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Segmentation of Glioma Tumours Using Deep CNN Architecture

V Vinamraa, Th Sandeep and K Nayana

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Vinamraa V
ECE, SVIT.
vinamraav.18ec@saividya.ac.in

Sandeep TH
ECE, SVIT.
sandeepth.19ec@saividya.ac.in

Prof.Nayana K
Assistant Professor, Dept. of ECE, SVIT.
nayana.k@saividya.ac.in

***Abstract*— We present a fully automated model for the task of segmentation and classification of Glioma tumours based on Deep CNN architecture and Fractal dimensional analysis. Glioma tumours are heterogeneous in shape and vary in location & early diagnosis of gliomas is essential to improve the treatment procedures. The proposed model is the result of a through examination of shortcoming of existing models for similar applications. The suggested approach uses 3-D MRI scans from the BraTS 2015 dataset to divide the tumour into four regions: edema, enhancing, non-enhancing and necrotic, as well as classify whether it is a High-Grade Glioma or Low-Grade Glioma. This model is computationally efficient and allows its adoption in a variety of research.**

Keywords—Tumours, Glioma, CNN, MRI.

I. INTRODUCTION

Tumours are clumps of aberrant cells that have grown and proliferated out of control. Primary and secondary brain tumours are the two types of brain tumours. A primary brain tumour begins in the brain and only rarely spreads to other parts or organs of the body. Secondary brain tumours are cancers that start in another part of the body and then move to the brain. These tumours are typically divided into two categories: "low grade" and "high grade." In most situations, a low-grade tumour grows slowly, although it can advance to a high-grade tumour over time. A high-grade tumour grows faster compared to a low-grade tumour. The problem in this brain tumour is, it varies in size, shape, appearances, color and orientation which is precisely the reason why the segmentation and classification of tumours are challenging. Brain tumours are one of the leading causes of death in both adults and children all over the world. In 2015, about 296,851 new cancer cases of the brain and nervous system were recorded and it was reported by the WHO. Manual segmentation of a brain tumour from radiological images is the common procedure in clinical practice, which is very time-consuming, hence, automated tumour segmentation methods are used to save time and improve the consistency of the results. However, because tumours vary in shape and location within the brain, automated brain tumour segmentation remains a difficult process. Discriminative and generative approaches are among the current/existing brain tumour segmentation methods. We have seen an increased use of the Convolutional Neural Network (CNNs) in recent years for this task of tumour segmentation, but most of them make use of 2D networks which requires relatively low memory requirement than 3D CNNs, but, the accuracy will be less compared to 3D CNNs. We can extract better 3D features from the input MRI picture by utilising 3D CNNs, however this needs a lot of memory, which may limit the input depth or feature counts, as well as the CNN patch size. We use/introduce the Deep learning algorithm like CNN, which is an advanced concept for this assignment, to solve the complexities and challenges of the brain MRI segmentation problem. We present a model that performs both classification and segmentation of brain tumours using Deep CNN architecture and Fractal dimensional analysis to differentiate High-Grade from Low-Grade Glioma tumours in order to obtain higher accuracy with lower processing times.

II. LITERATURE SURVEY

[1] The model described in this paper is used to provide segmentation results that are very similar to the original input data, and it is trained using the Multimodal Brain Tumour Segmentation Challenge (BraTS) dataset to improve accuracy and precision. Each of the 335 examples in the training set has four different MRI modalities: T1, T1ce, T2, and FLAIR. The issue is that within the same brain tissue, the intensity, contour, or contrast value, which can be white or black, can vary. This is a low-frequency bad signal which acts as noise or distortion in the MRI image. To overcome the above-mentioned problem, preprocessing of the data and augmentation is done. The 3D U-Net with Deep Supervision architecture is employed in this paper. The suggested method's output has an average better performance in the dice scores of 0.737 and 0.807, respectively, in boosting tumour and tumour core.

[2] To tackle the challenge of brain tumour segmentation, the model suggested in this paper uses residual blocks to extract deep features from visuals, convolutions with dense connections to increase feature map reuse, and thoroughly supervised outputs. The dataset from BraTS 2015 is used to train and examine the suggested model. A total sample of 285 is considered with each sample containing 4 MRI nodes which are called as t1, t1ce, t2 and flair. The problem is that the local information of different sequences of tumour images is extracted well in the 2D segmentation networks, but the spatial information of the tumour images is neglected, while the 3D segmentation networks are difficult to train as they have a large amount of data for computation. When compared to the other networks, the proposed technique's output has the best average progressive performance in the dice scores of 0.884 for the entire tumour, 0.806 for the tumour core, and 0.702 for augmenting the tumour core.

[3] The model proposed in this paper provides a new approach that detects the pathologies present in the cerebral tissue of the brain as bright structures based on the spectral energy distribution and fractal geometry of edges in brain MR

images. Using geometrical fractals and signatures of spectrum, this model distinguishes between normal and abnormal anatomical edges in human brain MR data. A sample or database consisting of 31 images is considered in which ten are normal, twelve are abnormal which is glioma and nine are abnormal ones. The problem is that in order to access the generality of reported results no cross-validation was used and these reported results were obtained with test sets and training sets.

[4] For the segmentation of glioma tumours, the model suggested in this research uses a DNN algorithm technique. A DNN network is implemented for glioma tumour segmentation of 2-D MRI images. The accuracy of the model is determined by two parameters: dice score co-efficient and sensitivity. Pre-processing, CNN network, and post-processing are the three processes in the proposed paradigm. The model employs image processing techniques such as convolution, max-pooling to downscale the picture, and upsampling. The model is trained and tested using the BraTS 2015 dataset. It contains 285 scans, with 210 of them being cancerous(HGG) and 75 being non-cancerous(LGG). T1, T1C, T2, and Flair are the four MRI modalities included in the dataset. The model predicts the label of each pixel based on information from the tissue of the brain , which improves the accuracy of segmentation results.

[5] For the segmentation of Brain lesion, the model suggested in this research is totally automatic, two pathway, multiple layer deep, and uses the 3D CNN algorithm. The model employs a two pathway architecture, which simultaneously analyses the 3D image , as well as conditional random fields for post-processing to eliminate false positives. The model is validated using data from real patients from the BraTS 2015 dataset, which has 220 HGG and 54 LGG. T1, T1C, T2, and T2FLAIR are the four MRI modalities included in each dataset. The model consists of input segmentation layers, a Convolutional layer, a fully connected layer, and a classification layer, all of which are piled on top of one another to form a features in order of importance. This model is mainly used to evaluate Brain lesion segmentation into brain injuries, brain tumour & ischemic strokes.

[6] This study presents a model that integrates ROI extraction and 3D segmentation into a single architecture. This approach is evaluated using the BraTS 2017 dataset. In the current 3D Segmentation, there is a problem with classes that are imbalanced. To address the above-mentioned issue, the Dice loss will be combined with a weight, which will increase the focus on tumour subregions while reducing background influence. The U-Net architecture is employed in this work, and it is made up of ROI (Region of Interest). For the overall tumour, tumour core and enhancing tumour the suggested technique yields average dice scores of 0.908, 0.716 and 0.839, respectively. This approach can automatically segment brain tumours without the assistance of a trained physician, and it can help doctors diagnose and plan treatment for brain tumours.

[7] The study investigated in this paper is precise and dependable segmentation of gliomas from magnetic resonance imaging data.The enormous variability of tumour location, size, form, and appearance, as well as the altered position of normal tissues, make segmentation difficult. The method is divided into three steps. The first step of the pre-processing is to prepare the MRI data for pattern recognition, the second phase completes the main classification process by using ensembles of binary decision trees and provides a first, interim labelling for each pixel of test data. The final phase uses a random forest classifier to review these intermediate labels, resulting in a high-quality final segmentation result. The procedure's accuracy is assessed using the BraTS 2016 training data sets' multi-spectral MRI recordings. The accuracy of the model is evaluated based onthree parameters namely Dice score co-efficient, sensitivity and precision.

[8] The objectives of this paper is to design a web-based software that uses a CNN from a deep learning model to classify brain tumours into glioma, meningioma, andpituitary on basis of T1 contrast MRI . The method in this software is built using the Keras library, which is written in the Python. Image processing is done with the Keras library.In addition, the libraries Tensor Flow, Keras, Scikit learn, Opencv, pandas, Numpy and Flask were used in the creationof this software. The output of the model can accurately segment the region of tumour into different regions with the help of colours into edema, enhancing core,non- enhancing,necrotic. The accuracy of the model is evaluated using two parameters namely Dice score co-efficient and sensitivity. The output of the suggested strategy performs better and has a dice scores of 0.757.

[9] The wide residual & pyramid pool network (WRN-PPNet) is an automatic technique used in this paper's model that can segment glioma from end to end. On (BraTS) 2015 databases, the proposed approach is validated. WRN-PPNet is trained using a cross-validation approach with 90% of the training data. The problem with the comparison networks is that they are part of a patch-based technique that mostly uses local information in patches and is limited by patch size. To address the above-mentioned issue, the suggested architecture mixes global priors with local features at different pyramid scales. As a result, brain tumour has a larger representation. The WRN-PPNet architecture is the one employed in this paper. The trial findings suggest that the proposed strategy can produce more accurate and faster segmentation results.

[10] In this paper, one-of-a-kind architecture to confront the dilemmas of complicated brain MRIs. The sculpture on show is a cross among two different types. The first is a densely connected inception-like model, whereas the second is built on element-wise addition connections. Using unimodal and multimodal algorithms, fusion from many paths can be achieved with short connections. From the bottom up, the entire system has been retrained. To deal with the imbalanced labels task during training, we use. To compensate for the lack of data, we apply augmentation techniques such as distortion and flipping. We have the highest dice scores for enhancing tumours, necrotic tumours, and non-enhancing tumours. Our primary goal is to improve the ratings for these two designations, tumour and necrotic.

III. METHODOLOGY AND IMPLEMENTATION

The BraTS 2015 data set was used for this project, which comprised Flair, T1C, OTMultiClass, and masked image sequences for each patient.

Data Processing:

Pre-processing of the input image includes 2 steps mainly:

1. Brain Extraction
2. The intensity inhomogeneity in the brain images was then adjusted.

Both the raw MR images and the segmentation ground truth tumour pictures were downloaded from the BRATS 2015 dataset. The ITK snap tool was used to segment the tumour areas from our clinical MR images. Following that, the pre-processed images were fed into three different brain tumour segmentation network namely,

[1] Region growing
[2] Fuzzy C-means and
[3] Deep convolutional neural network

1. Region growing

Brain tumour segmentation was achieved using this method. The following assumptions were used to implement the algorithm:

1. Tumours can be seen in either the left or right hemispheres, but not both.
2. The brain's left and right hemispheres are symmetrical.

The image processing steps in the algorithm are as follows:

(a) Bias correction and Skull tripping
(b) Geometrical transformation
(c) Separating left and right brain hemispheres and
(d) Contrast stretching and region growing operation

2. Fuzzy C-means

The fuzzy C-means clustering technique (FCM) algorithm which is the second algorithm we have utilised. FCM separates voxels in an image into clusters using an unsupervised statistical classification algorithm.

When voxels within a cluster are compared to voxels between clusters, this approach is based on the concept that voxels within a cluster are more similar. Unlike K-means, which assign a degree of membership value to each picture voxel to the clusters' centre points, FCM is a gentle clustering approach.

The membership value indicates how closely the picture voxels are linked to a single cluster centre. FCM is an iterative algorithm that uses the cost function in **Eq. (1)** to update the cluster centre and membership value on a continuous basis.

$$J = \sum_{J=1}^{N} \sum_{i=1}^{C} (w_{ij}{}^{m} ||x_j - c_i||^2) \qquad \textbf{(1)}$$

Where the $w_{ij}{}^{m}$ $w_{ij}{}^{m}$ variable indicates the membership of the ***ith*** cluster's $x_j x_j$ data point, ci is the centroid point value of a cluster centre, and m determines the partition's fuzziness. The intensity values of image voxels are grouped into separate clusters depending on their similarity. Using **Eqs. (2 and 3)**, the cluster centroids and membership values of data points were iteratively updated.

$$C_i = \frac{\sum_{J=1}^{N} x_i w_{ij}^{m}}{\sum_{J=1}^{N} w_{ij}^{m}} \qquad \textbf{(2)}$$

$$W_{ij} = \sum_{k=1}^{c} \left(\frac{||x_j - c_i||}{||x_j - c_k||} \right) \times \left(\frac{||x_j - c_i||}{||x_j - c_k||} \right) \qquad \textbf{(3)}$$

3. Deep Convolutional neural networks

A cutting-edge multiple scale 3D CNN neural network with a completely interconnected Conditional random field (CRF) developed by Kamnitsas et al was the third algorithm whose performance was examined using our clinical dataset. There are two pathways in the algorithm, each with 11 layers. Despite the fact that the parallel pathways have the same number of deep layers, their activity is varied, with each pathway executing a separate task. In contrast to the first pathway, which was created to handle local information from multimodal MRI 3D patches, the second pathway was designed to extract global spatial information from downsampled pictures. In order for the Convolution using 3D input patches should be faster, and the number of trainable parameters should be reduced, the network utilises tiny 33 kernels in both parallel routes.

The convolutional layers soft segmented feature maps are fed into completely interconnected CRF to eliminate false positives outcomes and classify the tumor into edema, active, nectrotic and entire tumor region.

- We began by installing the necessary libraries and softwares:
  - ❖ Python 3: Used for coding.
  - ❖ TensorFlow: Backend Deep Learning library.
  - ❖ NiBabel: This is the library that is used to load NIfTI files.
  - ❖ Scipy :It is a scientific package and many operations of the images, such as augmentation, are performed with this library.
  - ❖ numpy : It is a Python library for array processing.
- On the CPU, small networks may be run. However, large-scale 3D CNNs need GPU computation. This necessitates the installation of Nvidia's CUDA.
- After that, we installed CUDA in a version that worked with our GPU drivers.
- cuDNN 8.4.1 was also installed as it is easy and really offers high acceleration and each training session takes about one day.
- We examined the performance of the Python code from Kamnitsas K's GitHub repository on our dataset. and made necessary changes according our requirements of the project.
- Because large 3D CNNs are computationally costly, we downsampled the pictures (i.e., reduced the size of the network) to avoid the problems.
- Scans are usually configured to be roughly 200*200*200 in size by default.
- After that, we trained a small CNN model to ensure that everything works as it should.
- Initially, the dataset which was downloaded was in a Zip file format. We extracted the files to the folder.
- After extraction, we got access to the BRATS 2015 dataset.
- Each patient dataset was included with T1c, FLAIR and T2c regions which is nothing but different contrasts of the MRI images.
- The dataset which was downloaded was divided in the ratio of 80 : 10 : 10 for training, validation and testing respectively.
- The files were in a format called MetaImage (mha), which later was converted to NifTI (nii) file format, as NIfTI is a type of file format for neuroimaging and is commonly used in imaging informatics for neuroscience and even neuroradiology research.
- The mha formatted files were converted to nii formatted files using ITK Snap Software.
- Then the next step is to mask the Brain MRI images, which isolates the brain from surrounding tissue in MRI scans, and its precision is crucial for further imaging data analysis.

- Later, we began training the model using the 40-patient dataset, which yielded required segmentation results.

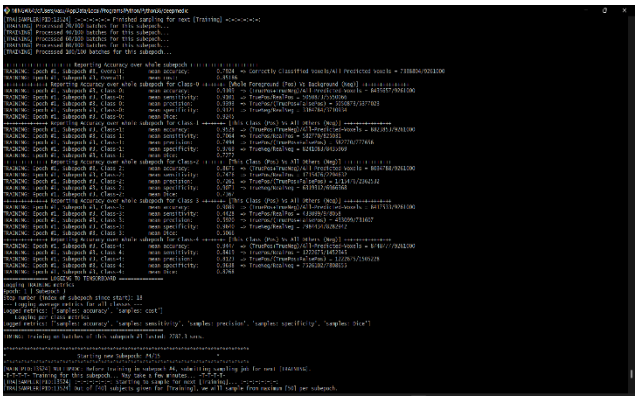

Fig: Training process

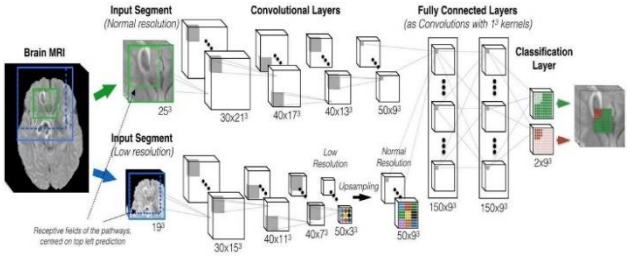

Fig: Multi-scale 3D CNN architecture for brain tumour classification

The use of 3-D convolutional neural networks helps to provide more context to the network. We have exploited the 3D nature of the input dataset, so the image slices are correlated upon one another across the volume. We have implemented a two-path way network, the first pathway gives local features at High resolution and the other pathway gives global features at low resolution, the kernels of both the pathway here are of size 5^3 and receptive fields of 17 voxels. The inputs of both pathways are centered at the same image location. The local features are extracted from patches of size 25^3 whereas the global features are extracted from the patches of size 51^3. The larger patches are reduced in size to 19^3 and fed into the network. After a series of convolution layers, the neural network's residual connections, global and local pathways are linked. Convolutional kernels with 1^3 kernels are used in the classification layer. The output patch of the network is of size 9^3 voxels.

IV. RESULTS

We have used 3D CNN architecture for semi-autonomous Glioma tumour segmentation. The proposed learning model is not only efficient computationally but also provides an alternate way of partially addressing imbalance segmentation difficulties. We looked into the advantages of utilizing tiny convolutional kernals in the 3D CNN and more discriminative network by not increasing the computational cost or the amount of parameters which are trainable. We addressed about the difficulties involved in the training of the deep neural networks and the solutions that have developed as a result of recent developments in deep learning. In addition, we suggested an effective strategy for large image contexts processing by employing parallel convolutional pathways for multi-scale processing, overcoming this primary computational constraints of earlier 3D CNNs. Finally, we demonstrate a fully connected 3D CRF on the BraTS 2015 dataset that can effectively segmenting the regions of the tumour.

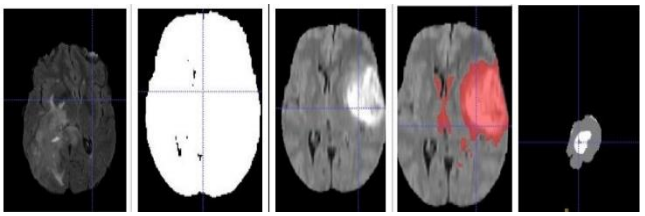

Fig: Segmented Results

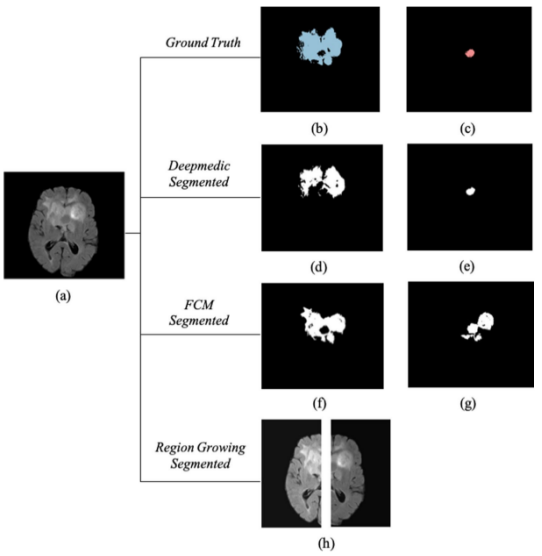

Fig : a .Input Flair image , b. The edema region's segmented ground truth using ITK snap tool, c .Segmenting the ground truth of the necrotic area with the tool called ITK snap, d .Region of segmental edema, e .region of segmented necrotic, f .Segmented edema region using FCM, g .Region of segmented necrotic using FCM, h. We attempted to segment the brain tumour location using the half-brain asymmetrical property. As a corollary, in these types of images, the tumour is not segmented by the region-growing algorithm.

V. CONCLUSION

On the patient data, we present a 3D CNN architecture that is cutting-edge for automatic glioma tumour segmentation and classification. Not only is the suggested unique training technique computationally efficient, but it also provides an adaptive way of partially reducing segmentation class imbalance and challenges. The fractal dimension's application for characterization of abnormalities in tumours has been shown to be effective in categorising tumours.

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