B.Sc. in Computer Science and Engineering Thesis

# Study on Brain Tumor Segmentation Using MRI Images


Submitted by

Pronob Das
201605098

Akid Abrar
201605100

Tasnim Doha
201605108

Supervised by

Dr. Md. Monirul Islam

**Department of Computer Science and Engineering**
**Bangladesh University of Engineering and Technology**

Dhaka, Bangladesh


May 2022

# CANDIDATES' DECLARATION

This is to certify that the work presented in this thesis, titled, "Study on Brain Tumor Segmentation Using MRI Images", is the outcome of the investigation and research carried out by us under the supervision of Dr. Md. Monirul Islam.

It is also declared that neither this thesis nor any part thereof has been submitted anywhere else for the award of any degree, diploma or other qualifications.

_____

Pronob Das
201605098

_____

Akid Abrar
201605100

_____

Tasnim Doha
201605108

# CERTIFICATION

This thesis titled, **"Study on Brain Tumor Segmentation Using MRI Images"**, submitted in May, 2022 by the group as mentioned below has been accepted as satisfactory in partial fulfillment of the requirements for the degree B.Sc. in Computer Science and Engineering .

**Group Members:**

**Pronob Das**

**Akid Abrar**

**Tasnim Doha**

**Supervisor:**

---

Dr. Md. Monirul Islam
Professor
Department of Computer Science and Engineering
Bangladesh University of Engineering and Technology

# ACKNOWLEDGEMENT

First of all, we have to thank our thesis supervisor, Dr. Md. Monirul Islam. Without his guidance and dedicated involvement in every step throughout the whole process, this thesis book would not have been accomplished. We would like to thank him for his guidance, support and understanding during the whole journey.

We are also grateful to our Department of Computer Science and Engineering, BUET. We would like to take this opportunity to thank to all of the Department faculty members and also all of our fellow students and our seniors for their help and support.

Most importantly, none of this could happened without the constant support of our family members. We want to thank our parents for the ceaseless encouragement, support and attention.

Dhaka
May 2022

Pronob Das

Akid Abrar

Tasnim Doha

# Contents

# List of Figures

# List of Tables

# List of Algorithms

# ABSTRACT

Brain Tumor is a deadly disease.There are mainly three parts of a brain tumor which needed to be segmented for the treatment. It is very hard and error prone to segment different parts of a brain tumor manually. Brain tumor segmentation is really important to determine the plan of treatment. In our thesis work, after studying and analyzing many existing models, we came up with a model which can successfully segment different parts of a brain tumor with comparable accuracy but with less computational complexity. Most of the implemented and well known models have the disadvantage of either being less accurate or being computationally complex. We compared our performance with some other papers and showed how well our model performed in spite of having very little computational complexity and cost.

# Chapter 1

# Introduction

## 1.1 Brain Tumor Segmentation

Brain tumor and substructure segmentation from MRI images has the potential for accurate and reproducible tumor identification, which can aid in more efficient and better diagnosis, surgical planning, and therapy assessment of brain tumors. However, reliable automatic segmentation of brain tumors is a difficult task for a variety of reasons. First, because of smooth intensity gradients, partial volume effects, and bias field artifacts, the boundary between brain tumor and normal tissues is often ambiguous. Second, brain tumors vary greatly between people in terms of size, form, and location. This precludes the use of strong priors on form and localization, which are frequently employed for robust segmentation of many other anatomical structures, including the heart and liver.

Deep Convolutional Neural Networks (CNNs) have recently attained state-of-the-art performance for multi-modal brain tumor segmentation. They require a set of annotated training images for learning as a form of machine learning approach. They do not rely on hand-crafted features like typical machine learning algorithms and can learn features automatically.

## 1.2 Background and Motivation

Brain tumors form when the brain's regular growth and division processes go awry. Tumors are categorised as malignant or benign (non-cancerous). Brain malignancies are classified into two types: primary tumors that begin in the brain and spread to other regions of the body, and secondary tumors that begin elsewhere in the body and spread to the brain. All types of brain tumors can induce a wide range of symptoms, depending on their size and location. Brain tumors are becoming increasingly prevalent. In the United States this year, an estimated 25,050

people (14,170 men and 10,880 women) were diagnosed with primary brain and spinal cord malignant tumors. This type of tumor affects less than 1% of people at some point in their lives. The brain is home to 85 to 90 percent of all primary central nervous system (CNS) malignancies. An estimated 308,102 people worldwide were diagnosed with a primary brain or spinal cord tumor in 2020.

In fact, not just adults but children are predisposed to brain tumor-related issues that eventually appear as cancer. This year, around 4,170 children under the age of 15 have been diagnosed with a brain or CNS tumor in the United States. Typically, primary CNS tumors account for about 20% of juvenile malignancies and 25% of adolescent cancer mortality. Brain tumors are the second most prevalent type of cancer in children under the age of 15 years old, after acute lymphoblastic leukemia.

And identifying and Segmenting Brain tumor manually is highly exhaustive and error prone. Thus the need of automated segmentation of Brain Tumor seems to be a crying need.

## 1.3 Organization of the rest of the Thesis

The rest of the thesis is organised as follows: In Chapter 2, we briefly discussed the related works about Brain Tumor segmentation.

Chapter 3 represents the main methodology of our work and corresponding explanations.

The experimental results and comparison of our result with others is provided in Chapter 4.

Finally, the conclusion and possible future work is mentioned in Chapter 5.

# Chapter 2

# Related Works

## 2.1 Introduction

Studying papers and articles about a few groundbreaking works on this relevant field helps understanding the problems. Also it is beneficial to decide on which sub-area there is still scope for contribution and more research work.

## 2.2 Related Works

Brain tumor segmentation is an issue where so many influential works are being performed. A solid understanding of the classifications are necessary for further understanding.

Edema (whole tumor), non-enhancing solid core (tumor core), necrotic/cystic core, and enhancing core are the four tumor components divided and classified by brain tumor segmentation. [1]

Medical imaging of brain tumors is critical for assessing disease progression both before and after treatment. Magnetic Resonance Imaging (MRI) with several sequences, such as T1-weighted, contrast enhanced T1-weighted (T1ce), T2-weighted, and Fluid Attenuation Inversion Recovery (FLAIR) images, is currently the most extensively utilized imaging modality for brain malignancies. [2] These MRI contrast modes work in a way such that FLAIR images indicate whole tumors, contrast enhanced T1ce indicate enhancing tumor and T1 T2-weighted indicate core tumors.

The challenge of brain tumor segmentation was solved using machine learning and image processing. Support Vector Machines were successfully utilized to segment brain tumors [3], while Conditional Random Fields were employed to refine the segmentation as well [4]. K-means, as shown in [5], is another effective way for addressing this problem. Level Sets (LS) is a classic method for segmenting brain tumors among several image processing methodologies [6], [7].

We have seen a lot of deep learning in the last several years, and it has become one of the most productive approaches in many domains [8–12], including segmenting brain tumors [13–15],. Convolutional Neural Networks (CNNs) are developed to combine with other classification methods or clustering methods in order to increase performance and overcome the limitations of training data [16]. In the BRATS 2015 challenge, Havaei et al. [17] created one of the first deep network architectures for segmenting brain tumors.

In case of brain tumor, accurate automatic segmentation is difficult to achieve for a variety of reasons. At first, because of smooth intensity gradients, partial volume effects, and bias field abnormalities, the distinction between brain tumor and normal tissues is frequently difficult.

Then, the size, shape, and location of brain tumors differ significantly amongst patients. Strong priors on shape and localization, which are routinely utilized for useful efficient segmentation of many other anatomical structures, such as the heart [18] and the liver [19] are not allowed when it comes to the case of brain tumor.

Deep Convolutional Neural Networks (CNNs) have made significant progress in recent years in course of performance for multi-modal brain tumor segmentation using cutting edge technologies [20, 21]. They require a set of annotated training photos for learning as a form of machine learning approach.

Later, Pereira et al. [22] tested an 11-layered CNN design on the BRATS dataset by incorporating small 3 x 3 sized filters in the convolutional layers, lowering the overall number of network parameters. The first patch-based 3D CNN for brain tumor segmentation was proposed by Kamnitsas et al. [23].

Rather than analyzing MRI images slice by slice as in earlier 2D approaches, 3D patches from each MRI channel are extracted and passed through four 3D convolutional layers.

DeepMedic employs a dual route 3D CNN with 11 layers to separate brain tumors using multi-scale characteristics. It employs a 3D fully linked Conditional Random Field (CRF) [24] for post-processing, which helps to eliminate false positives. DeepMedic outperformed 2D CNNs in terms of performance.

Recently, Le et al. [25] effectively segmented a brain tumor using Gated Recurrent Unit to rebuild Level Set curve evolution. Their network is based on the Fully Convolutional Network (FCN) in the context of a recurrent network described by Level Set curve evolution.

The cascaded network is a traditional yet powerful architectural network that has improved performance on a variety of jobs. Wang et al. [26] suggested a cascaded anisotropic convolutional neural network in which the entire tumor is segmented in the first stage and the result's bounding box is used for tumor core segmentation in the second step. The augmenting tumor core is then segregated based on the tumor core segmentation result's bounding box.

A triple cascaded architecture for brain tumor segmentation was presented in [21]. The architecture employs three networks to progressively segment the total tumor, tumor core, and augmenting tumor core. To cope with 3D pictures, it employs a network structure with anisotropic convolution, as well as dilated convolution, residual connection and multi-scale fusion [27–29]. It revealed a beneficial trade-off between receptive field, model complexity, and memory use. This approach additionally integrates the output of CNNs in three orthogonal perspectives for more robust brain tumor segmentation.

Kamnitsas, et al. [21] used Ensembles of Multiple Models and Architectures to achieve robust performance by aggregating predictions from a variety of methodologies (EMMA). This method seeks to reduce the impact of individual model meta-parameters and the risk of overfitting the configuration to a specific database.

Wang, et al. [30] have proved the utility of test-time augmentation in improving CNN performance for brain tumor segmentation. They also used different foundation network topologies and enhanced the image with 3D rotation, flipping, scaling, and random noise at both training and test time in their suggested method.

For training neural networks, [31] proposed mix-up, a simple and data-agnostic data augmentation procedure. Several studies have recently revealed that integrating predictions of numerous modified versions of a test image can increase the performance of deep learning-based image recognition algorithms, such as in lung nodule identification [32] and skin lesion classification [33]

Unet, proposed by Ronneberger et al. [13], is one of the most successful deep networks in medical imaging. The network's contractive and expansive routes are made up of a downsampling FCN followed by an upsampling FCN.

Many additional brain tumor segmentation algorithms, such as [34] and [14] updated the U-Net design for 3D convolution as a result of its success on BRATS.

## 2.3 Summary

In summary, we observed the gradual improvement of technologies used on solving this classic problem efficiently. Later, tried to evaluate the effectiveness of one of the cutting edge technology regrading this aspect.

# Chapter 3

# Methodology

## 3.1 Introduction

In this chapter, we present a detailed overview of the model architecture that we have worked on.Our model is based on CNN.

## 3.2 Main Methodology

There are five main basic components in the segmentation network including 2D convolution layers, 2D dilated convolution layers, pooling layers, fully connected layers and feature map concatenation.

In this model, vanilla convolutions are used in the shallower layers because they have a small receptive field. So they can learn local features. The dilated convolutions with larger receptive fields are used in the deeper layers to learn longer-range contextual information (global feature) without the need for pooling. In this model, we concatenate features of very different depths to the final output. By concatenating features from different scales, the semantic meaning of features is also preserved throughout the whole network.

### 3.2.1 Input

The dimension of the input in the model is 128X128. Here the size of the input image is 128X128 pixels.

### 3.2.2 Design of the Model

The block diagram of the whole model is as follows:

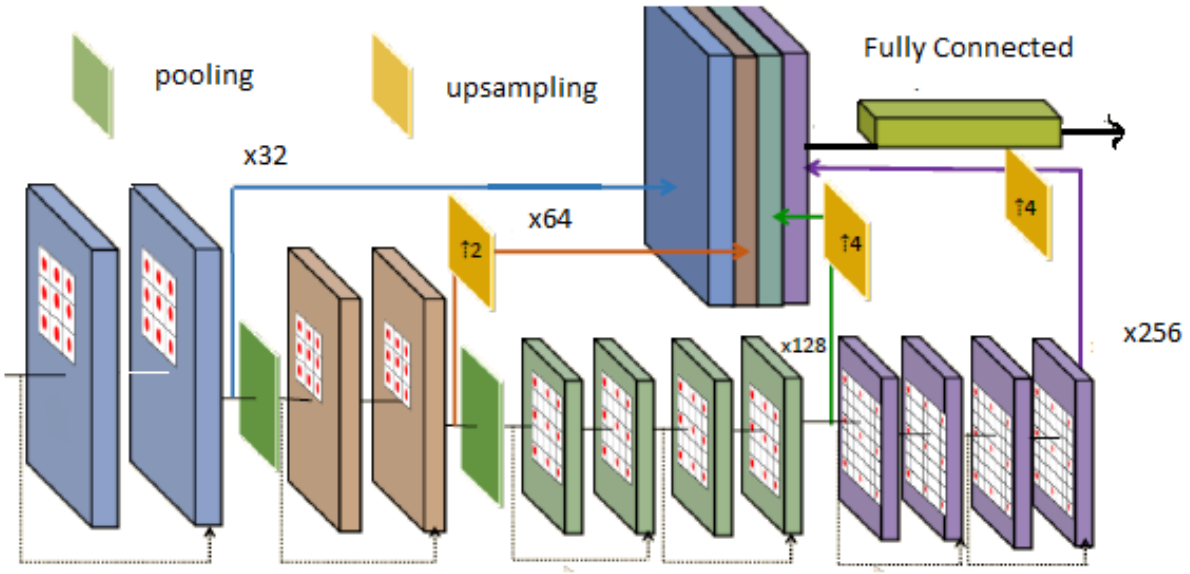


Figure 3.1: Whole Model

We see there are 12 CNN layers in total along with a concatenation layer with upsampling.

Description of each block:

**Block-1**

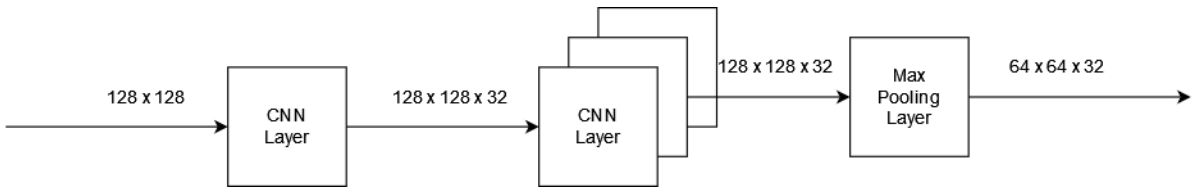


Figure 3.2: Block 1

The first block consists of 2 CNN layer followed by a max pooling layer.each CNN layer introduces 32 filters.the dimension of the input image is 128X128.as there are 32 filters in each CNN layer,the output is 128X128X32.We used stride 1 and same padding that conserves the dimension of the input.After the Max pooling layer the dimension becomes 64X64X32.

**Block-2**

The second block also consists of 2 CNN layer followed by a max pooling layer.Each cnn layer introduces 64 filters.The dimension of the input of the first CNN layer is 64X64.as there are 64

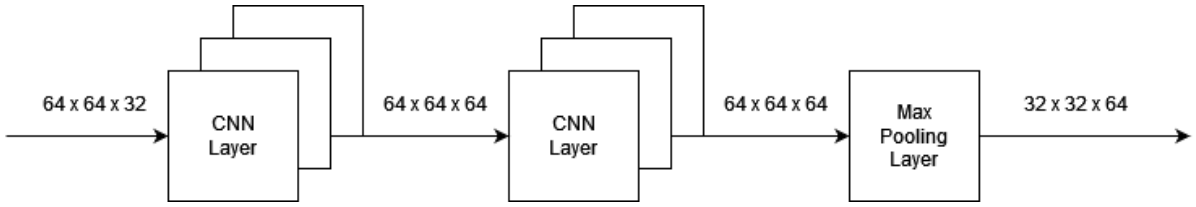


Figure 3.3: Block 2

filters in each cnn layer, the output is 64X64X64.After the Max pooling layer the dimension becomes 32X32X64.

**Block-3**

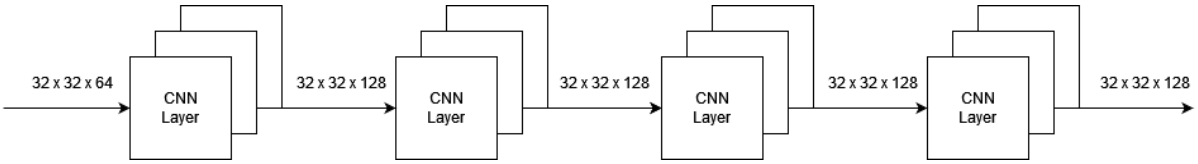


Figure 3.4: Block 3

In the third block there are 4 CNN layers. Each CNN layers introduces 128 filters.The input dimension of the 1st cnn layer is 32X32X64 as it comes from the pooling layer of the 2nd block.The output of the 1st CNN layer is 32X32X128.and the dimension of all other cnn block's output is the same.

**Block-4**

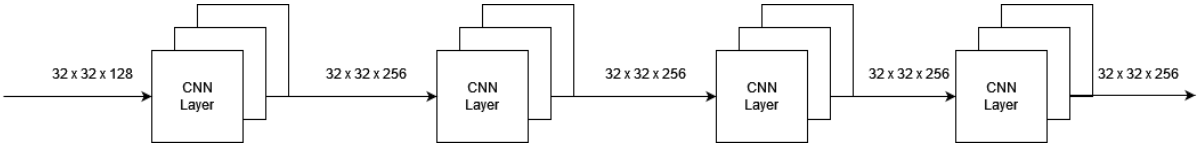


Figure 3.5: Block 4

The 4th block is quite similar to the 3rd block,except each layer introduces 256 new filters.The input dimension of the 1st cnn layer is 32X32X128 as it comes from the last cnn layer of the 3rd block.The output of the 1st CNN layer is 32X32X256.and the dimension of all other cnn block's output is the same.

**Whole Model**

Here the full model with 4 blocks are shown.We upsampled every last cnn layer of the block 2,3 and 4.Then we concatenated them with the last cnn layer of the 1st block.Thus we get a

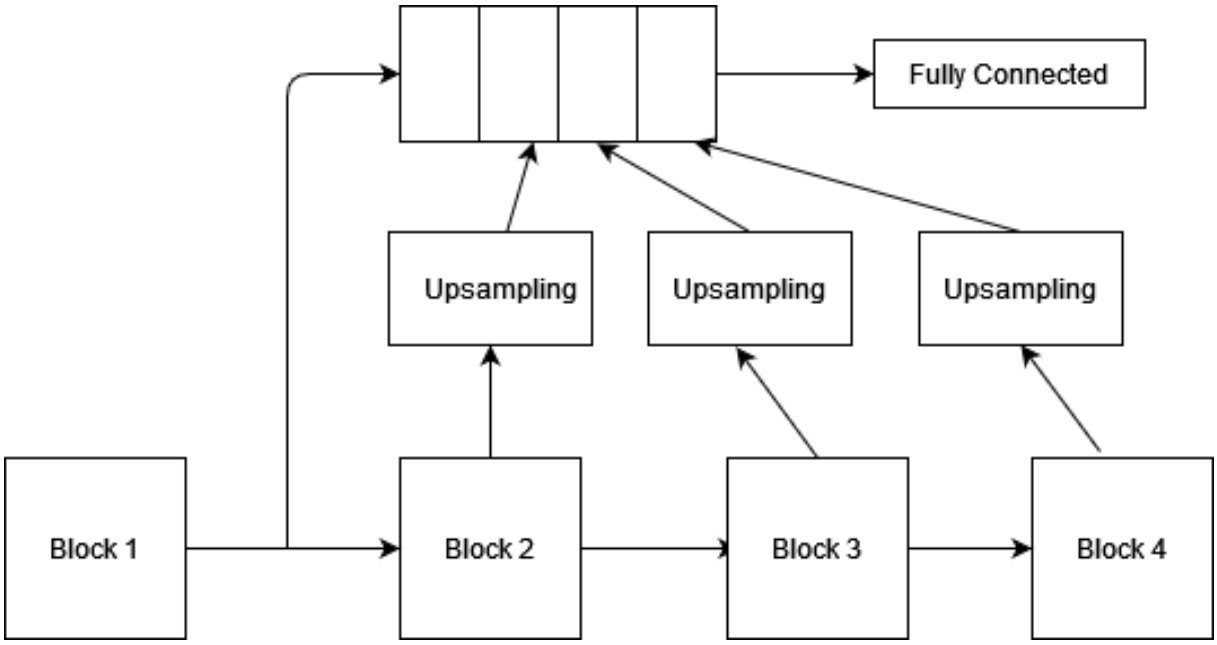


Figure 3.6: Whole Model

merged layer and this merged layer is then connected to a fully connected layer which gives us the output.

## 3.3 Summary

The choice of number of blocks, number of layers and other constructing elements of this entire network structure were tuned towards achieving the best performance considering the limited resources used.

# Chapter 4

# Experimental Results

## 4.1 Introduction

In this chapter, we will discuss about the result that was produced during testing.

## 4.2 Data Set

We used ”BraTS MICCAI 2018” data set for our training and testing.

Dataset can be found here: ”https://www.kaggle.com/datasets/awsaf49/brats18-dataset-training-validation”

Dataset consists of 2349 files and in each file there are 4 types of images, which are FLAIR, T1-weighted, T2-weighted and T1ce.

We split the data set in three parts, the partition is mentioned below.

Table 4.1: Data Set Spliting

| Task | Data set used |
|---|---|
| Train | 75 % |
| Validation | 15 % |
| Test | 10 % |

## 4.3 Performance Metrics Used

For the evaluation of our results, we choose three performance metrics which are:

- Dice Coefficient
- Precision
- Sensitivity

We used Dice Coefficient over Accuracy because it is known that in terms of image segmentation, Dice Coefficient is better over Accuracy.

**Dice Coefficient**

Dice Coefficient is calculated as:

$$\frac{2|P1T1|}{|P1| + |T1|}$$

where îs the logical AND operator, || is the size of the set (i.e., the number of pixels belonging to it), and P1 and T1 represent the set of pixels where P=1 and T=1, respectively.

**Precision**

$$Precision = \frac{TruePositive}{TruePositive + FalsePositive}$$

**Sensitivity**

$$Sensitivity = \frac{TruePositive}{TruePositive + FalseNegative}$$

## 4.4 Our Test Result

We have train and test our model with "BraTS MICCAI 2018" data set, the results are mentioned below:

Table 4.2: Experimental Results on BraTS MICCAI 2018

| | EDEMA | NECROTIC | ENHANCING |
|---|---|---|---|
| DICE Coefficient | 88.76 | 85.10 | 77.21 |
| Precision | 88.51 | 86.20 | 76.21 |
| Sensitivity | 90.10 | 86.46 | 77.38 |

## 4.5 Experimental Result Comparison with other references

We compared our result with some reference papers, Here are the comparison of Dice Coefficient values with our results and theirs.

Table 4.3: Experimental Result Comparison with others

| Reference | EDEMA | NECROTIC | ENHANCING |
|---|---|---|---|
| [1] | 90.95 | 88.88 | 81.41 |
| [2] | 86.38 | 76.58 | 73.44 |
| [13] | 90.05 | 83.78 | 78.59 |
| [5] | 85.87 | 88.61 | 77.08 |
| [14] | 90.10 | 79.70 | 73.80 |
| [18] | 90.50 | 83.80 | 78.60 |
| [21] | 90.44 | 84.94 | 80.52 |
| [Ours] | 88.76 | 85.10 | 77.21 |

# Chapter 5

# Conclusion

## 5.1 Summary

We implemented the segmentation part of the paper [1] without the background removal and showed that we get comparable performance with less computational complexity. Another thing is needed to keep in mind that, for getting this result we used only free tools, we have not used any local GPU to train or test the model. Whereas according to the paper, they have trained their model in local machines with GPU support. So we believe we can achieve accuracy much more close to the paper if we could train this model in local GPU.

## 5.2 Suggestion for Future Work

With a model that can segment different parts of a tumor, it is possible to build another model which can successfully predict the survival rate of the patient.

# References


[1] N. Le, K. Yamazaki, K. G. Quach, D. Truong, and M. Savvides, "A multi-task contextual atrous residual network for brain tumor detection & segmentation," in *2020 25th International Conference on Pattern Recognition (ICPR)*, pp. 5943–5950, IEEE, 2021.

[2] G. Wang, W. Li, S. Ourselin, and T. Vercauteren, "Automatic brain tumor segmentation using convolutional neural networks with test-time augmentation," in *International MICCAI Brainlesion Workshop*, pp. 61–72, Springer, 2018.

[3] M. Havaei, H. Larochelle, P. Poulin, and P.-M. Jodoin, "Within-brain classification for brain tumor segmentation," *International journal of computer assisted radiology and surgery*, vol. 11, no. 5, pp. 777–788, 2016.

[4] S. Bauer, L.-P. Nolte, and M. Reyes, "Fully automatic segmentation of brain tumor images using support vector machine classification in combination with hierarchical conditional random field regularization," in *international conference on medical image computing and computer-assisted intervention*, pp. 354–361, Springer, 2011.

[5] V. Anitha and S. Murugavalli, "Brain tumour classification using two-tier classifier with adaptive segmentation technique," *IET computer vision*, vol. 10, no. 1, pp. 9–17, 2016.

[6] S. Taheri, S. H. Ong, and V. Chong, "Level-set segmentation of brain tumors using a threshold-based speed function," *Image and Vision Computing*, vol. 28, no. 1, pp. 26–37, 2010.

[7] S. Ho, E. Bullitt, and G. Gerig, "Level-set evolution with region competition: automatic 3-d segmentation of brain tumors," in *Object recognition supported by user interaction for service robots*, vol. 1, pp. 532–535, IEEE, 2002.

[8] K. He, X. Zhang, S. Ren, and J. Sun, "Deep residual learning for image recognition," in *Proceedings of the IEEE conference on computer vision and pattern recognition*, pp. 770–778, 2016.

[9] T. H. N. Le, C. Zhu, Y. Zheng, K. Luu, and M. Savvides, "Deepsafedrive: A grammar-aware driver parsing approach to driver behavioral situational awareness (db-saw)," *Pattern Recognition*, vol. 66, pp. 229–238, 2017.

[10] K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," *arXiv preprint arXiv:1409.1556*, 2014.

[11] T. H. N. Le, C. N. Duong, L. Han, K. Luu, K. G. Quach, and M. Savvides, "Deep contextual recurrent residual networks for scene labeling," *Pattern Recognition*, vol. 80, pp. 32–41, 2018.

[12] T. H. N. Le, K. G. Quach, K. Luu, C. N. Duong, and M. Savvides, "Reformulating level sets as deep recurrent neural network approach to semantic segmentation," *IEEE Transactions on Image Processing*, vol. 27, no. 5, pp. 2393–2407, 2018.

[13] O. Ronneberger, P. Fischer, and T. Brox, "U-net: Convolutional networks for biomedical image segmentation," in *International Conference on Medical image computing and computer-assisted intervention*, pp. 234–241, Springer, 2015.

[14] Ö. Çiçek, A. Abdulkadir, S. S. Lienkamp, T. Brox, and O. Ronneberger, "3d u-net: learning dense volumetric segmentation from sparse annotation," in *International conference on medical image computing and computer-assisted intervention*, pp. 424–432, Springer, 2016.

[15] T. Le, R. Gummadi, and M. Savvides, "Deep recurrent level set for segmenting brain tumors," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pp. 646–653, Springer, 2018.

[16] P. Dvořák and B. Menze, "Local structure prediction with convolutional neural networks for multimodal brain tumor segmentation," in *International MICCAI workshop on medical computer vision*, pp. 59–71, Springer, 2015.

[17] M. Havaei, A. Davy, D. Warde-Farley, A. Biard, A. Courville, Y. Bengio, C. Pal, P.-M. Jodoin, and H. Larochelle, "Brain tumor segmentation with deep neural networks," *Medical image analysis*, vol. 35, pp. 18–31, 2017.

[18] D. Grosgeorge, C. Petitjean, J.-N. Dacher, and S. Ruan, "Graph cut segmentation with a statistical shape model in cardiac mri," *Computer Vision and Image Understanding*, vol. 117, no. 9, pp. 1027–1035, 2013.

[19] G. Wang, S. Zhang, H. Xie, D. N. Metaxas, and L. Gu, "A homotopy-based sparse representation for fast and accurate shape prior modeling in liver surgical planning," *Medical image analysis*, vol. 19, no. 1, pp. 176–186, 2015.

[20] G. Wang, W. Li, S. Ourselin, and T. Vercauteren, "Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks," in *International MICCAI brainlesion workshop*, pp. 178–190, Springer, 2017.

[21] K. Kamnitsas, W. Bai, E. Ferrante, S. McDonagh, M. Sinclair, N. Pawlowski, M. Rajchl, M. Lee, B. Kainz, D. Rueckert, *et al.*, "Ensembles of multiple models and architectures for robust brain tumour segmentation," in *International MICCAI brainlesion workshop*, pp. 450–462, Springer, 2017.

[22] S. Pereira, A. Pinto, V. Alves, and C. A. Silva, "Brain tumor segmentation using convolutional neural networks in mri images," *IEEE transactions on medical imaging*, vol. 35, no. 5, pp. 1240–1251, 2016.

[23] K. Kamnitsas, C. Ledig, V. F. Newcombe, J. P. Simpson, A. D. Kane, D. K. Menon, D. Rueckert, and B. Glocker, "Efficient multi-scale 3d cnn with fully connected crf for accurate brain lesion segmentation," *Medical image analysis*, vol. 36, pp. 61–78, 2017.

[24] P. Krähenbühl and V. Koltun, "Efficient inference in fully connected crfs with gaussian edge potentials," *Advances in neural information processing systems*, vol. 24, 2011.

[25] T. Le, R. Gummadi, and M. Savvides, "Deep recurrent level set for segmenting brain tumors," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pp. 646–653, Springer, 2018.

[26] G. Wang, W. Li, S. Ourselin, and T. Vercauteren, "Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks," in *International MICCAI brainlesion workshop*, pp. 178–190, Springer, 2017.

[27] F. Yu and V. Koltun, "Multi-scale context aggregation by dilated convolutions," *arXiv preprint arXiv:1511.07122*, 2015.

[28] H. Chen, Q. Dou, L. Yu, J. Qin, and P.-A. Heng, "Voxresnet: Deep voxelwise residual networks for brain segmentation from 3d mr images," *NeuroImage*, vol. 170, pp. 446–455, 2018.

[29] G. Wang, W. Li, M. A. Zuluaga, R. Pratt, P. A. Patel, M. Aertsen, T. Doel, A. L. David, J. Deprest, S. Ourselin, *et al.*, "Interactive medical image segmentation using deep learning with image-specific fine tuning," *IEEE transactions on medical imaging*, vol. 37, no. 7, pp. 1562–1573, 2018.

[30] G. Wang, W. Li, S. Ourselin, and T. Vercauteren, "Automatic brain tumor segmentation using convolutional neural networks with test-time augmentation," in *International MICCAI Brainlesion Workshop*, pp. 61–72, Springer, 2018.

[31] H. Zhang, M. Cisse, Y. N. Dauphin, and D. Lopez-Paz, "mixup: Beyond empirical risk minimization," *arXiv preprint arXiv:1710.09412*, 2017.

[32] H. Jin, Z. Li, R. Tong, and L. Lin, "A deep 3d residual cnn for false-positive reduction in pulmonary nodule detection," *Medical physics*, vol. 45, no. 5, pp. 2097–2107, 2018.

[33] K. Matsunaga, A. Hamada, A. Minagawa, and H. Koga, "Image classification of melanoma, nevus and seborrheic keratosis by deep neural network ensemble," *arXiv preprint arXiv:1703.03108*, 2017.

[34] H. Dong, G. Yang, F. Liu, Y. Mo, and Y. Guo, "Automatic brain tumor detection and segmentation using u-net based fully convolutional networks," in *annual conference on medical image understanding and analysis*, pp. 506–517, Springer, 2017.

Generated using Undegraduate Thesis LaTeX Template, Version 1.4. Department of Computer Science and Engineering, Bangladesh University of Engineering and Technology, Dhaka, Bangladesh.

This thesis was generated on Sunday 3rd September, 2023 at 7:52am.