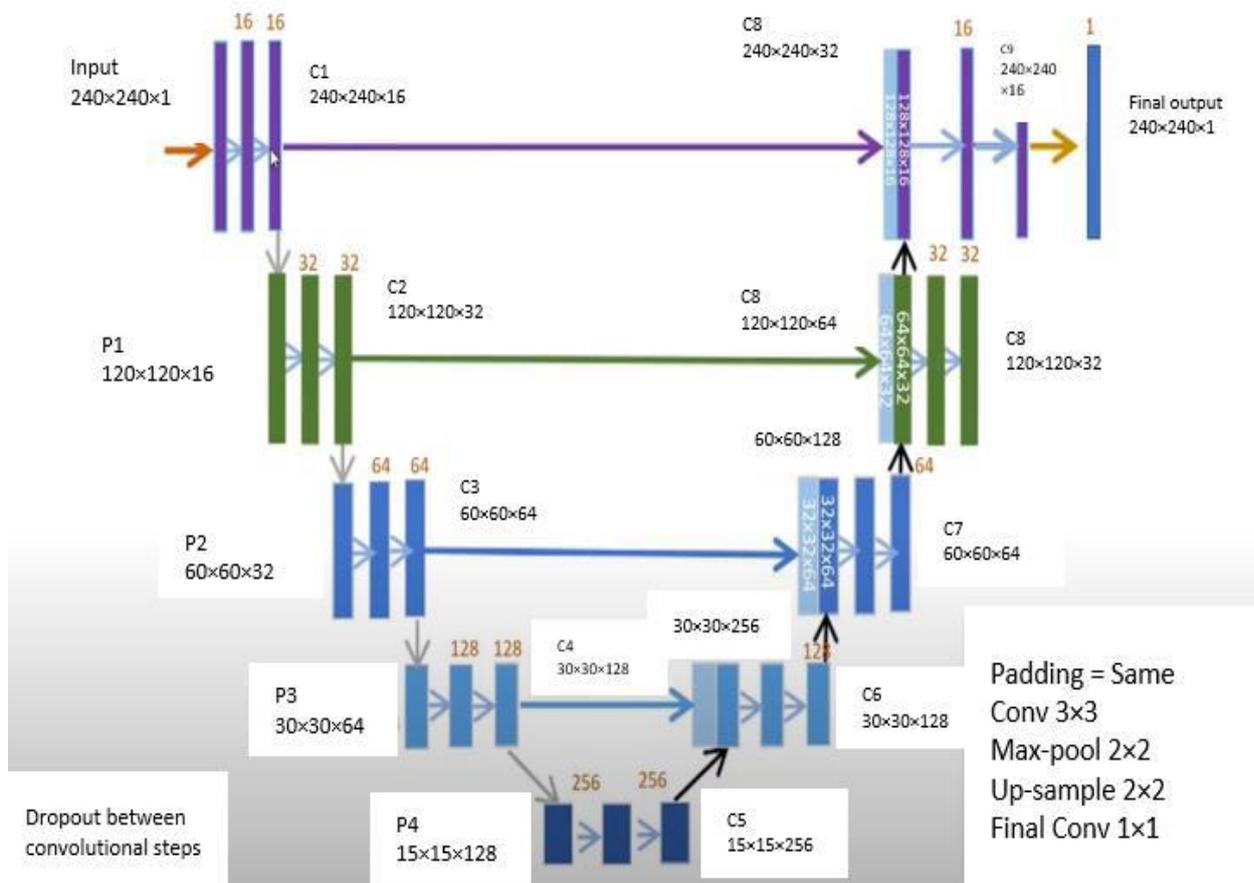

Fig 2. Encoder-Decoder Type U-Net architecture for segmenting tumor region

2.3 Data Augmentation

Due to the scarcity of the training samples in BraTS 2018 dataset, it is intended to apply augmentation techniques for generating suffcent amount of training samples. In this work, we have utilized the augmentation parameters as summarized in table 1. The flips operations basically flip the tumor images horizontally and vertically to alter the tumor location and this is the most commonly employed data augmentation approach. Also, horizontal axis flipping is much more prevalent than vertical axis flipping. Shearing deforms the tumor shape horizontally. Zooming typically zooms out a small region of the image whereas in cropping a small rectangle shaped region is cropped out and image is scaled up. The samples can be rotated at different angles like 45°, 90° or 180° for increasing the size of training dataset. In experiments, we have chosen fill mode as reflect. It should be noted that aggressive augmentation may also leads to poor accuracies.

Hence, the combinations of these augmentation approaches should be selected appropriately.

3 Results and Discussions

In this work, we have explored the various data augmentation techniques that can be applied to the brain tumor MRI scans as shown in fig 3. Multiplicating the avaliable training samples by artifically augmenting

the images lead to some improvements in the accuracies of the training, validation and test images as depicted in table 2 and 3. To examine the efficiency of data augmentation approaches, the images were divided as 20% of training images for validation and 10% for testing. Keras, a deep learning framework in python is used for implementing the CNN. For training, adam optimizer and a dropout of 0.1 was used. The hyper-parameters for optimizer were set to 0.00001 as learning rate with epochs and batch size as 10 and 3 respectively. In case when the number of training images were enhanced (6060 training images) using DA, the learning rate and batch size were changed to 0.001 and 500 respectively.
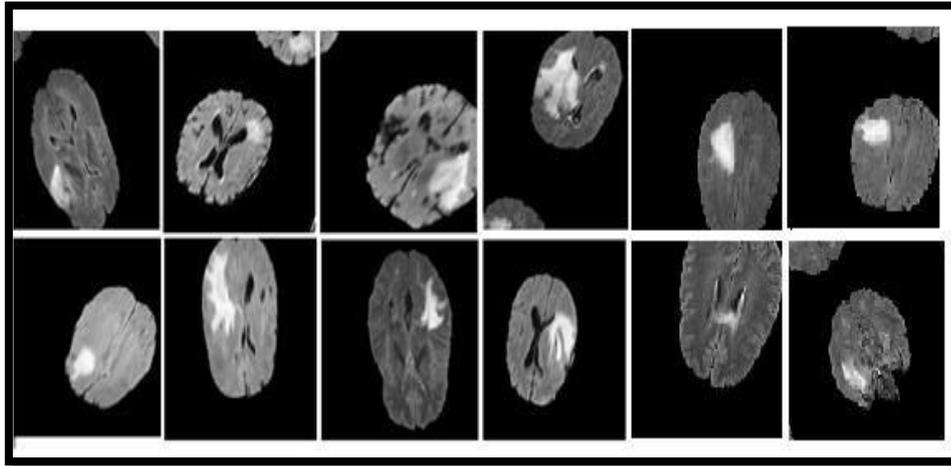

Fig 3. Augmented training samples using different DA approaches.

Table 1. Data augmentation parameters

Sr. No	Parameters Utilized	Values
1.	Rotation_range	45
2.	Width_shift_range	0.2
3.	Shear_range	0.2
4.	Zoom_range	0.2
5.	Fill_mode	Reflect
6.	Height_shift_range	0.2

Table 2. Segmentation results without DA approaches

Sr No.	Samples	Accuracy	Loss
1.	Training	96.74	0.4064
2.	Validation	96.85	0.3751
3.	Test	97.37	0.3185

4   Conclusions

Deep learning is an exponentially growing domain that has achieved remarkable progress in addressing many problems. In the present work, we tried to enhance the number of training samples for brain tumor segmentation using DA approches. The results were evaluated using a U-net architecture on BraTS2018

dataset. Improvement in the accuracy and loss values cleary indicates the efficacy of DA techniques in medical imaging. Future work may include exploring more DA based approches for brain tumor related problems and incorporating other MRI modalities (T1,T1-CE or T2) in U-Net based models.

Table 3. Segmentation results with DA approaches

Sr No.	Samples	Accuracy	Loss
1.	Training	97.12	0.0408
2.	Validation	97.25	0.0347
3.	Test	97.8781	0.0275

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