ANALYSIS OF BRAIN MR IMAGES FOR TUMOUR DETECTION

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ABSTRACT

Detection of brain tumor using a segmentation based approach is critical in cases, where survival of a subject depends on an accurate and timely clinical diagnosis. Gliomas are the most commonly found tu- mors, which have irregular shape and ambiguous boundaries, making them one of the hardest tumors to detect. The automation of brain tumor segmentation remains a challenging problem mainly due to signif- icant variations in its structure. An automated brain tumor segmentation algorithm using deep convolu- tional neural network (DCNN) is presented in this paper. A patch based approach along with an inception module is used for training the deep network by extracting two co-centric patches of different sizes from the input images. Recent developments in deep neural networks such as dropout, batch normalization, non-linear activation and inception module are used to build a new ILinear nexus architecture. The mod- ule overcomes the over-fitting problem arising due to scarcity of data using dropout regularizer. Images are normalized and bias field corrected in the pre-processing step and then extracted patches are passed through a DCNN, which assigns an output label to the central pixel of each patch. Morphological opera- tors are used for post-processing to remove small false positives around the edges.

Keyword : - MRI, CNN, Segmentation,MATLAB.

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1. INTRODUCTION

In the age of machines, where most tasks are being automated, the automation of image segmentation is of substantial impor- tance. This is significant in medicine field, due to the sensitiv- ity of underlying information. Segmenting lesions in medical im- ages provide invaluable information for lesion analysis, observing a subject's condition and devising a treatment strategy. Brain tu- mor is an abnormality in brain tissues, which leads to a severe damage to the nervous system, and in extreme cases can cause death. Gliomas are the most common and threatening brain tu- mors with the highest reported mortality rate due to their quick progression . These are infiltrative in nature and mostly esca- late near the white matter fibre, but can spread to any part of the brain making them very difficult to detect. Glioma tumors are generally divided into four grades by the world health organiza- tion (WHO). Grade one and two tumors refer to the low grade gliomas (LGG), whereas grade three and four are known as the high grade gliomas (HGG), which are severe tumors with a life expectancy of about two years . Grade four tumors are addition- ally called glioblastoma multiforme (GBM) and have an average life expectancy of around one year . GBM and the encompassing edema can lead to a major impact, devouring healthy tissues of the brain. High grade gliomas show conspicuous micro-vascular multi- plications and territories of high vascular thickness. Treatment al- ternatives for gliomas incorporate surgery, radiation treatment, and chemotherapy . Magnetic resonance imaging (MRI) is a commonly used imag- ing technique for detection and analysis of brain tumors. MRI is a non-intrusive system, which can be utilized alongside other imaging modalities, such as computed tomography (CT), positron emission tomography (PET), and magnetic resonance spectroscopy (MRS), to give accurate data about tumor structure . However, use of these modalities alongside MRI is expensive and in some cases can be invasive such as PET. Therefore, different MRI modal- ities that are non-invasive and image both structure and functions are mostly used for brain imaging. MRI machines themselves come with different configurations and produce images with varying

intensities. This makes tumor detection a difficult task, when different MRI configurations (such as 1.5, 3 or 7 T) are used. These configurations have different intensity values across voxels, which result in masking the tumor regions . MRI can be normalized to harmonize tissue contrast, making it an adaptable and widely used imaging technique for visualizing regions of interest in the hu- man brain. MRI modalities are combined to produce multi-modal images giving more information about irregular shaped tumors, which are difficult to localize with a single modality. These modal- ities include T1-weighted MRI (T1), T1-weighted MRI with contrast improvement (T1c), T2-weighted MRI (T2) and T2-weighted MRI with fluid attenuated inversion recovery (T2-Flair) . This multi- modal data contains information that can be used for tumor segmentation with a significant improvement in performance. The human brain is usually segmented into three regions i.e., white matter (WM), grey matter (GM) and cerebrospinal fluid (CSF) . Tumor regions normally reside near the white matter fibre and have fuzzy boundaries, making it a challenging task to segment them accurately. Different tumor regions include necrotic center, active tumor region, and edema, which is the surrounding area swelled by the effects of tumor. A correctly segmented tumor region is significant in medical diagnosis and treatment planning, hence it has drawn huge focus in the field of medical image analysis. Manual segmentation of glioma tumors across the MRI data, while dealing with an increasing number of MRI scans is a near to impossible task. Therefore, many algorithms have been de- vised for automatic and semi-automatic segmentation of tumors and intra-tumor structures. Historically, standardized datasets have not been available to compare the performance of such systems. Recently, the medical image computing and computer assisted in- tervention society (MICCAI) has started a multi-modal brain tumor segmentation challenge (BRATS), which is held annually and pro- vide a standard dataset used as a benchmark for the evaluation of automated brain tumor segmentation task .

2. Proposed Methodology

The proposed methodology elaborates on the effectiveness of convolutional neural networks in brain tumor segmentation task and consists of three steps i.e., pre-processing, CNN, and post- processing as shown in Fig. 1 . The input images are pre-processed and divided into patches, which are then passed through a convo- lutional neural network to predict the output labels for individual patches. The details of each step are as follows.

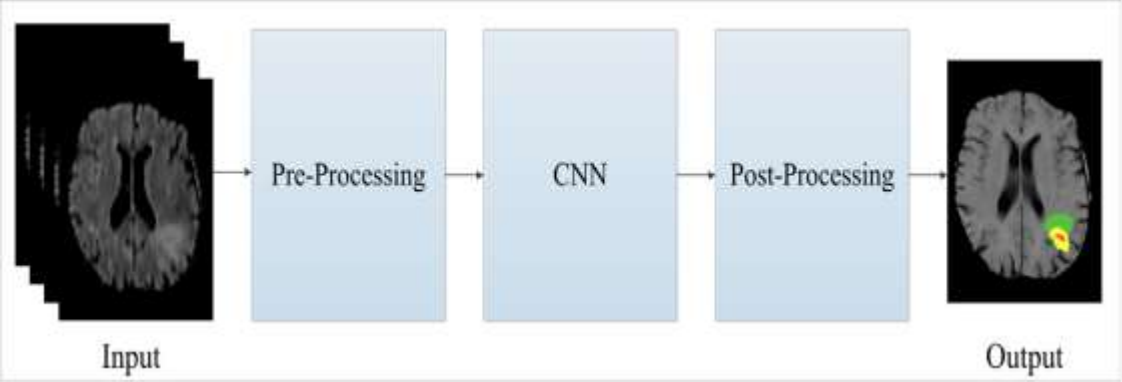

Fig.1 Block Diagram.

2.1 Pre-processing: Images acquired from different MRI modalities are affected by artefacts, such as motion and field inhomogeneity [45] . These arte- facts cause false intensity levels, which leads to the emergence of false positives in the predicted output.

1) De-noise the image: Median Filter is used for de-noising the image.

$$\hat{f}(x,y) = \underset{(s,t)\in S_{xy}}{median}\{g(s,t)\}$$

Gaussian low pass filter is used for smoothening the image.

$$G(x,y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}}$$

2) Intensity Normalization : A normalized slice *Xn* is generated as follows,

$$x_n = \frac{x - \mu}{\sigma},$$

where *x* represents the original slice, μ and σ are the mean and standard deviation of *x*, respectively.

2.2 Convolutional Neural Network: The convolution layers are the main building block of a CNN. These layers are stacked over one another in a hierarchical fashion forming the feature maps. A feature map *Oa* is obtained as,

$$O_a = b_a + \sum_r F_{ar} * I_r,$$

where *Far* is the convolution kernel, *Ir* is the input plane

- These maps are passed to the max- pooling layer, which retains the relevant features and discards the rest. The shrinking factor is controlled by hyper-parameters i.e., pool- ing size, which controls the size of the pooling window, and stride for the subsequent window. The features from the max-pooling layer are converted into one dimensional feature vector in the fully connected layer, which are then used to compute the output probabilities.
- A CNN kernel can be designed having different dimensions such as 3 ×3, 5 ×5 and 7 ×7 etc.
- The weights on connections as well as kernels are learned through a method called back-propagation
- A non-linear activation function is used at the end of the network to convert features in to class probabilities.
- The ReLU activation function converts the output values in to soft class probabilities . The class with the largest probability after applying ReLU is assigned to the central pixel in the corresponding input patch.

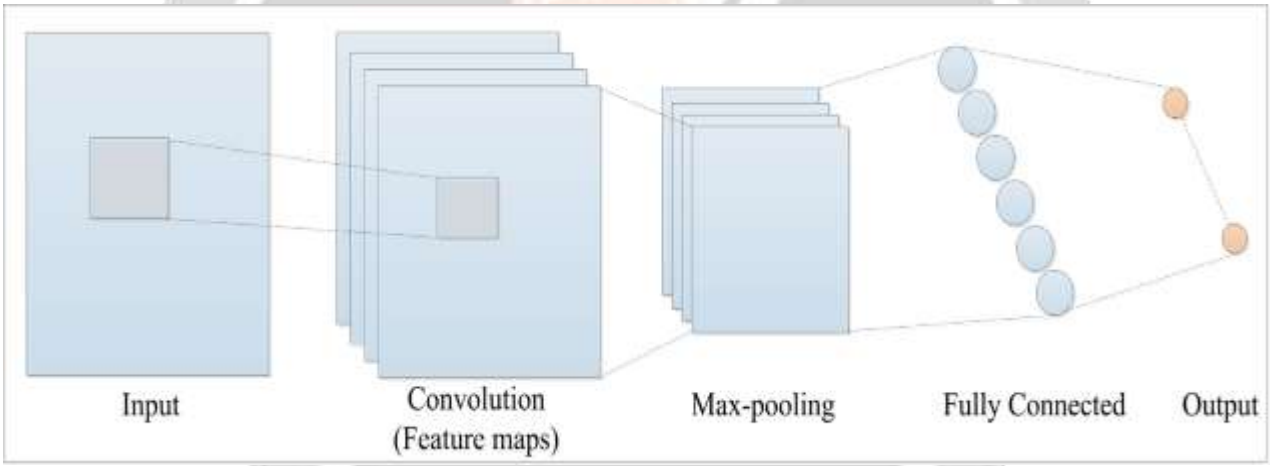

Fig 2. CNN Architecture.

2.3 Post Processing: In the post-processing step, simple morphological operators are used to improve the segmentation results.

3. Experimental setup

3.1 Dataset: Experiments are carried out on and BRATS 2015 datasets , which contain four MRI modalities i.e., T1, T1c, T2 and T2flair, along with segmentation labels for the training data. The BRATS 2015 dataset comprises of a total of 274 training MR images, out of which, 220 are HGG and 54 are LGG images.

Convolutional layers	Dropout Layer	Convolutional kernels	Max pooling	Fully connected Layer	No of parameters
3	3	3x3,5x5	2x2	1	407,210

Table 1.Structural summaryof the proposed deep architecture.

3.2 Graphical User Interface(GUI):In this GUI there are five push buttons, first for loading the image from dataset,second for pre-processing,third for patch Extraction,fouth for feature Extraction and last for CNN classification.

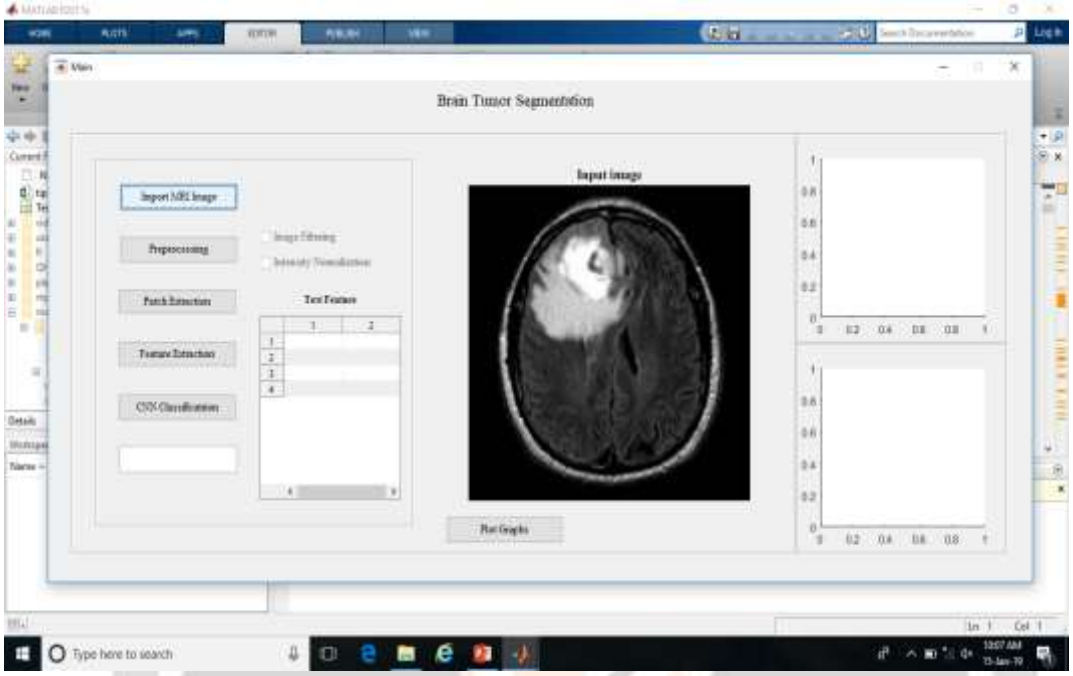

Fig 3. Graphical user Interface for proposed system.

Neural network parameters:The proposed methodology is implemented in MATLAB. which provides numerous methods and pre- trained models to implement convolutional neural networks.

3.3 Neuronal activation: A neuronal activation function is used to control the output of neurons in the neural network. A ReLU activation function has either a zero or a positive value output. It is a non-linear activation function, which calculates a maximum of zero and the input z as follows;

$$f(z) = max\ (0\ ,\ z)\ .$$

3.4 Normalization: Batch normalization is used to normalize the activations after every batch of input data. Batch normalization utilizes an ac- tivation function to maintain the mean and standard deviation of activations near zero and one, respectively. Due to a large learning rate, layer weights change significantly, which can amplify small changes in layer parameters causing the weights to explode. Batch normalization hinders gradient from blowing out of proportions and keeps it within an acceptable limit during back-propagation. A normalized feature map *N* is obtained as,

N = nl(BN(W a))

where BN () represents batch normalization on weight parameter Wa and nl is the ReLU non-linearity.

3.5 Regularizer :Regularizers are used to reduce over-fitting by imposing penal- ties on layer weights during network optimization. A dropout layer canbe used as a regularizer on feature maps obtained from the convolution layer. This layer drops a certain percentage of activations randomly at each update during training by setting dropped units to zero. This reduces over-fitting as units have to learn independently, instead of relying on each other for produc- ing an output.

3.6 Optimizer: An optimizer is used to compute the loss function at the output layer of the network and distribute the updated values throughout the network. Stochastic gradient descent (SGD) is used along with the loss function in the back-propagation algorithm. The loss function *L i* is computed as

$$L_i = \frac{-1}{B} \sum_{i=1}^{B} \log(P(Y_i = y_i))$$

where *Y i* is the target class label, *y i* is the predicted class label and *B* represents the mini-batches of data.

3.7 Training:For training the network 256 FLAIR images are used because in FLAIR modality the CSF is black and tumour is white which helps in segmentation.
3.8 Testing:For testing the network 100 images are used validation.
3.9 Evaluation parameters: Segmentation results are evaluated based on three metrics namely sensitivity, and specificity.
Sensitivity is a measure of accuracy of correctly classified tumor labels. It determines, how well the model has performed to detect tumor in a given image and is given as,

$$\text{Sensitivity} = \frac{|L| \cap |G|}{|G|}$$

Specificity computes the accuracy of correctly classified labels of normal output class. It determines, how well the model has per- formed to specify tumor to its labelled area. It is computed by tak- ing intersection of predicted normal label *P o* with actual normal label *L o* as,

$$\text{Specificity} = \frac{|Lo| \cap |Go|}{|Go|}$$

Where L is predicted output image and G is manually segmented label.

4. RESULTS

The results obtained on BRATS 2015 datasets for the proposed architecture are reported in this section.

Sensitivity			Specificity		
Complete	Core	Enhancing	Complete	Core	Enhancing
0.80	0.83	0.83	0.92	0.91	0.89

Table 2. Segmentation results of the proposed architecture in terms of sensitivity and specificity on MICCAI BRATS 2015 dataset.

5. CONCLUSION

Automated methods for brain tumor segmentation can play a vital role in future diagnostic procedures for the brain tumor. In this paper, an automated method for segmenting brain tumor us- ing deep convolutional neural networks has been presented. Dif- ferent architectural settings have been explored and the effect of using multiple parallel paths in an architecture are validated. The segmentation results on two datasets i.e., BRATS 2013 and BRATS 2015 verifies that the proposed architecture improves the perfor- mance, when compared with state-of-the-art techniques.

6. REFERENCES

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