Feedforward Model of Deep Learning Strategy for Brain Tumor Segmentation on MRI Images

Archana, K. V.,^{1*} Pandey, B.¹ and Komarasamy, G.²

¹School of Computer Science and Engineering, Jain University, Bangalore, India E-mail: archanakv101991@gmail.com,^{*} p.biswajeet@jainuniversity.ac.in ²School of Computing Science and Engineering, VIT Bhopal University, Bhopal-Indore Highway Kothrikalan, Sehore, Madhya Pradesh – 466114, E-mail: komarasamy.g@vitbhopal.ac.in **Corresponding Author*

DOI: https://doi.org/10.52939/ijg.v19i7.2751

Abstract

Computer Aided Diagnosis (CAD) systems are extensively used in the biomedical area. These systems collect and analyze various kinds of images in order to increase the accuracy and speed of diagnostic procedures. Because it can gather comprehensive data on a human organ, magnetic resonance imaging (MRI) is one of the most versatile diagnostic tools available today and is often regarded as a potentially useful method. Due to the fact that brain tumors are now one of the major causes of death in humans, early stage diagnosis and prediction of brain tumors may assist to lower the overall mortality rate. During the course of the last ten years, a number of methodologies have been introduced, the primary emphasis of which has been on the segmentation and categorization of brain tumors. However, the accuracy of classification is dependent on the segmentation; hence, we will be concentrating on the segmentation of brain tumors in this study. Recently, there has been a rise in popularity for semantic segmentation approaches that are based on deep learning. Nevertheless, obtaining the requisite level of performance in terms of precise segmentation is still seen as a difficult undertaking. Introduce a deep learning-based scheme that is primarily based on the encoding and decoding process utilizing cascade approach in order to solve the problem of tumor segmentation. This will allow you to overcome the issue of tumor segmentation. Introduce a new design for the encoder and decoder module, one that makes advantage of 3x3 kernels and stride 2 In addition to that, the model that has been developed makes use of the ResNet model for learning as a residual learning process. The proposed method obtains an average dice score of 0.95, which demonstrates a substantial improvement in comparison to the strategies that are currently in use.

Keywords: Brain Tumor Segmentation, Classification, Deep Learning, Feature Extraction, MRI Images

1. Introduction

The human brain is not only recognized as the dominating management for the central nervous system, but it is also accountable for all actions that are carried out by humans. On the other hand, several factors have contributed to the fact that diverse areas of the body are afflicted with distinct cancers [1]. It is possible for these cancer cells to spread uncontrollably across several regions of the body, including the breasts, lungs, and brain, amongst others [2] [3] and [4]. A tumor is the name given to this kind of uncontrolled proliferation of cells. Surgeons and professionals in the field of medical study have distinguished between a number of distinct forms of tumors. Because the brain is such an important component of the human body, the

investigation of brain tumors will be the primary emphasis of our effort. At the moment, brain tumors may be divided into two categories: primary [4] and metastatic [5] brain tumors. In most cases, only the patient's brain is affected by a primary brain tumor, but metastatic tumors have the potential to spread to other areas of the body. According to research published in 2012 by the Central Brain Tumor Registry of the United States (CBTRUS), brain tumors are the second greatest cause of mortality due to cancer among children, both male and female, of any age group. A total of 69,720 new instances of primary brain tumors were identified in 2013 [6]. Benign and malignant brain tumors are the two categories that are used to classify this condition.



According to a standard grading system that was devised and published by the World Health Organization, brain tumors are rated from grade I (the least severe) to grade IV (the most severe), with grade I being the least severe and grade IV being the most severe (WHO). Brain tumors that have been graded as I and II are considered to be benign, but brain tumors that have been graded as III and IV are considered to be malignant [7]. Research that was carried out not too long ago, published not too long ago, and can be found in [8] determined that the incidence of benign and malignant tumors combined was 23.03 instances per 100,000 people. This information can be found in [8]. Finding brain tumors at an early stage is vital for obtaining an accurate diagnosis and, ultimately, creating a treatment strategy that will be beneficial in the battle against the illness. The earlier the tumors are found, the more time there is to formulate an effective treatment plan.

This is due to the fact that it is general known that brain tumors have the potential to have such a huge influence on a person's life for the whole of their disease. Consequently, this is the reason why this is the case. In order to ease the execution of a wide variety of activities, a wide variety of applications that can image the brain have been developed. Some of the tasks that come under this area include the mapping of the brain, the detection of brain abnormalities, the categorization of the various kinds of brain tissue, the assessment of the volume of brain tumors, and the segmentation of brain tumors. Mapping the brain and dividing up brain tumors are two of the other responsibilities. Among other things, there is the task of mapping the brain. In addition, a number of applications have been developed expressly with the goal of completing certain obligations and duties. These apps may be downloaded through the app store. On the other hand, distinguishing brain cancers manually presents a significant challenge for human professionals due to the wide variety of sizes and shapes that brain tumors can take, in addition to the locations and intensities of the tumors in images. This is due to the fact that brain tumors can take on many different forms. This is owing to the fact that brain tumors may manifest themselves in a wide variety of various ways. This is owing to the fact that there are many different ways in which brain tumors may present themselves to the patient. Because of this factor, it is quite challenging for human experts to carry out this task [The chain of causation]. As a direct consequence of these problems, the process of segmentation consumes a large amount of time and only provides an accuracy level that is below average. This is an issue since the process of segmentation costs time. As an immediate result of this reality, the method in question is not one

that is encouraged. The imaging modalities in question play a very big role in the diagnosis process because of their ability to conduct in-depth investigations of specific parts of the body. As a consequence of this ability, the diagnostic method is highly important. The magnetic resonance imaging (MRI) method is a painless imaging tool that does not need any intrusive procedures and provides a significant amount of information about the brain and spinal cord.

The term "magnetic resonance tomography" may also be used to refer to this imaging technology. In a separate setting, this technique is referred known as "magnetic resonance tomography," which is a mouthful. Radio waves and magnetic fields are used during the imaging process that is referred to as magnetic resonance imaging (MRI). This technique is used to get images of an individual's internal anatomy. The technology known as magnetic resonance imaging (MRI) makes use of both of these components. When compared to other imaging modalities, this imaging approach is regarded to be the most effective one since it detects the full structure of the brain, which allows it to convey the information in the most comprehensive manner that is imaginable to human beings. Other imaging methods are not capable of detecting the whole of the brain's structure. There are many different kinds of magnetic resonance imaging (MRI) that can be performed today. Some examples of these include T1-weighted magnetic resonance imaging (MRI) (T1w), T1-weighted magnetic resonance imaging (MRI) with contrast enhancement (T1wc), and T2weighted magnetic resonance imaging (MRI). T1weighted magnetic resonance imaging (MRI) (T1w), fluid attenuated inversion recovery, and T1-weighted magnetic resonance imaging (MRI) with contrast enhancement are some of the other types of MRI modalities (T2w). Combining contrast enhancement with T1-weighted magnetic resonance imaging (MRI) is yet another approach that might be used (T1wc). On the other hand, this list does not include all of the potential options that may be taken into consideration. In addition to that, magnetic resonance imaging (MRI) scans may also be of the fluid attenuated inversion recovery (FAI) and T1-weighted forms respectively (FLAIR). In the Figure 1 that can be found lower down on this page, you will find some examples of photographs that were obtained by making use of each of the four unique MRI modalities. These examples were used to create the images. You may discover this image by scrolling farther down on this page. You may get a better idea of what they seem to be like by looking at these images, which are available for your perusal.



Figure 1: Image examples from various imaging modalities: (a) T1-Weighted (b) T2-Weighted (c) FLAIR (d) FLAIR with contrast



Figure 2: Map of research on brain tumor detection dataset in different countries in the world

When it comes to the investigation of brain tumors, the imaging sequence known as T1W is the one that is used most often. This is because it is much simpler to annotate in this format than in others. On the other hand, images with a greater contrast make the boundary of the brain tumor more apparent, which contributes to an increase in the accuracy of the processes of identification and segmentation.

In the realm of applications pertaining to medical imaging, computer vision techniques are now garnering an increasing amount of interest these days. In Figure 2. Taken dataset from MICCAI, CBICA Brats data set from USA North Continent. Done Research in South India. Deep learning [9], feature analysis [10], support vector machines [11], as well as a great number of other techniques, are among the many different methodologies that are accessible and might be used in order to segment brain tumors [9] [10] and [11]. The majority of the currently available techniques for tumor segmentation are built on top of deep learning. These techniques include: 3x3 kernel CNN [12], cascaded anisotropic convolutional neural networks (FCNNs) and Conditional Random Fields (CRFs) [14], and DeepMedic, which uses multiscale 3D CNN with fully connected CRF. Chen et al., [15],

who compared the DeepMedic model to the Multi-Level DeepMedic model, offered a dual-force model [16]. In this particular field, the segmentation of brain tumors may take either a two-dimensional or a threedimensional approach. It is challenging to find a solution to the issue of computational complexity since the processing of the massive amount of MRI data that hospitals generate requires additional time. Razzak et al., [18] built a CNN-based architecture, and while they got decent results for tumor segmentation, complexity is still a challenging problem. The use of MLDeepMedic, as stated by the authors of reference 16, contributes an additional 10% in complexity to both the spatial and temporal aspects of the DeepMedic method. To continue in this vein, improving the level of segmentation accuracy is a hard process.

As a direct result of this, the application of the deep learning approach to the process of extracting information about brain tumors from MRI scans needs to be the primary focus of our investigation. This method's overarching objective is to cut down on the number of erroneous positive results, which, in turn, will lead to an increase in the segmentation's precision. This article will provide a novel CNNbased architecture with the intention of presenting encoder and decoder models together with particular strides and convolution blocks. The purpose of this presentation is to introduce these models. Rest of the article is arranged as follows: section II presents brief literature review about various schemes of brain tumor segmentation, section III presents proposed solution and CNN architecture for brain tumor segmentation, section IV presents comparative analysis of segmentation performance, finally, section V presents concluding remarks and future work.

2. Literature Survey

In this part, we will investigate the many different methods now available for segmenting brain tumors. Because the deep learning methods that were presented in the preceding part are frequently used in the job of segmenting brain tumors, the emphasis here will be exclusively on those deep learning approaches.

Imaging methods in both the two-dimensional and three-dimensional planes need to be used in order to provide an appropriate diagnosis in the area of medicine. The use of deep learning algorithms is making a significant contribution to the conversation that is taking place around this issue, as was said before. Pereira et al., [12] created a CNN-based technique that uses kernels that are three by three. The cluster is not very large, which makes it easier to implement its intricate design. This is due to the fact that it is not to spread out. In addition to this, it helps to lower the risk of making the mistake of overfitting the data. Wang et al., [13] developed Cascaded Anisotropic Convolutional Neural Networks with the goal of segmenting the multi-modal MRI images into three unique categories: overall tumor, tumor core, and enhancing tumor core. In order to accomplish the task of segmenting the photos, this step has to be taken. The multi-modal MRI scans were used in order to classify each of these categories into their appropriate subsets. In order to design a deep learning model for the segmentation of medical images, Zhao et al., [14] used image patches and slices in two dimensions as its building blocks. In order to separate the photos, the model was used. This model was used in the process of creating the model that was developed. Image segmentation was accomplished successfully with the assistance of the model, which eliminated any potential for errors. This model is trained in three stages: first, an FCNN is trained by making use of image patches; next, the parameters of the trained FCNN are employed for training the CRF as an RCNN; and finally, a finetuning approach is applied to these two trained models.

Initially, an FCNN is trained by making use of image patches; next, the parameters of the trained FCNN are employed for training the CRF as an RCNN. First, an FCNN is trained by using image patches; next, the parameters of the trained FCNN are used for training the CRF as an RCNN. Finally, the trained FCNN is evaluated to determine its accuracy. First, a fully convolutional neural network (FCNN) is built by employing image patches; next, the learned parameters of the FCNN are utilized for further training of the CRF as an RCNN. At long last, the trained FCNN is put through its paces in order to discover how accurate it is. This model is often trained with the assistance of two-dimensional image patches and slices that are created from axial, coronal, and sagittal angles of view. After that, the patches are joined, and a voting-based fusion process is utilized in order to separate the brain tumor into its component pieces. This is done in order to remove the tumor. In order to conduct out segmentation, Chen et al., [16] put their attention on the hierarchical qualities that are evident in MRI. This allowed them to see what they were looking for. After that, a distribution-based loss function is presented, a dualforce learning model is presented to improve the learning of multi-level features, and finally, a postprocessing approach that uses Multi-Layer Perceptron is developed to improve the prediction results. All of these are presented in the following order: The completion of each of these processes occurs directly after the one before it.

The Deep Medic model will serve as the primary focus of this investigation. Research done in various parts of world USA, UK, South Africa and India using ResNet.

Following this step, the model is extended so that it may make use of information on several levels in order to improve the accuracy of the segmentation. The presently accessible methods for segmentation are based on three different types of strategies: ensemble, cascaded, and three-dimensional convolutions. Nevertheless, the segmentation process becomes more computationally complicated as a result of these tactics. As a direct result of this, Luo et al., [19] developed a hierarchical decoupled convolution network, also known as an HDC-Net. This is a neural network that makes use of hierarchical decoupled convolutions rather than 3D convolutions. The "Ensemble" and "Cascaded" techniques of segmentation are both based on the same fundamental principle of hierarchical decoupled convolution, which may be explained as follows: (HDC).

3. Proposed Method

In this part, we will show the solution that we have developed for the automatic segmentation of brain tumors. Recently, U-Net based models have become more popular for use in biomedical image segmentation; nevertheless, these models are susceptible to loss as a result of the many different types of up and down sampling. Introduce an innovative strategy for the segmentation of brain tumors so that these problems may be resolved. In order to segment the image, the suggested method utilizes the auto encoder architecture as its foundation. Image segmentation, in general, is also known as a pixel classification issue, which is when a machine learning model classifies the pixel to determine whether or not it belongs to the mask. Up sampling and down sampling, which are often referred to as encoder operations and decoder operations, are both carried out by the proposed network. The primary objective of the encoding module is to acquire knowledge of the low-level feature representation, which is accomplished via the use of a number of different convolutional layers and a non-linear activation function. In this case, the kernel size should be set to 3, so that the dimensions of the input images may be decreased. The decoder portion, on the other hand, is responsible for restoring the dimensions of the data all the way up to the size of the original input, which is then used to the process of fitting the mask to the ground truth. The overall structure of the suggested method is shown in Figure 3, which can be seen below.

The primary goal of using this method is to build a cascade architecture so that the information may be passed on to further modules. The purpose of this section is to demonstrate encoding and decoding blocks that have varied configurations. The output of encoder block is sent to encoder block 2, which in turn sends it as input to decoder block 1, which also receives it. The architecture of the encoder block is shown in Figure 4(a), and the design of the decoder block is shown in Figure 4(b).



Figure 3: Brain tumor segmentation using a proposed cascaded CNN architecture



Conv[(1x1),(m, m/4),/2]

(b)

Block	E	Encoder		Decoder	
	m	Μ	n	n	
1	64	64	64	64	
2	64	128	128	64	
3	128	256	256	128	
4	256	512	512	256	

Figure 4: (a) Encoder module and (b) Decoder module Table 1: Encoder and decoder module count for input and output

(a)

Filters stands for the input channel, and n, which stands for the output channel. The encoder block has a typical convolutional layer after an upsampling of the input with stride 2; the output channels are taken into consideration for this layer. The encoder block also has a 3x3 convolution layer. The strategy that is used in this method involves cascading the input of the first layer that undergoes the convolution process so that it becomes the input of the next layer that undergoes the convolution process after the output of the layer that came before it. This is done so that the input of the layer that came before it is used as the input of the layer that comes after it. In a manner that is analogous to this, the decoder block consists of not just one but two convolution layers, as well as a fullconvolution layer that employs down sampling. The information that can be found in Table 1 pertains to the number of inputs and outputs that can be found on the encoder module as well as the decoder module.

Conv[(3x3),(n, n)]

Conv[(3x3),(n, n)]

Conv[(3x3),(n, n)]

Conv[(3x3),(m, n),/2]

The encoder module of the envisioned design is based on the ResNet paradigm. This information is also cascaded to earlier inputs with the assistance of connection models. The ResNet module has many encoding blocks, which are used to feed the information using convolution. Additionally, this information is cascaded to earlier inputs. The suggested model begins with a convolution operation that has a kernel size of 7 and uses stride 2; the result of this model is 64 channels, and it is then followed by 3x3 max-pooling while using stride 2. On the other hand, the output module is made up of a deconvolution block that has 32 filters and stride 2, a traditional convolution layer that also has 32 filters, and a 2x2 deconvolution layer that has a single output channel and stride 2 at the very end. The ResNet model consist a sequence of residual units where the output of a specific residual unit can be computed in Equation 1:

$$x_n = x_{n-1} + \mathcal{F}(x_{n-1}; \mathcal{W}_n)$$

Equation 1

Where x_n denotes the output of n^{th} RU, $\mathcal{F}(x_{n-1}; \mathcal{W}_n)$ is the residual whose parameters are provided as \mathcal{W}_n . Hence, do not compute the output x_n directly and \mathcal{F} computes the residual that is added to the previous input as represented in (1). This process is known as skip-connection because of unavailability of connection between input x_{n-1} and output x_n which skips the computation of \mathcal{F} . Let us consider n^{th} and m^{th} residual units by assuming that the m^{th} layer is near to the output layer. The outcome of m^{th} unit can be expressed in Equation 2:

$$x_m = x_n + \sum_{i=n}^{m-1} \mathcal{F}(x_i; \mathcal{W}_{i+1})$$

Equation 2

International Journal of Geoinformatics, Vol.19, No. 7, July, 2023 ISSN: 1686-6576 (Printed) | ISSN 2673-0014 (Online) | © Geoinformatics International The training process considers training loss as l, then use the chain rule to represent the loss of derivative that is corresponding to the output is represented in Equation 3:

$$\frac{\partial l}{\partial x_n} = \frac{\partial l}{\partial x_m} \frac{\partial x_m}{\partial x_n} = \frac{\partial l}{\partial x_m} + \frac{\partial l}{\partial x_m} \sum_{i=n}^{m-1} \frac{\partial \mathcal{F}(x_i; \mathcal{W}_{i+1})}{\partial x_n}$$
Equation 3

This can be rewritten and to find a relation between residual and output as represented in Equation 4:

$$\frac{\partial l}{\partial x_n} = \frac{\partial l}{\partial x_m} \frac{\partial x_m}{\partial x_n} = \frac{\partial l}{\partial \mathcal{W}_m} \left(\frac{\partial l}{\partial x_m} + \frac{\partial l}{\partial x_m} \sum_{i=n}^{m-1} \frac{\partial \mathcal{F}(x_i; \mathcal{W}_{i+1})}{\partial x_n} \right)$$

Equation 4

From Equation (4), can conclude that the weight update process depends on the two parameters such as:

$$\frac{\partial l}{\partial x_m} \text{and} \frac{\partial l}{\partial x_m} \sum_{i=n}^{m-1} \frac{\partial \mathcal{F}(x_i; \mathcal{W}_{i+1})}{\partial x_n}$$
Equation 4

Further, to present loss function modeling to reduce the training error. Consider three different loss functions dice loss, L2 loss and KL divergence. The dice loss L_{Dice} is a soft loss which is applied to the output of decoder module to match the predicted segmentation. This can be given in Equation 5:

$$L_{Dice} = \frac{2 * \sum p_{gt} * p_{predict}}{\sum p_{gt}^2 + \sum p_{pred}^2 + \alpha}$$
Equation 5

 p_{gt} denotes the ground truth of segmentation, $p_{predict}$ denotes the predicted segmentation mask and α is a small constant. Similarly, the L2 loss is measured based on the input image and predicted segmentation mask. This is given in Equation 6:

$$L_{L2} = \left\| I_{inp} - I_{pred} \right\|_{2}^{2}$$
Equation 6

Finally, the KL divergence is computed between normal and prior distribution which can be represented in closed form as mentioned in Equation 7:

$$L_{KL} = \frac{1}{N} \sum \mu^2 + \sigma^2 - \log \sigma^2 - 1$$
Equation 7

Where *N* represents the total number of image voxels, noraml distribution is $\mathcal{N}(\mu, \sigma^2)$ and prior distribution is $\mathcal{N}(0,1)$. The loss optimization process uses Adam optimizer with the learning rate of 1e-5, given in Equation 8:

$$\alpha = \alpha_0 * \left(1 - \frac{e}{N_e}\right)^{0.9}$$

Equation 8

Where e denotes the epoch counter, N_e denotes the total number of epochs.

4. Results

In this section, describe the experimental study of proposed cascading approach of brain tumor segmentation. The proposed approach is implemented on GPU enabled operating system the complete implementation details are as follows: windows operating system, PyCharm IDE, 8 GB RAM and 8 GB NVDIA graphics card. Simulation parameter for CNN architecture is presented in below given Table 2. The data should be divided in a ratio of 70% to 30%, with 70% of the data being used for training and 30% of the data being used for testing.

Parameter	Value
Batch Size	1
Epochs	30
Learning rate	5e-4
Drop out	0.2
Convolution	3
De-convolution	3
Activation function	ReLU
Optimizer	Adam

Table 2: Parameter for CNN architecture simulation

During testing, in order to measure how well the proposed method performs in terms of the Dice score, which can be calculated using Equation 9:

$$DICE = \frac{2 * TP}{FP + FN + 2 * TP}$$
Equation 9

Where TP denotes the true positive which is the measurement of correctly segmented tumor pixels, FP denotes the fasle positives which is a measurement of pixels which are not in the tumor class but classified as tumor and FN denotes the false negative which is measurement of pixels that are turmor but classified as non-tumor. Consider using the T1-weighted CE-MRI dataset that is readily available to the public for this experiment [30]. There are a total of 3064 grayscale photographs acquired, 1047 of which are coronal images, 1027 of which are sagittal images, and 990 of which are axial images.

These images are collected from three distinct orientations. Meningiomas, pituitary tumors, and gliomas are the three different classes of tumors that may be seen in these photos. The sample results obtained using the suggested approach are shown in Figure 5, which may be seen below. Similarly, present comparative performance for training loss and dice score for the given number of iterations. This analysis given in Table 3 and the graphical representation is presented in Figure 6.

According to the findings of this research, the DICE score improves as the number of epochs rises, while the training loss for both the training dataset and the validation dataset decreases. The acquired performance is compared with that of other ways, which are laid out in table-4 below. This is done such that the average DICE score may be reached, which is 0.95.

Ground Truth	Predicted Mask	Difference between Masks	Dice Score
			0.949
			0.876
			0.909
		•	0.929
			0.95

Figure 5: Sample of the proposed approach's results

 Table 3: DICE Score Comparison

Method	DICE Score
LinkNet (LN)	0.76
Dual-Scale LinkNet (DS-LN)	0.78
Triad-Scale LinkNet (TS-LN)	0.77
Multi-Scale LinkNet (MS-LN)	0.77
Cascaded Dual-Scale LinkNet (CDS-LN)	0.80
Proposed Cascaded Model	0.95



Figure 6: Comparative performance for training loss and DICE score



Figure 7: Comparative performance of DICE, Sensitivity and Specificity

Test	Hausdorff (mm)	Accuracy	Computational Time(s)
LN	63.27	83.3	46
DS-LN	61.87	86.5	54
TS-LN	55.67	89.8	38
MS-LN	43.27	91.3	46
CDS-LN	41.87	92.5	39
Proposed Model	33.45	97.3	13

Table 4: Comparative quantitative results of performance measure

Figure 7 shows the proposed algorithm validation performance dice score, Sensitivity, Specificity with the compared algorithms. The proposed method attains promising results in terms while comparing with the other approaches. Table 3 shows the compared the quantitative performance of the proposed framework compared with the well-known segmentation algorithm. The testing was performed on the standard MR images dataset. The results show that the proposed model outperforms the existing compared methods in terms of Hausdorff (mm), Accuracy and computational time. Figure 8 shows axial, coronal, sagittal views of segmented MRI images using the proposed framework. Figure 9 shows the tumor segmented images obtained by the proposed approach under different views.



Figure 8: (a) Axial, (b) Coronal, (c) Sagittal view of the extracted brain tumors



Figure 9: Results obtained by our proposed ResNet approach in different views

5. Conclusion

The purpose of this study effort is to offer an automated approach for segmenting brain tumors using the Deep Learning scheme. The currently available methods (such as morphological analysis), however, have an issue with their low accuracy. As a result, deep learning strategies have been developed, however the most recent deep learning strategy calls for a significant amount of computing time and is unable to provide the expected results. As a result, the

International Journal of Geoinformatics, Vol.19, No. 7, July, 2023 ISSN: 1686-6576 (Printed) | ISSN 2673-0014 (Online) | © Geoinformatics International objective is to create an unique deep learning scheme that makes use of a cascade process and in which encoder and decoder models extract and learn highlevel characteristics. The encoder and decoder architectures that have been developed make use of convolution layers that have strides in a cascading fashion. Learning is accomplished by the usage of ResNet architecture in this model. According to the findings of the comparison study, the suggested method gets a higher dice score when compared to the methods that are already in use.

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