JADAVPUR UNIVERSITY

Brain tumor segmentation using CNN

BY

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EXAM ROLL-226047

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To whom it may concern

I hereby recommend that the project "Brain tumor segmentation using CNN" has been carried out by ***ABHISHEK MANDAL*** *(Reg. No. 149908 of 2019-2020, Roll No: 001910503048,* **EXAM ROLL-226047***) under my guidance and supervision and be accepted in partial fulfillment of the requirement for thedegree of* ***MASTER of COMPUTER APPLICATION*** *in* ***DEPARTMENT ofCOMPUTER SCIENCE and ENGINEERING, JADAVPUR UNIVERSITY*** *during the academic year 2021-2022.*

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CERTIFICATE OF APPROVAL

This is to certify that the project entitled "***Brain tumor segmentation Using CNN***" is a bonafide record of work carried out by **ABHISHEK MANDAL** in fulfillment of the requirements for the award of the degreeof ***MASTER of COMPUTER APPLICATION*** in the ***DEPARTMENT ofCOMPUTER SCIENCE & ENGINEERING, JADAVPUR UNIVERSITY.*** It is understood that by this approval the undersigned do not necessarily endorse or approve any statement made, opinion expressed or conclusion drawn therein but approve the project work only for the purpose for which it has been submitted.

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CONTENTS

ABSTRACT

The determination of tumor extent is a major challenging task in brain tumor planning and quantitative evaluation. Magnetic Resonance Imaging (MRI) is one of the non-invasive technique that has emanated as a front line diagnostic tool for brain tumor without ionizing radiation.

Among brain tumors, gliomas are the most common aggressive, leading to a very short life expectancy in their highest grade. In the clinical practice manual segmentation is a time consuming task and their performance is highly depended on the operator’s experience.

This project proposes fully automatic segmentation of brain tumor using convolutional neural network. Further, it uses high grade gliomas brain image from BRATS 2015 database. The project accomplishes brain tumor segmentation using tensor flow, in which the anaconda frameworks are used to implement high level mathematical functions. The survival rates of patients are improved by early diagnosis of brain tumor.

Hence, this project segments brain tumor into four classes like edema, non-enhancing tumor, enhancing tumor and necrotic tumor. Brain tumor segmentation needs to separate healthy tissues from tumor regions such as advancing tumor, necrotic core and surrounding edema. This is an essential step in diagnosis and treatment planning, both of which need to take place quickly in case of a malignancy in order to maximize the likelihood of successful treatment.

INTRODUCTION

Brain tumor is the abnormal growth of cells within the brain. Generally, tumor is classified into primary and secondary tumor. Primary tumor starts within the brain and secondary tumor will spread to the other parts of the body. There are many medical imaging methods available like X-ray, CT (Computed Tomography) and MRI (Magnetic Resonance Imaging). This project uses MRI brain images, because of its high resolution and good quality of an image. After capturing MRI brain image, it is necessary to separate the tumor region from the MRI brain image. This presented work mainly segments glioma types of brain tumor. The manual segmentation of brain tumor is labor sensitive and the segmentation results based on the operators experience and their subjective decision making. Hence there is a need for fully automatic, objective and reproducible segmentation method. This work uses fully automatic convolutional neural network. The convolutional neural network is implemented in python programming. The anaconda is one of the frameworks for machine learning concept, in which neural network tool for training of BRATS database is implemented using tensor flow. By using this, the accuracy of segmentation is improved and it has the features to process the larger dataset. The performance of the segmentation of MRI brain tumor is compared with the ground truth images of BRATS database 2015. The dice co-efficient is the parameter to define the accuracy of automatic segmentation.

MATERIALS & METHODS

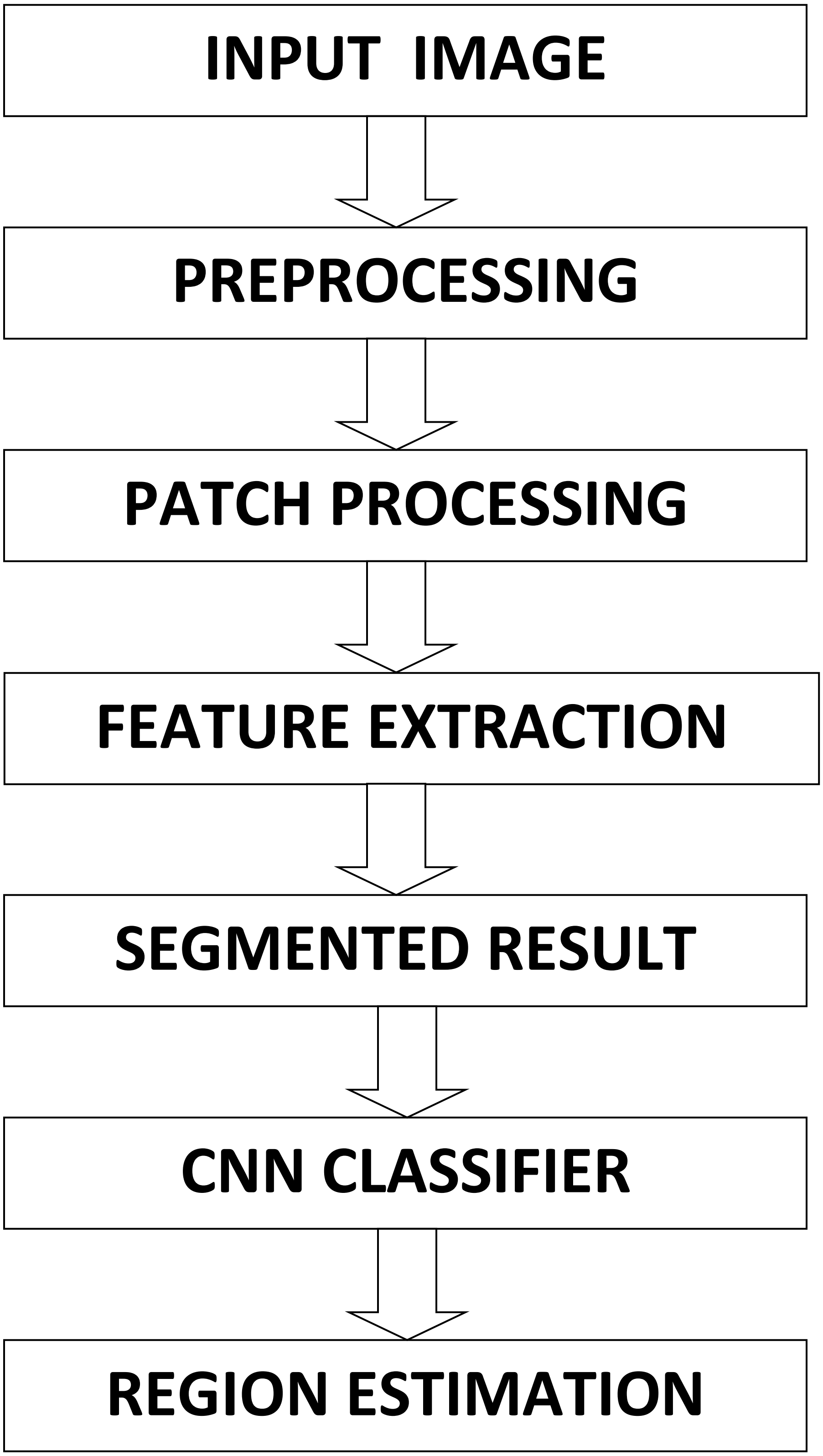
This project uses convolutional neural network for MRI brain tumor segmentation. It uses tensor flow based MRI brain tumor segmentation in order to improve segmentation accuracy, speed and sensitivity. Segmentation is performed on BRATS MRI brain images and results are compared in terms of dice co-efficient.

PYTHON BASED CONVOLUTIONAL NEURAL NETWORK

This project work utilizes the python programming to implement the segmentation of MRI brain tumor. The features are listed below in order to choose python programming to implement the project work:

1. Python code is more compact and readable.
2. The python data structure is superior.
3. It is an open source and also provides more graphic packages and data sets.

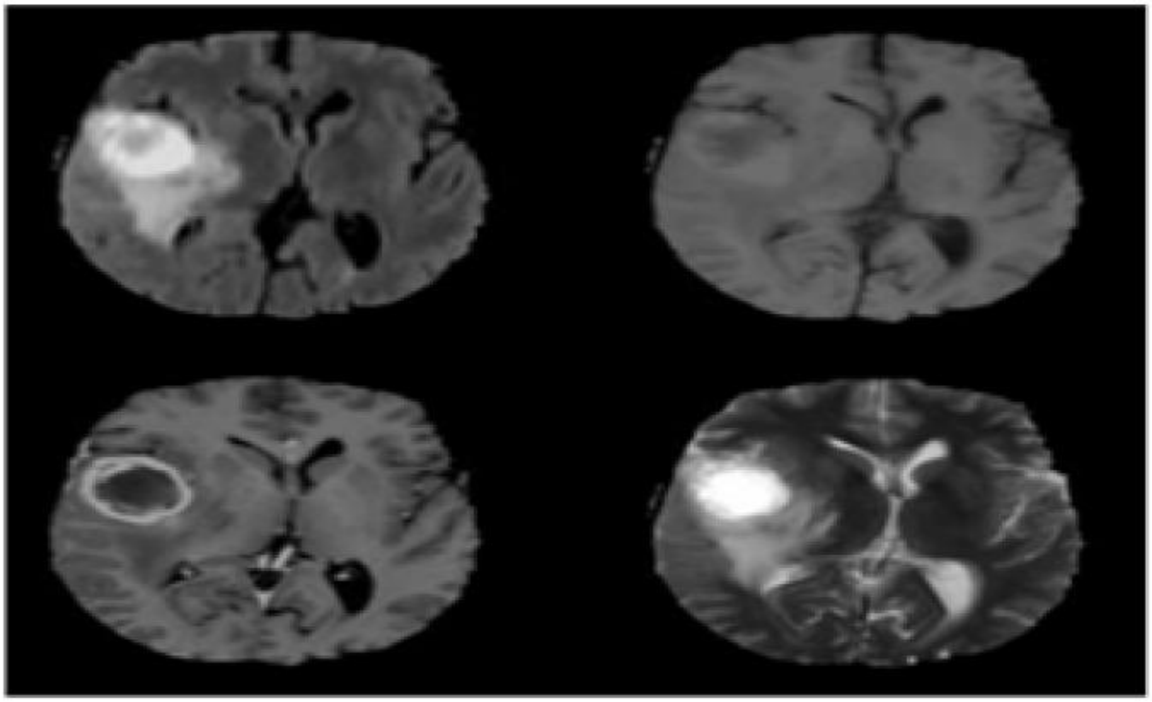
FLOW DIAGRAM OF THE PROPOSED WORK



MRI BRAIN DATA ACQUISITIONS

This recommended method is tested and implemented on the BRATS 2015 dataset, which had 220 high grade glioma (HGG) and 54 (LGG) low grade glioma patient scanned images. Each patient in the BRATS 2015 dataset multimodal MRI was available and also four scanning sequences were implemented for every patient using T1 weighted (T1), T1 weighted imaging with gadolinium enhancing contrast (T1C), T2 weighted and FLAIR. This uses the HGG image of BRATS 2015.

Pulse sequence images of brain tumor:

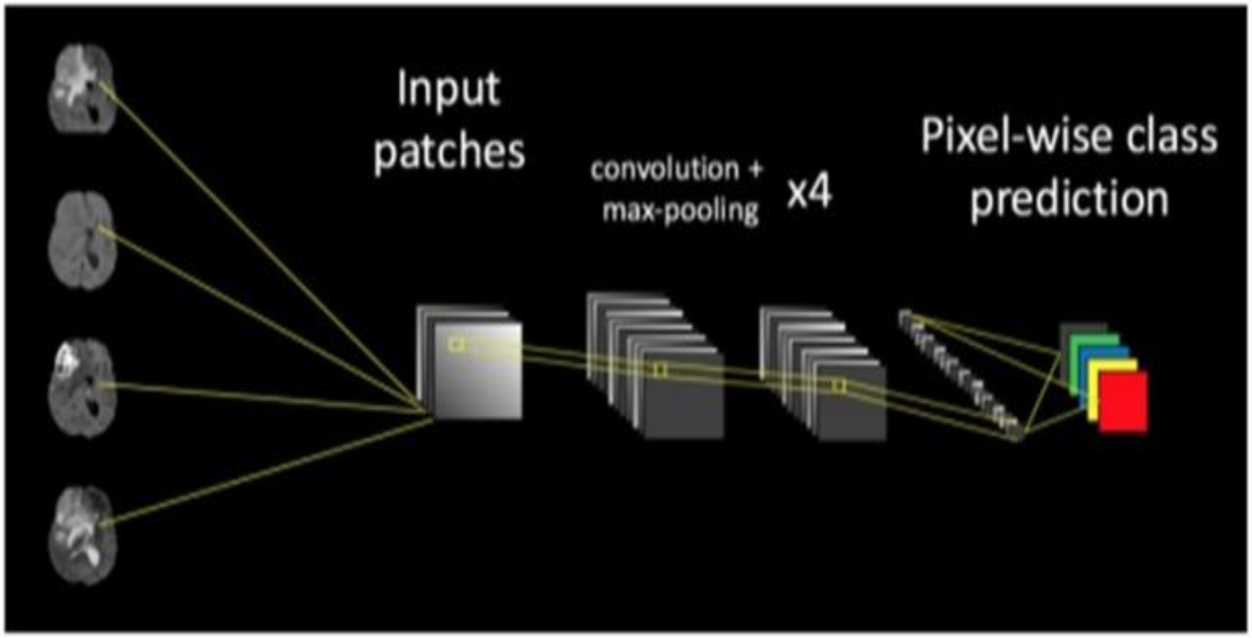


PREPROCESSING

The main challenging task is removing artifacts produced by in-homogeneity in a magnetic field or small movements created by the patient during scanning. Many time biases are present in the scanning results, which affect the segmentation results, particularly in the computer n-based models. Demonstrated work uses n4ITK bias correction for the T1 and T1C images in the data set. The n4ITK bias correction removes the intensity gradient on each scanning images. Additionally, noise reduction is also performed by median filter in order to standardize the pixel intensities. Hence, noise reduction and bias correction helps to improve the data processing and provides the better segmentation.

In BRATS data base there are four different sequences available for each image like Fluid Attenuated Inversion Recovery (FLAIR), T1, T1 contrasted and T2. The chemical and physiological characteristics can be obtained from these pulse sequences, which result in contrast between the individual classes.

ARCHITECTURE OF CNN



NEURAL NETWORK

For image recognition, neural network is one of the powerful tools to perform segmentation. MRI is one of the most commonly used imaging techniques to capture MRI brain images. Automatic segmentation is a challenging task because of its large spatial and structural variability. Hence, this proposed system implements the automatic segmentation method based on CNN exploring small 3×3 kernels. The small size kernels help to design deeper architecture by using fewer numbers of weights in the network.

CNN ALGORITHM

CNN algorithm performs the voxel-wise classification problem. The tumor or lesion portion is separated from the background by calculating the probability of each image voxel belonging to the target is known. The CNN network has four sections. The input layer processes the input image in order to produce the designed image patches. The convolution section process the designed image patches, in which multilayer convolutional filters operates and output feature maps. Further, the fully connected layer that groups all feature maps. The classification section estimates a prediction score to classify the every image voxel and provides a segmentation map.

INPUT SECTION

The input section generates the image patches for the remaining of the network. The method performs the classification based on voxel-wise, where each voxel is classified based on the linear and non-linear relationship between the focal voxel's intensity and its neighbors. The input 3D image size is large; hence, calculation of linear and nonlinear relationship between all voxels in the complete image is complex. Hence, the entire image is divided into smaller patches in order to find the relationship within a particular region instead of the entire image.

It reduces the computational time and also memory space. It separates both local and global patches as input for the convolution section. For every extraction process, the central voxel is chosen randomly and extracted concentric local and global image patches. The neighboring voxel around the central voxel provides the local information and global patch covers larger region and provides global information. In order to reduce the computation burden produced by the larger global patch, I have used down sampling of all global patches. The down sampling process is also called as pooling.

CONVOLUTION SECTION

There are multiple layers in the convolution section, which help to sequentially identify the features using convolution operations. The captured features are low level features like edges and corner relationship between neighboring voxels. The feature maps are the output of the convolutional layer. The complete convolution region consists of three different sub paths. The path 1 and 2 utilize the same local patch with various filter sizes to internment various neighborhood patterns, at the same time sub path 3 uses down sampled global patch to provide global features. The convolutional layer calculates the output of the neurons that are connected to either local or global regions in the input. The convolution is the process of performing dot product between their inputs and their respective field to which they are connected to in the input volume. For my project work,

L- be the depth of the convolution filter stack

a^1 ($1 \mathcal{E}$ [1,L]) represents the number of feature maps in the l^{st} layer and

F_i^l ($i \mathcal{E}$ $[1,\alpha^l]$) represents the i^{th} feature map of the l^{st} layer F_i^l is calculated by

$$F_i^l = g\Big(\sum_{j=1} \propto^{l-1} F_j^{i-1} * w^l_{j^1} + b_i^i$$

……………………………………(1)

Where g(.) is the PReLU function. The PRELU is a neuron activation function defined by

$g(x)= x, x >0$

$ax\ x\leq 0$

a is the network parameter

$W_{j1}{}^{l}$ is the filter connecting the j^{th} feature map in the $l\text{-}1^{th}$ layer and $b_i{}^{l}$ is the bias of the artificial neuron model

ReLU is the rectified linear units.

It is one of the most popularly used activation functions. It is represented as

$R(x)= \max(0, X)$ ie

If $X < 0$ $R(x)=0$

If $X>=0$, $R(x)=X$

Most of the machine learning techniques refers to this function because of its simplicity and also it avoids vanishing gradient problem. But, it should be used only within the hidden layer of neural network model. For example, output layers, softmax function will be used to calculate the probabilities for the classes. During the training phase, some gradients can be fragile and die. Hence, it needs a weight update, further, it never activates on any data point again. It can be avoided by another modification called leaky ReLU. It provides small slope to keep updates alive.

FULLY CONNECTED REGION

The operation of fully connected section is similar to the convolution section in which each co-efficient node performs like a convolution filter with the size (1,1,1).

CLASSIFICATION SECTION

The classification section helps to provide probability for each voxel. Most of the Convolutional neural network uses softmax function in order to map the feature maps into categorical probabilities.

$$J_p(\emptyset.I_s.C_s)= -\frac{1}{B\bullet w}\sum_{S=1}^{B}\sum_{V=1}^{V}\log\left(P_{C_s^v}\left(x^v\right)\right)$$

Where x^V and C_S^V are the v^{th} target voxel's position and ground truth,

$$V \in [1.V] \bullet V = f_1^L \times f_2^L \times f_3^L$$

…

………………………………………………………(2)

Where (f_1^L, f_2^L, f_3^L) is the L^{th} layer feature map size. $S \in [1, B]$ where the B is the size of a batch, $P_{C_S^v}$ is the output of the softmax function.

The parameter θ is denoted as filter co-efficient and bias. It can be found by training through the stochastic gradient descent method. SGD is one of the stochastic approximations of the gradient descent optimization method in order to minimize an objective function iteratively. For every iteration, the method estimates the gradient from a subset of labeled dataset and also it helps to increase the speed of training in a huge training set.

TRAINING OF NETWORK

The training model is created using Keras. The 4 layer sequential model was trained on selected 33× 33 patches of MRI images in order to classify the center pixel. Every input has 4 channels, among four, one channel helps for each imaging sequence and the network can learn the relative pixel intensities of each given class.

VALIDATION OF DATA SET

This proposed method uses BRATS database for evaluating the brain tumor segmentation methods. BRATS provides each patient's T_1 weighted MRI with gadolinium contrast (T_{1c}) and T_2 weighted fluid attenuated inversion recovery (FLAIR) images. This kind of data set compares our automatic delineation method with other algorithms.

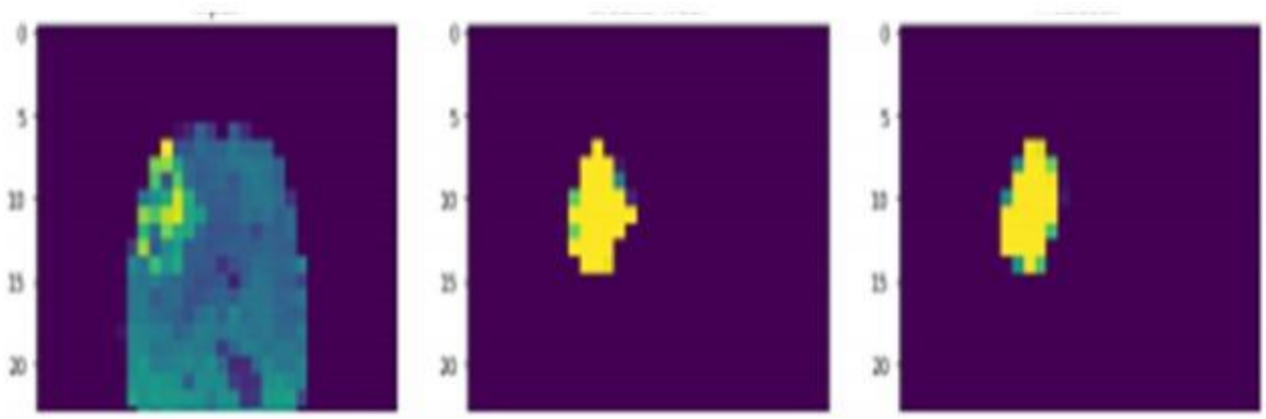
RESULTS & ANALYSIS

This project uses either color or gray scale intensity images with a default size of 220×220. The automatic brain tumor detection of a patient consists of two important stages, namely, image segmentation and edge detection. The next important step is adding path from the image data set file to the system directory. It can be implemented by an anaconda frame work to allocate data sets from computer memory. It can be performed either manually or by programming using the python OS inbuilt operation.

The main objective of segmentation is to cluster pixels into image region and it helps in identifying a region of interest i.e. to locate tumor and other abnormalities. The pixels segmented portion is compared with normal brain image in the jupytor note book. This kind of comparison helps to locate abnormal parts of brain tumor in patient. The next step is edge detection. It uses cannon edge detection in order to classify the brain tumor portion of the segmented image.

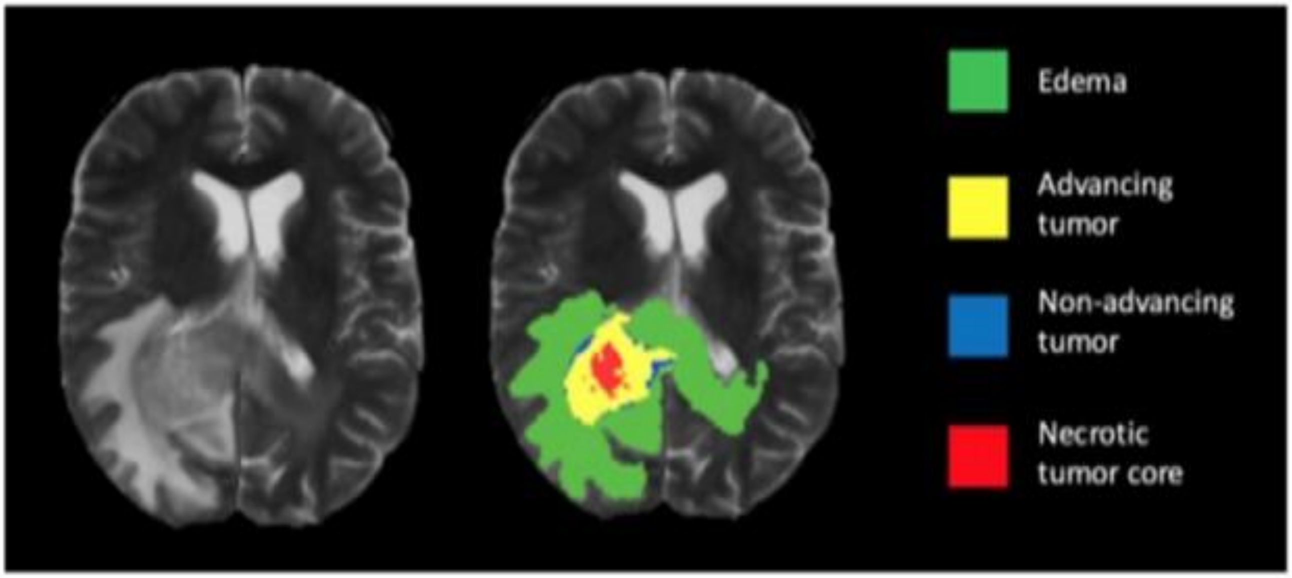
The white portion shown is tumor. In the resultant, red represents the necrotic core of the tumor, yellow represents the advancing tumor, and blue represents non-advancing tumor and green represents the swelling part of the tumor called edema.

SEGMENTED IMAGE OF BRAIN TUMOR



Input image Ground truth image Prediction

RESULT OF BRAIN TUMOR SEGMENTATION



DICE SIMILARITY COEFFICIENT

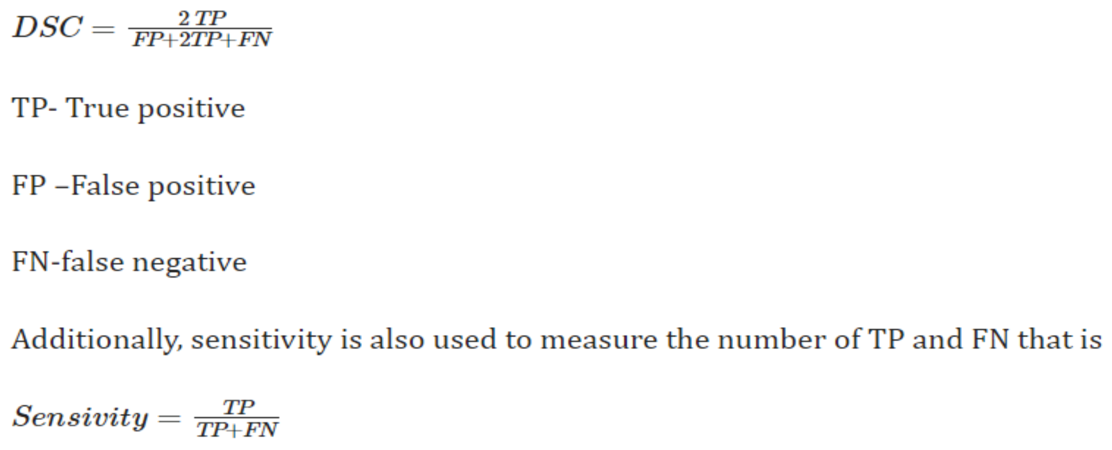
In mathematical notation, dice score is the number of false positives divided by the number of positives added with the number of false positives.

Experiments & performance evaluation

Five-fold cross validation method is used for evaluation of HGG and LGG data respectively. For every patient, four subnormal regions are validated. It is represented by

1. The complete tumor region.
2. The core tumor region.
3. The advancing tumor.

For every tumoral region, the performance of segmentation has been evaluated using the dice similarity co-efficient and the sensitivity. The DSC measures the overlap between the manual delineated brain tumor regions and the segmentation results of fully automatic method that is



$$DSC = \frac{2\,TP}{FP+2TP+FN}$$

TP- True positive

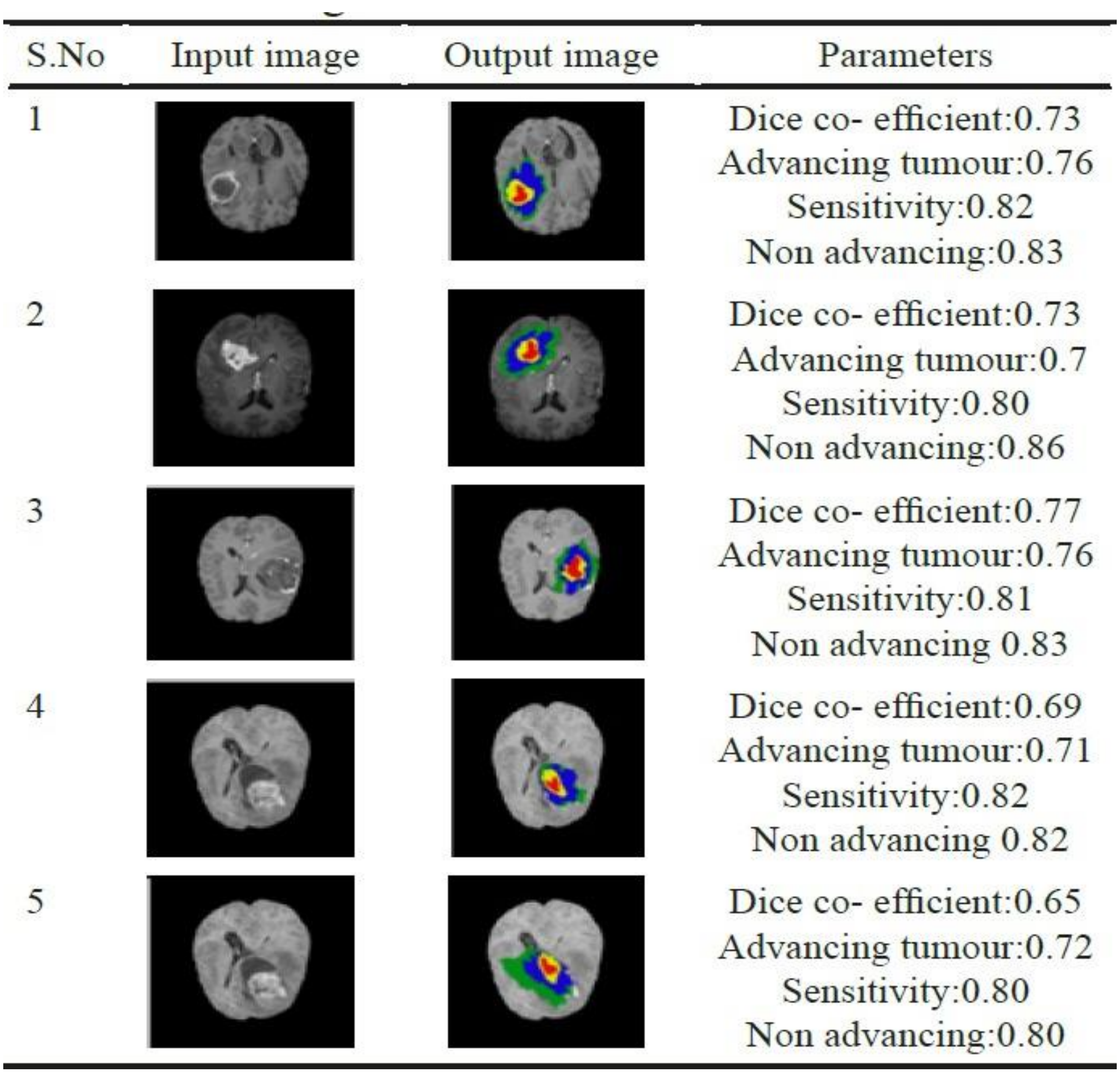
FP –False positive

FN-false negative

Additionally, sensitivity is also used to measure the number of TP and FN that is

$$Sensivity = \frac{TP}{TP+FN}$$

This table provides the Dice co-efficient value for different ground truth brain images.



S.No	Input image	Output image	Parameters
1			Dice co- efficient:0.73 Advancing tumour:0.76 Sensitivity:0.82 Non advancing:0.83
2			Dice co- efficient:0.73 Advancing tumour:0.7 Sensitivity:0.80 Non advancing:0.86
3			Dice co- efficient:0.77 Advancing tumour:0.76 Sensitivity:0.81 Non advancing 0.83
4			Dice co- efficient:0.69 Advancing tumour:0.71 Sensitivity:0.82 Non advancing 0.82
5			Dice co- efficient:0.65 Advancing tumour:0.72 Sensitivity:0.80 Non advancing:0.80

CONCLUSION

In conclusion, the segmentation of brain tumor plays an important role in diagnostic procedures. The accurate segmentation helps in clinical diagnostic, but also helps to increase the lifetime of the patient. In this project work a segmentation of brain tumor is implemented using CNN architecture. The algorithm relates both local and global features, because it helps to perform the segmentation accurately. The training and testing speed is increased by using max pooling, maxout and dropout. The speed is also increased by reducing the features in the fully connected layer. Reduction of parameters also causes the reduction of over fitting. The result shows that the implemented method helps in detection of enhancing tumor as well as specifying tumor to the actual tumor region only.

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