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Deep CNN architectures building blocks for implementing automatic Brain tumor segmentation

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ABSTRACT:

A brain tumor is a major death cause of cancerous disease. The tumor division and its quantitative measurements are the great challenges in biomedical analysis. Since manual division would be tedious and unreasonable for broad examinations. Deep learning is a field which gives optimized solution for the intracranial tumor analysis. This paper shows a review of cutting-edge architecture of deep learning for intracranial tumor division, with the existing methodologies. Brain tumor is also known as intracranial tumors. The proposed methodology gives better results when related to the present methodologies. The results show the performance of the fully convolutional network which is derived by the analysis of different deep learning models through different datasets. The conclusion section also discussed the open challenges faced in brain lump division.

Keywords: CNN Architecture, tumor division, intracranial tumors, Deep learning,

INTRODUCTION

A brain lump or tumor is the abnormal growths of tissue in the cerebrum and affects function of brain and causes death. Tumor cells may be cancerous (malignant) or non-cancerous (benign). Mutationsin genes may cause a mass of cells to grow in and around the cerebrum to cause a tumor. Primarytumor & secondary tumor are two different types of tumor. The first one appears in the cerebral matter and the secondary tumor is spread to different organs of the biological structure. Medulloblastoma is a fast-growing cancerous intracranial tumor among children.

Tumor detection by manual systems is time-consuming, non-automated, stagnant and tedious, and error-prone. Researchers from all over India are trying to find an automated system to predict and identify the disease. Tumors can be diagnosed by MRI, CT and PET test. For fast-growing tumors, Surgery is the common treatment, whereas radiation andchemotherapy are used for slow-growing tumors. Moreover, identifying the tumor becomes complex depending on the large variability in shape, location, and size.

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1. RELATED WORKS

A machine learning technique focus on the medical image analysis and depends on the built in methods in the image processing techniques and also needs human assistance for processing the data [3].

Over the past few years, Deep Learning based approaches perform an important role in brain lump division. As compared earlier, DL approaches relies on a large dataset for training and fewer pre-processing steps, this become the main reason to popularized upcoming deep learning technique used for automatic detect brain tissue abnormal growth division.

In the past few years, massive research was going on deep learning architecture to generate optimized results in intracranial tumor division. In previous investigations, modeling a network to categories many image patches, a fully convolutional neural network (FCN) proposed an automatic generate the map slice by slice. Ronnerberger et al, who proposed the architecture withsymmetric FCN named U-Net and used it in challenging tasks [5].

2. METHODOLOGY

1. Deep CNN architectures:

1. U-Net:

This is basically a convolutional network architecture for semantic division. U-Net was designed and applied in 2015 to process biomedical image division. U-net works on classification of each and every pixel to distinguish the borders; therefore they share the same size for input and output dataset. The U-Net organization doesn't have a completely associated layer. As shown in figure 1, U- net has two paths. The left hand side path is called contracting path and right hand side path is called expansive path. Both the paths perform encoding and decoding process. Earlier path i.e. left side performs encoding and the former right side path performs decoding. After that max pooling and ReLU activation function has been performed.

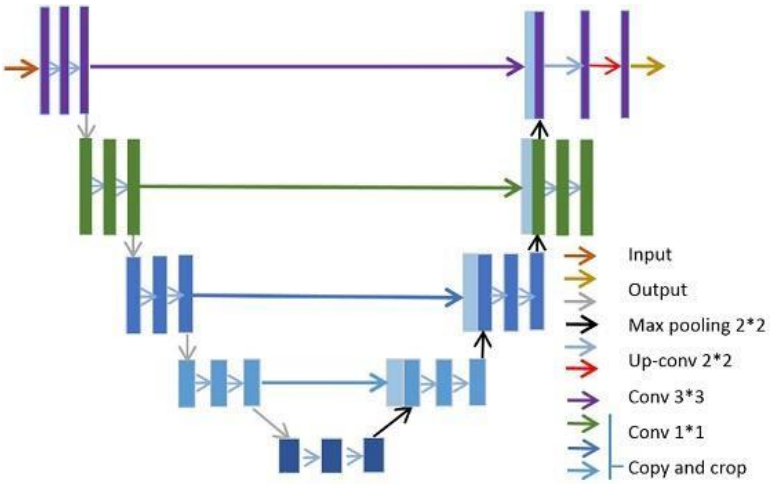

Fig.1. Building block of U-Net

U-Net takes its name from the engineering, which when pictured, seems like the letter U, as demonstrated in the figure1 above. Info pictures are acquired as a fragmented yield map.

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2. S3DU-Net:

Ronnerberger proposes the new architecture which is based on the U-net, i.e. Separable 3D U-Net architecture. It contains both encoder and decoder to analyze the convolutional and de-convolutional layer of the intracranial tumor division.

The encoder has a 128x128x128 voxel block with 4 channels and 5 levels. Every level contains 2 Separable 3D U-Net architecture block except for the level 1 of the left side i.e. contracting path.

The transition down module is usedto reduce the resolution of the feature map and doubling the number of channels. It consists of 3x3 convolutions with stride2, followed by normalization and Leaky ReLU. The feature map sizeis reduced to 8x8x8.

To recover the input resolution of the decoder, adopt the up sampling and halve the number of channels. The decoder uses a 1x1x1 convolution with stride 1 to reduce the channel numbers. The transition up module consists of transposed 3x3 convolutions with stride2, followed by normalization and Leaky ReLU. Then the featured maps are concatenated through the long skip connections. The final step is done by 1x1x1 convolutional layer with softmax operation.

2. SegNet:

The SegNet architecture comprises the grouping of encoders and decoders followed by a pixel wise classifier. Each encoder way has at least one convolutional layer and a ReLU non-linearity. The decoder utilizes the pooling files to process the max-pooling lists for up-sampling theelement maps. The last yield was taken care of into a softmax classifier layer.

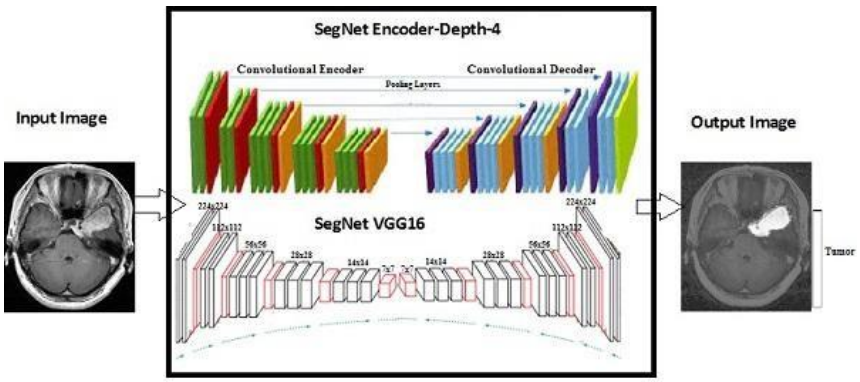

Figure 2. Division using SegNet

Figure 2 shows the pipeline of the SegNet networks. The encoder way comprises at least one convolution block, each of which is trailed by a maximum pooling activity for down examining. . The convolutional decoder was regularly constructed to the convolutional encoder path except that the maximum pooling activity is removed by an up-sampling activity. Up-sampling gives the pooling records of the relating encoding layer as info. The output of the last decoder, which is a high dimensional element representation, is taken care of into the softmax classifier layer, which groups every pixel freely.

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a. MCCNN and CRF:

The Multi Cascaded Convolutional Neural Network (MCCNN) architecture assists us with removing more multi-scale features for tumor division. MCCNN and completely associated contingent irregular fields (CRFs) are joined to introduce a coarse to fine division. The Division interaction predominantly incorporates two stages. To start with, they plan a multi-cascaded network architecture by consolidating the transitional consequences of a few local dependencies of labels into account and make use of multi-scale features for the coarse division. Second, they apply CRFs to think about the spatial relevant data and remove some deceptive yields for the fine division. The proposed technique utilizes picture patches got from pivotal, coronal, and sagittal perspectives. The epic strategy is assessed on the accessible datasets BRATS 2013, BRATS 2015, and BRATS 2018

2. **Suggested Methodology:**

1. Improved Fully Convolution Network:

This methodology is presumed on U-Net structure which was extended and modified by introducing cross-layer architecture incorporating up skip connection and inception modules [5]. The module between the convolutional and the de-convolutional is prone to comprehend multi- scale characteristics for intracranial tumor division. The forward propagation approach permitsthe encoder to extract low-level features and restore spatial information. The up skip connection also helps to ameliorate the gradient flow in the back propagation process. The proposed technique adopts a 3x3 de-convolution layer with stride 2 to acquire the same size of outputs, meanwhile, the skip connection adopts a 1x1 convolutional layer with stride 1 to stabilize the featured maps[5].To optimize the performance The inception module is used and to capture more information under computational complexity. This module is designed with a 7x7 convolutional layer to maximize the field. They adopt Batch normalization operations to stabilize the feature maps[5]. Cascaded strategy is also added in the training phase for segmenting whole, core, and enhances tumor regions.

2. EVALUATION METRICS

The execution model was estimated on the image database from the Multimodal Intracranial tumor division challenge BRATS 2015, BRATS 2017, and BRATS 2018[5][7].

Each patient had a different type of MRI sequences (i.e T1-weighted (T1), T1 contrast-enhanced (T1c), T2-weighted (T2), and Fluid Attenuated Inversion Recovery (FLAIR)). For practical clinical applications, the evaluation task is grouped into three sub-regions:

- Whole tumor contains all four intratumor regions.(label,2,3,4)
- Core tumor consists of three intratumor regions exclusive of (label 2)edema.
- Enhancing tumor consists of enhancing tumor (label4)

For the intracranial tumor region division results, the evaluation was done on quantitative measurement using the Dice score, sensitivity, and specificity[5].The Dice score estimates the similitude of two segmented maps. It goes from 0 to 1, and higher dice esteem shows a superior match. As to every tumor sub-region, given the paired division map A Ɛ (0,1) acquired from forecasts of division models and the comparing ground truth B Ɛ (0,1), the Dice score is defined as follows:

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$$\text{Dice(A,B)} = \frac{2 * |A1 \cap B1|}{(|A1| + |B1|)} \quad (1)$$

Where $|A1 \cap B1|$ described the number of factors observed in each unit and $|A1|and|B1|$arethe cardinalities of the two units (i.e. Pixels are A=1 and B=1).

3. RESULT

The learning ability of the architecture will improve by expanding the intricacy of the methods. Table.1 Shows the comparison of the MCCNN & CRF method with other approaches in terms of Dice score. On the Overall performance, the MCCNN & CRF method dice scores exceed all the other methods in the Table1.

Table 1.Assessment of MCCNN+CRF+Postprocess method with other approaches [2].

Dataset	Method	Dice score		
		WT	TC	ET
BRATS 2015	Zhao et al.	0.84	0.73	0.62
	Chen et al.	0.85	0.70	0.63
	Kamnitsas et al.	0.847	0.670	0.629
	MCCNN+CRF+Post-Process	**0.87**	**0.76**	**0.75**
BRATS 2018	Zhou et al.	0.907	0.835	0.792
	Wang et al	0.896	0.730	0.770
	Chandra et.al	0.871	0.794	0.740
	Zhang et.al	0.889	0.739	0.749
	MCCNN+CRF+Post-Process	**0.882**	**0.748**	**0.717**

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Table 2: Assessment based on the dice score

Dataset	Method	Dice score		
		WT	**TC**	**ET**
BRATS 2015	U-Net	0.864	0.694	0.664
	SegNet	0.856	0.670	0.612
	3D U-Net	0.856	0.618	0.655
	FCN	**0.890**	**0.733**	**0.726**
BRATS 2017	U-Net	0.848	0.726	0.549
	SegNet	0.833	0.703	0.496
	3D U-Net	0.835	0.655	0.551
	FCN	**0.876**	**0.763**	**0.642**
BRATS 2018[9]	3D U-Net without proposed S 3D Block	0.899	0.868	0.684
	3D U-Net with S 3D Block	0.838	0.783	0.689

Table 1 obtained values MCCNN +CRF are compared with the following dice score and table 2 upgrade the esteem values. Existing methodologies show the dice score for the different datasets and comparing all these methods, FCN enhances the optimized results. The measurable test outcomes further shows, that the improved fully convolutional network presents huge upgrades contrasted and existing profound learning-based methods.

Table.3 shows that this technique accomplishes the following results, by using the FCN - Inception based U-Net method, the dice score is about 0.838(whole tumor),0.676(core tumor), and 0.586(Enhance tumor) whereas by including the up skip connection and cascaded training strategy, the result achieves the better performance of the dice scores 0.845(whole tumor),0.698(core tumor), and 0.600(Enhancing tumor), suggesting that the proposed strategy can accomplish a performance that can contend with existing intracranial tumor division methods. This model (Improved FCN-Inception-based U-Net +up skip connection + cascaded training strategy[5]) can automatically generate division maps slice by slice for the simplified procedures.

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Table 3: Performance of the framework of BRATS 2015

Dataset	Method	Dice score		
		WT	TC	ET
BRATS 2015	Zhao et al.(2017)	0.80	0.66	0.57
	Kamnitsas et al(2016)	0.836	0.674	0.629
	FCN(Inception based U-Net)	0.838	0.676	0.586
	FCN(Inception based U-Net + up skip Connection)	0.844	0.693	0.595
	FCN(Inception based U-Net + up skip connection + cascaded training strategy)	**0.845**	**0.698**	**0.600**

In the above, all methods, the proposed methodology (i.e.) the improved fully convolutional Network shows the optimization results with existing methods. Quantitative Analysis has revealed that this model can complete with state-of-the-art methods.

4. CONCLUSION

This article has examined a few Deep CNN architectures, cutting-edge strategies, and building blocks for implementing automatic intracranial tumor (**Intracranial tumors)** division. The vigor of the deep learning approach is as yet substandard compared to master execution. In the present study, BRATS 2015, 2017, 2018 datasets are in the way of comparing with the state-of-the-art methods. Moreover, an improved Fully Convolutional Network was based on modifying the U-Net architecture to accomplish execution that can contend with cutting-edge intracranial tumor division methods. The analytical results have shown that the cluster of data from various perspectives can improve the presentation of tumor division, but not every single view can accomplish great division results. For future development, the cluster of data can be segmented with a large set of training datasets. The lack of large training datasets is open cutting-edge for deep learning methods. The labeling of tumor images is a great challenge in intracranial tumor analysis. Modifications in the Fully convolutional Network (FCN) eventually leading to better diagnosis in intracranial tumor division.

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