

A Novel Approach to Glioma Grading using MR Images with Deep Neural Networks

Aneeta Christopher¹, Dr. Sreelatha G²

¹P G Scholar, College of Engineering Trivandrum, Kerala, India

²Associate Professor, College of Engineering Trivandrum, Kerala, India

Abstract - The field of medical imaging is gaining significance with an increase in the demand for automated, reliable, fast, concise and efficient diagnosis which can provide insight into the biomedical image better than human eyes. Brain tumors are the largest cancer killer of children and adults under the age of 40 years and it reduces the life expectancy by an average of 20 years. Early diagnosis and timely treatment play vital roles in the survival rate of cancer patients. A system to classify gliomas based upon the WHO (World Health Organization) grading using Deep Learning is proposed. The brain MRIs are obtained from the BraTS 2018 database which provides both High Grade and Low Grade glioma MRIs. The preprocessing is carried out using bias field correction. The 3D segmentation is performed using 3D ESPNet that enables the inclusion of fine and coarse features. The classification of the gliomas as benign and malignant (High Grade Glioma and Low Grade Glioma) is implemented using the 3D Multi scale convolutional network. The segmentation has obtained a Whole Tumor Mean Dice score of 0.92 and the grading system provides an accuracy of 80.86%.

Key Words: Glioma, Deep Neural Networks, 3D Multi scale convolutional Network, 3D ESPNet, Dice score.

1. INTRODUCTION

Primary malignant brain tumors are among the most dreadful types of cancer, not only because of the forlorn prognosis, but also due to the direct consequences on decreased cognitive function of the individual and poor quality of life. The most frequently occurring primary brain tumors in adults are primary central nervous system lymphomas and gliomas, of which the latter account for almost 80 percent of the malignant cases occurring among humans. Gliomas are primary tumors that affect the glial cells in the central nervous system and based on the aggressiveness, they are classified as low grade gliomas (LGG) and high grade gliomas (HGG). The term 'glioma' comprises many sub-types of the primary brain tumor, which vary from relatively slow-growing "low-grade" tumors to heterogeneous, highly aggressive and intrusive malignant tumors. Despite prominent advances in biomedical imaging, radiotherapy, chemotherapy and surgical procedures, certain cases of malignant brain tumors, e.g., high-grade glioblastoma multiforme and metastasis, are still perceived to be incurable with a 2.5-year cumulative relative survival rate of 8 percent and 2 percent at 10 years. Moreover, there are varying prognosis

results for patients with low-grade gliomas (LGG) with an overall 10-year survival rate of about 57 percent.

Magnetic Resonance Images (MRI) are widely used for diagnosis and the treatment of brain tumors. MRI provides with vital information about location, shape, and size of tumors without exposing the patient to a high ionization radiation as is with other modalities like: CT, PET, or SPEC. The MRI characteristics of newly identified brain tumors can be used to point out the likely diagnosis and treatment strategy for the patient. Moreover, multimodal MRI protocols are commonly used to assess the brain tumor cellularity, vascularity, and blood-brain barrier (BBB) integrity. This is because variable image contrasts produced by multimodal MRI protocols can yield critical complementary information about the different tissues in the tumor region that enables distinguishing between different tumor types. Typical brain tumor MRI protocols, which are used often, include T1-weighted, T2-weighted (including Fluid-Attenuated Inversion Recovery, i.e., FLAIR), and gadolinium enhanced T1-weighted imaging sequences. These structural MRI images yield a vital diagnosis in the majority of cases.

According to the World Health Organization (WHO), the tumors are classified using the grading system that scales from Grade I to Grade IV. These grades classify the benign and malignant tumor types further depending on the differences in tissue cell constitution. The grade I and II are collectively known as low grade tumors while grade III and IV are grouped together as high grade tumors. Brain tumors can affect individuals at any age and the impact on every person may not be the same as this depends on the nature of the tumor occurring and the health of the individual. Due to the complex structure of human brain, diagnosis of tumor affected regions in brain is an exigent task. Hence automatic brain tumor detection system plays a vital role in today's medical scenario. The grades of gliomas have been determined based on the tissue histology according to the World Health Organization standard[1]. Since tumor grade relates heavily to prognosis, being able to distinguish non-invasively matters to clinical decision making and treatment planning.

2. LITERATURE REVIEW

Interpreting and processing brain tumor MR images are the most exacting and imminent field in biomedical imaging. Magnetic resonance imaging (MRI) is an improved biomedical imaging technique which is being used to

produce high-grade images of the human body parts especially the internal organs and it is very vital for deciding the correct therapy at the right stage for tumor-affected individual. Being less harmful than its contemporaries like CT, PET etc. has made it widely applicable for medical diagnosis.

A number of techniques have been proposed for classification of brain tumors from the MR images and CT scan images such as fuzzy clustering means (FCM), support vector machine (SVM), artificial neural network (ANN), expectation-maximization (EM) algorithm technique, Convolutional Neural Networks(CNNs) and Deep Neural networks(DNNs) which are some of the prevalent techniques used for region based segmentation of tumor regions in the brain and hence to extract important information from the medical imaging modalities which can further be used for related functions such as classification, detection and localization of brain tumors.

There are many processes involved in the brain tumor detection procedure namely, Pre-Processing, Segmentation, Feature Extraction and Classification. A lot many variants of the different phases of the detection process have evolved over time.

2.1 Preprocessing Techniques

Various preprocessing techniques have been employed for the enhancement of biomedical images. Pereira *et al.*[2] proposed Brain Tumor Segmentation using Convolutional Neural Networks in MR Image. In their work they preprocessed the MR images by using intensity normalization method. Havaei *et al.* [3] proposed Brain Tumor Segmentation with Deep Neural Networks and the preprocessing was carried out by using intensity inhomogeneity correction and also investigated on the normalization of data within each input channel provided. Vaidhya *et al.*[4] proposed Multimodal Brain Tumor Segmentation using Stacked Autoencoders. They investigated pre-processing techniques in MR images using the histogram matching techniques for the various MR input channels separately. Vaidya *et al.*[5] proposed Longitudinal Multiple Sclerosis Lesion Segmentation using 3D Convolutional Neural Networks and investigated the normalization of data in MR images using the ANTs normalization toolkit. ANTs[6] extracts information from complex datasets that include imaging. Paired with ANTsR, ANTs is useful for managing, interpreting and visualizing multidimensional data. ANTs is popularly considered a state-of-the-art medical image registration and segmentation toolkit. ANTsR is an emerging tool supporting standardized multimodality image analysis. ANTs depends on the Insight ToolKit (ITK), a widely used medical image processing library to which ANTs developers contribute. Darko *et al.*[7] proposed segmentation of brain tumor tissues with Convolutional Neural Networks and investigated on intensity

inhomogeneity correction in each MRI Channel and downsampling of MR image with Nearest Neighbor interpolation as pre-processing steps.

Bahadure *et al.* [8] proposed a method for MRI-based brain tumor detection and classification using Berkeley Wavelet Transform (BWT) and SVM techniques based image analysis. In this method, accuracy of 95 percent was achieved and the preprocessing of MR images was done using skull stripping that eliminated all non-brain tissues like the skull region and the cerebro spinal fluid (CSF) for the detection function.

2.2 Segmentation Techniques

For the brain tumor segmentation, Zanaty[9] proposed a hybrid approach, with the combination of seed growing, FCM(Fuzzy C Means) algorithm, and Jaccard similarity coefficient algorithm with the measure of gray and white segmented tissue matter from the tumor images. An average score of 90 percent segmentation was achieved with noise level of 9,3. To manage and to address protocols of different images and nonlinearity of real data an effective classification based on contrast of enhanced MRI images, Yao *et al.*[10] proposed a methodology which included extraction of textures features with wavelet transform and SVM with an accuracy of 83%. For the classification and brain tumor segmentation, Kumar and Vijayakumar[11] proposed methodology using principal component analysis (PCA) and radial basis function kernel with SVM. They obtained an accuracy of 94 percent with this method. An artificial neural network tool as both classifier and segmentation was used for the effective classification of brain tumor from MRI images was proposed by Sharma *et al.* [12] with the utilization of textural primitive features which achieved an accuracy of 100%. Dong *et al.*[14] proposed a fully automatic brain tumor detection and segmentation method using the U-Net based deep convolution networks. This method achieved a DSC value of 0.88 for HGG, 0.86 for LGG and 0.88 for combined occurrence cases. This result was way better than the conventional methods.

Joseph[13] proposed segmentation of MRI brain images using K-means clustering algorithm along with morphological filtering for the detection of tumor images. The automated brain tumor classification of MRI images using support vector machine was proposed by Alfonse and Salema [15]. The accuracy of the classifier was improved using fast Fourier transform for the extraction of features and minimal redundancy maximal relevance technique was used for reduction of features. The accuracy obtained from this work was 98%. Ouchtati *et al.* [16] proposed a method for brain tumor classification based on central moments using a neural network. The proposed

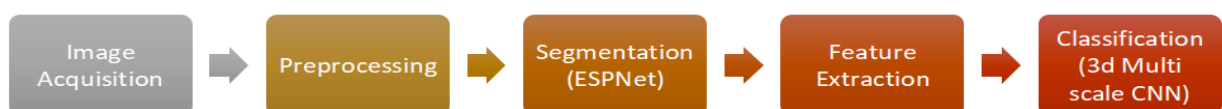


Fig - 1: Block diagram of the Proposed System.

system is based on the use of a new method for the features extraction. The principal objective is to calculate the histogram of each zone selected by sliding a window of size 16×16 pixels on the MR image of the brain, this allows us to obtain sixty four (64) histograms, and each obtained histogram will be considered as a sequence for which we calculate the central moments of order 1, 2 and 3. The classification is achieved by a multi-layer perceptron. The obtained results are very encouraging and promising. The system arrives to properly affect 88.333% of the images of the database.

For the medical image segmentation, a localized fuzzy clustering with the extraction of spatial information was proposed by Cui *et al.*[17]. The author used Jaccard similarity index as a measure of segmentation claiming an accuracy of 83.95% and differentiating into white, gray and cerebrospinal fluid. For the brain tumor image segmentation, active contour method was applied to solve the problem based on intensity homogeneities on MRI images was proposed by Wang *et al.* For the automatic extraction of features and tumor detection a with an enhanced feature using Gaussian mixture model applied on MRI images with wavelet features and principal component analysis was proposed by Chaddad[18] with an accuracy of T1- weighted 95% and T2 - weighted 92% for FLAIR MRI weighted images. Shaina Reji[19] proposed a brain tumor segmentation procedure based on the combination of W Net and U Net and Mask R-CNN based techniques in which W Net and U Net cascaded system outperformed the other system. The Multimodal Brain Tumor Segmentation Benchmark (BRATS)[20] enabled to provide an overview on the different brain tumor segmentation techniques prevalent today. Among the BRATS 2012 methods, only Hamamci and Geremia performed comparably in the “off-site” and the “on-site” challenges, while the other algorithms performed significantly better in the “off-site” test than in the previous “on-site” evaluation. This involved tumor - cut method that fuse different MR modalities so that it can be applied to each channel separately and then combine the segmented volumes by basic set operations based on the type of the modality. The dice score obtained was 0.72 for HGG and 0.59 for fused cases. For whole tumor segmentation Guo X. and B.[21] was the most accurate followed by Menze *et al.* [22]. Zhao *et al.*[23] proposed a semi-automatic segmentation method for multimodal brain tumors that requires only that a user manually draw a region of interest (ROI) roughly surrounding the tumor on a single image. The algorithm combines the image analysis techniques of region and edge-based active contours and level set approach, and has the advantages of easy initialization, quick segmentation, and efficient

modification. The typical run-time for each case in the training dataset can be within 1 minute.

2.3 Classification Techniques

Lavanyadevi *et al.*[24] proposed an automatic brain tumor classification system to classify the brain tumors as benign, normal and malignant using Probabilistic Neural Network (PNN) based classification technique. The features were extracted using the Gray Level Co-Occurrence Matrix (GLCM). Image recognition and image compression is done by using the Principal Component Analysis (PCA) method and also large dimensionality of the data is reduced. Segmentation process is done by using K-means clustering algorithm and also detects the brain tumor spread region. The system provided an accuracy of 72% in classification. Mengqiao *et al.*[25] proposed an automatic brain tumor segmentation algorithm based on a 22-layers deep, three dimensional Convolutional Neural Network (CNN) for the challenging problem of gliomas segmentation. To correct the bias field distortion of MRI images, N4ITK method was added before intensity normalization. During training, dropout was added to reduce over fitting, and adapt the batch normalization technique to speed up training. The validation process is carried out using BraTS 2015 database and the performance for the complete tumor, tumor core and enhancing tumor regions was evaluated by the online evaluation platform with Dice metric of 0.84, 0.79, 0.75, Positive Predictive Value metric of 0.88, 0.86, 0.70 and Sensitivity metric of 0.82, 0.75, 0.86. The total training time is about 140 min. The proposed system was found to be time-saving and efficient.

Varuna Shree and Kumar [26] proposed a brain tumor identification and classification based on feature extraction using DWT and Probabilistic Neural Network (PNN). The system had a test accuracy of 95% in identifying the normal and abnormal brains from MR images.

Kollerathu[27] proposed a DenseNet based fully automatic glioma classification based on transfer learning that provided with feature maps from the penultimate layer of the classification network for volumetric quantification of gliomas. The segmentation phase provide a Whole Tumor Mean Dice Score of 0.89 while the classification system had an accuracy of 79%. The proposed system was implemented based on 2D segmentation followed by 3D classification based on a few number of slices adjacent to the tumor assessed MRI slice.

A lot many paths have been undertaken for the analysis of biomedical images over time especially in the field of brain tumor analysis in order to help improve and fasten up the diagnosis process. These innovative methods have enabled

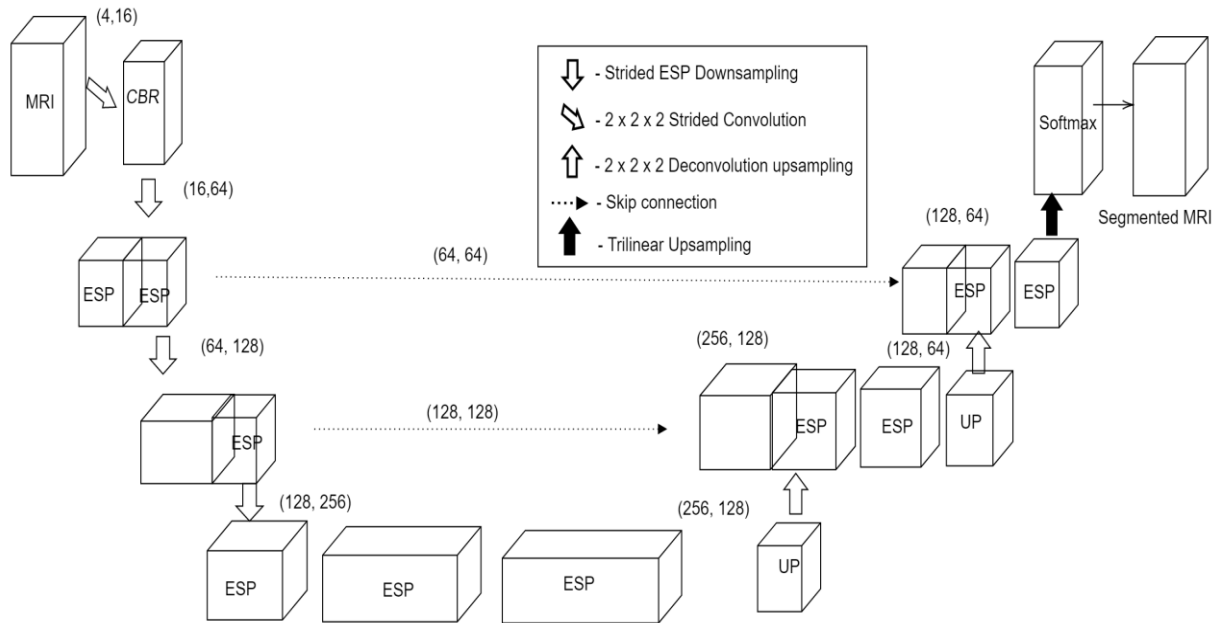


Fig-2 : The network architecture of 3D ESPNet based segmentation network. *Courtesy: Mehta et. al.[30]*

the medical experts to have a deeper insight into the condition of the patients. The recent advances in this field is brought about by Deep Neural Networks that mimics the working of neural networks in living beings.

3. PROPOSED METHOD

The overall system design of the proposed method is illustrated in Fig-1. Proposed system uses 3D ESPNet network for MRI segmentation and a 3D Multi Scale CNN Network for feature extraction and classification. Initially, preprocessing the brain MRI to remove noise is done using bias field correction and then the segmentation process is done on the enhanced image by 3D ESPNet Network. Finally the segmented images are to be trained and classified by Multi Scale 3D classifier system in order to classify the brain tumors based on WHO grading.

- Data Acquisition :** The brain MRIs for brain tumor classification (both training and testing phase datasets) are obtained from BraTS 2018 database[28] which provides two classes of brain tumor MRIs namely, those of the Low Grade Gliomas (LGG - Benign tumors) and those of the High Grade Glioblastomas (HGG - Malignant tumors).
- Preprocessing :** Preprocessing is the procedure to eliminate the noises and extracranial tissues in MRI and alter the heterogeneous image into homogeneous image.The preprocessing is carried out by using Bias field correction.
- Segmentation :** The segmentation is carried out by using 3D ESPNet network with pyramidal refinement . It enables classification of the proposal regions into object categories and background based on the intensity variations.

d) **Feature Extraction:** The 3D scaling features are extracted by using the 3D CNN network that enables to consider the fine and detail feites of the biomedical images.

e) **Classification:** The classification stage comprises of a Multi Scale 3D CNN Network that enables to classify the gliomas as High Grade Glioma(HGG, Malignant) and Low Grade Glioma(LGG, Benign).

3.1 Dataset

The dataset that is primarily considered is BraTS 2018 (Multimodal Brain Tumor Segmentation Challenge 2018) dataset[28] released in conjunction with the MICCAI 2018. BraTS 2018 utilizes multi-institutional pre-operative MRI scans and focuses on the segmentation of intrinsically heterogeneous(in appearance, shape, and histology) brain tumors, namely gliomas. Ample multi-institutional routine clinically-acquired pre-operative multimodal MRI scans of glioblastoma (GBM/HGG) and lower grade glioma (LGG), with pathologically confirmed diagnosis and available OS, is provided as the training, validation and testing data for BraTS 2018 challenge. These multimodal scans describe a) native (T1) and b) post-contrast T1-weighted (T1Gd), c) T2-weighted (T2), and d) T2 Fluid Attenuated Inversion Recovery (FLAIR) volumes, and were acquired with different clinical protocols and various scanners from multiple (n = 19) institutions.

All the imaging datasets have been segmented manually, by one to four raters, following the same annotation protocol, and their annotations were approved by experienced neuro-radiologists. Annotations comprise the GD-enhancing tumor (ET T label4), the peritumoral edema (ED D label2), and the necrotic and non-enhancing tumor core (NCR/NET T label1). The provided data are distributed after their pre-processing, i.e. co-registered to the same

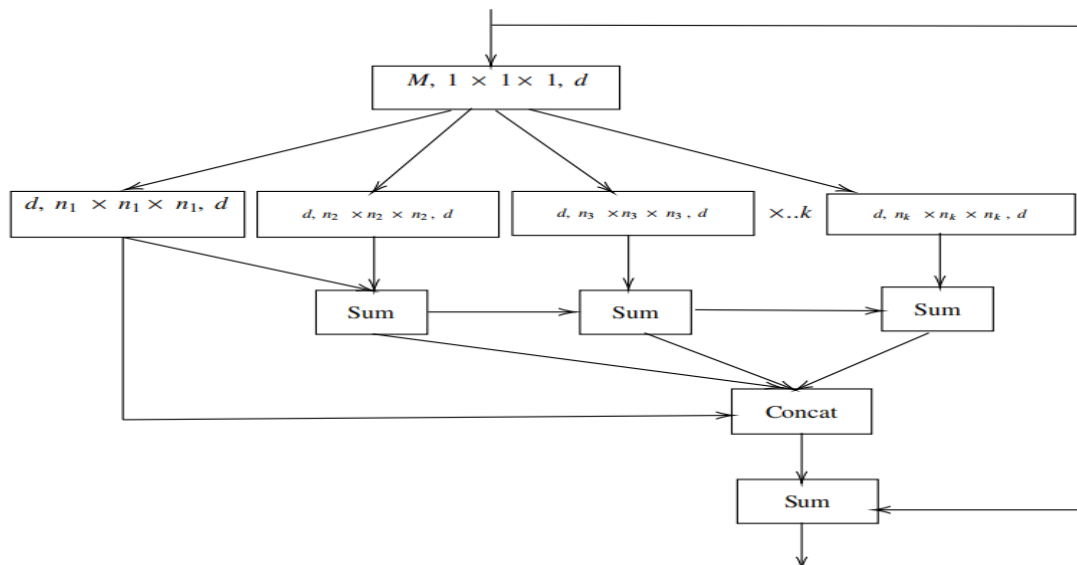


Fig - 3 :The Effective Spatial Pyramid Module. Courtesy: Nicholas et. al.

anatomical template, interpolated to the same resolution (1mm³) and skull-stripped. The expert neuroradiologists have radiologically assessed the complete original TCIA glioma collections (TCGA-GBM, n=262 and TCGA-LGG, n=199) and categorized each scan as pre-operative or post-operative. Subsequently, all the pre-operative TCIA scans (135 GBM and 108 LGG) were annotated by experts for the various glioma sub-regions and included in the BraTS 2018 datasets.

3.2 3D ESPNet based Brain Tumor Segmentation

The network for the 3D segmentation is an end-to-end system consisting of 3D implementation of ESPNet followed by pyramidal refinement, as shown in Fig-2. ESPNet Mehta et al. is a faster, more efficient take on U-Nets encoder-decoder architecture. 3D-ESPNet[29] is an encoder-decoder network that extends U-Net[30]. The primary distinction between 3D-ESPNet and U-Net is that 3D-ESPNet employs efficient convolutional blocks for aggregating features instead of stacking convolution layers (with or without residual connections) after the first layer. The Efficient Spatial Pyramid (ESP) module, shown in Fig.3, is an efficient convolutional module proposed by Mehta et al.[31] In the encoder stage, the network learns feature representations by performing convolutional and down sampling operations.

The encoder downsamples once with a strided convolutional layer and three subsequent times with strided ESP modules. In downsampling ESP modules, we use convolutions with $n_i \times n_i \times n_i$ sized kernels and stride of two, for $i \in \{1, \dots, K\}$, as shown in Fig.4. The combination of varying receptive fields allows 3D-ESPNet to learn feature representations at multiple scales.

In the decoder stage, the feature maps in the encoder is shared with same-level feature maps in the decoder via skip-connection concatenation. Skip-connections allow fine details lost in down sampling in the encoder to be

recovered in the decoder, which gives the segmentation maps a granularity that simple interpolation cannot achieve. The decoder uses $3 \times 3 \times 3$ deconvolution kernels to upsample the encoder output once, followed by trilinear upsampling layer to return to the resolution at the network's second level. The feature maps of the final ESP module in the decoder are passed into the pyramidal refinement module.

Pyramidal Refinement

Pyramid-based approaches sub-sample either the feature maps or the convolutional kernel to learn global contextual information. This approach is extended to volumetric data and is called pyramidal refinement. This module combines both feature map-based and convolutional kernel-based pooling methods in a novel fashion. Pyramidal refinement, as shown in Fig- 4, consists of three layers:

- Projection Layer:** This is a standard $3 \times 3 \times 3$ convolutional layer followed by batch normalization and ReLU that projects the feature maps from the previous ESP block to C-dimensional space, where C is the number of classes.
- Spatial Pyramid Pooling Block :** The input feature maps to this block are low dimensional ($C = 4$). We sub-sample them using convolutional kernels of different sizes and merge their output using sum operations as shown in Fig - 4.
- PSP Block:** A PSP block, sketched in Fig. 6, is based on the principle of *split-pool-transform-upsample*[23]. **Split:** A PSP block distributes the input feature maps across four parallel branches. **Pool:** Each branch downsamples the feature maps using a different pooling rate. **Transform:** The down sampled feature maps are transformed using point-wise convolutions. **Upsample:** The transformed feature maps are upsampled to the same resolution as the input feature maps using bilinear interpolation. **Merge:** The upsampled feature maps are then concatenated.

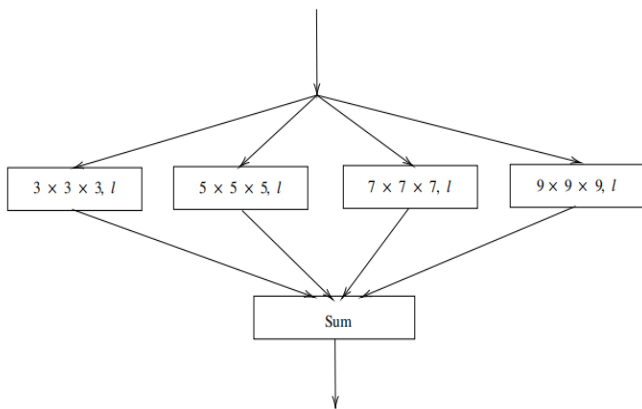


Fig - 4: Spatial pyramid Pooling block used in Pyramidal Refinement.

Pyramidal refinement is followed by a classification layer which pools the feature maps using another SPP block and then upsamples by a factor of two using trilinear

designed for fusing and refining multiscale features by using multi-scale fusion layers. Block-3 is designed for glioma grading/classification by using fully connected (FC) layers, whose output is the predicted class labels.

Network Architecture The architecture of the deep CNN and fusion network is described in Fig.5. The structure consists of eight convolutional layers.

Multi-scale convolutional layers (Block-1 in Fig. 6): The multi-scale convolutional structure consists of 5 bottom-up layers (Conv1-Conv5) and 3 merged layers (Conv6-Conv8), as shown in Fig.7. The first 5 convolutional layers are designed by using traditional CNN structure, where feature maps are generated in a coarse-to-fine manner. Since semantically strong features are often associated with relatively low resolution, while detail tissue features are often related to fine resolution, it is desirable to obtain

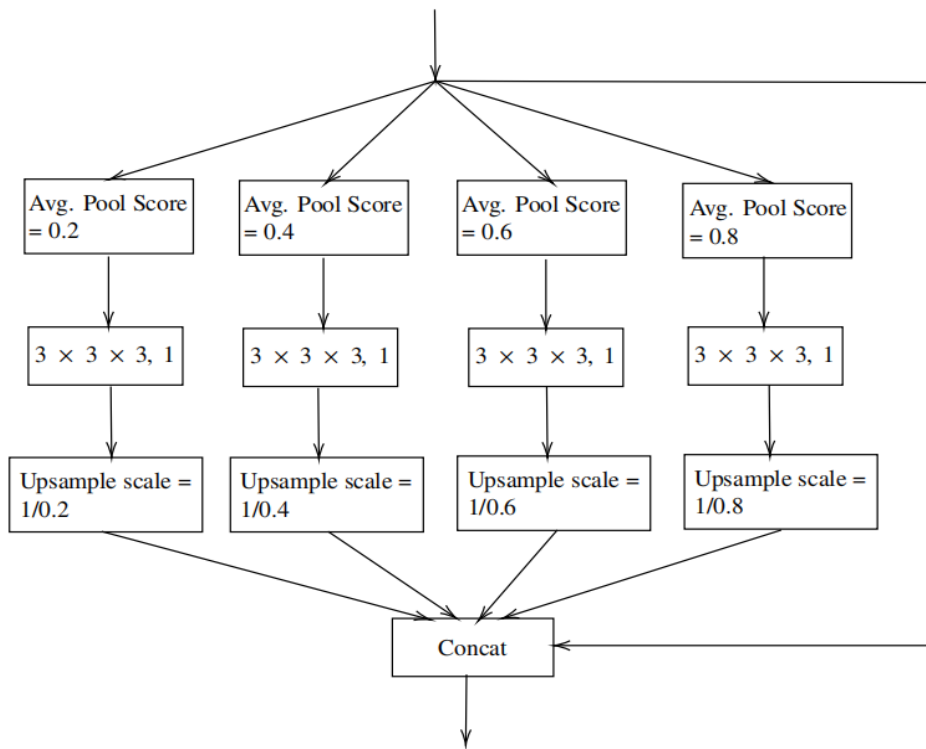


Fig - 5: PSP Module used in the Pyramidal Refinement block.

interpolation. Two convolutional layers are stacked on top of the upsampled feature maps before a softmax layer

3.3 Multiscale 3D CNN for Feature Extraction and Glioma Classification

Making use of multi-scale features that are rich in semantic and fine level information, the 3D multi-scale convolutional networks Ge *et al.*[32] could lead to learning more discriminative features for glioma grading/classification. The classification method consists of 3 modules as shown in Fig - 6, Block-1 is designed for extracting features by using multi-scale convolutional layers, whose input is 3D brain MR images. Block-2 is

features with both rich semantics and fine details for glioma classification. Hence, Conv5 is upsampled by a factor of 2 by a nearest neighbour up-sampling method. It is then merged with Conv4 features by element-wise addition and further convolved by a merged convolutional layer Conv6. In a similar way, features from the remaining two merged convolutional layers (Conv7 and Conv8) can be obtained.

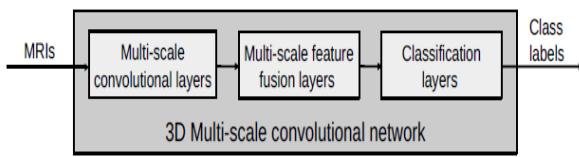


Fig - 6: Pipeline of the glioma classification network.

Feature fusion and classification layers (Blocks 2 and 3 of Fig-6): To make the full use of features from the multi-scale convolutional layers, the detailed fusion and classification architecture are shown in Fig-9. Features from different scales are separately pooled with the same pooling size to remain the multi-resolution structure, followed by individual fully connected layers to refine these dense features. After this, features are further concatenated and fed to the consequent FC layers for classification. The proposed scheme applies $3 \times 3 \times 3$ convolution before layer merging, resulting in deeper network and hence more powerful for feature learning. Furthermore, the proposed fusion and classification layers are specially designed for the task of glioma classification.

Layer	Kernel	Output Shape
Conv1+ReLU+BN	5*5*5*32	56*48*48*32
Conv2+ReLU+MaxPool+BN	3*3*3*64	28*24*24*64
Conv3+Relu+MaxPool+BN	3*3*3*128	14*12*12*128
Conv4+ReLU+MaxPool+BN	3*3*3*256	7*6*6*256
Conv5+ReLU+BN	3*3*3*256	7*6*6*256
UpSample1+MergeConv4+BN	-	14*12*12*256
Conv6+ReLU	3*3*3*128	14*12*12*128
UpSample2+MergeConv3+BN	-	28*24*24*128
Conv7+ReLU	3*3*3*64	28*24*24*64
UpSample3+MergeConv3+BN	-	56*48*48*64
Conv8+ReLU	3*3*3*32	56*48*48*32
FC1-1	-	256
FC1-2	-	256
FC1-3	-	256
FC1-4	-	256
Concatenation+BN	-	1024
FC2	-	256
FC3	-	2

Fig -7: Architecture of the Glioma Classification Network.

3.4 Saliency-Aware Enhancement of the Tumor Regions

A brain tumor often occupies a small regional area in a 3D brain MRI scan. To let the deep network focus on the tumor region instead of other brain parts, a saliency-aware approach is introduced to enhance the tumor region.

Based on tumor masks provided in the dataset, pixel intensity values in the non-tumor regions are scaled down by a factor (e.g., 1/3 of their original values in our tests). Tumor regions, considered as salient, are thus highlighted as shown in Fig-10 and Fig-11 for the high grade and low grade gliomas respectively. The saliency-aware tumor enhancement serves as a soft segmentation protocol,

where the contextual information of tumor (i.e., information on its surrounding tissues) is preserved. This enables us to take into consideration the neighbouring tissue nature for the glioma study as well.

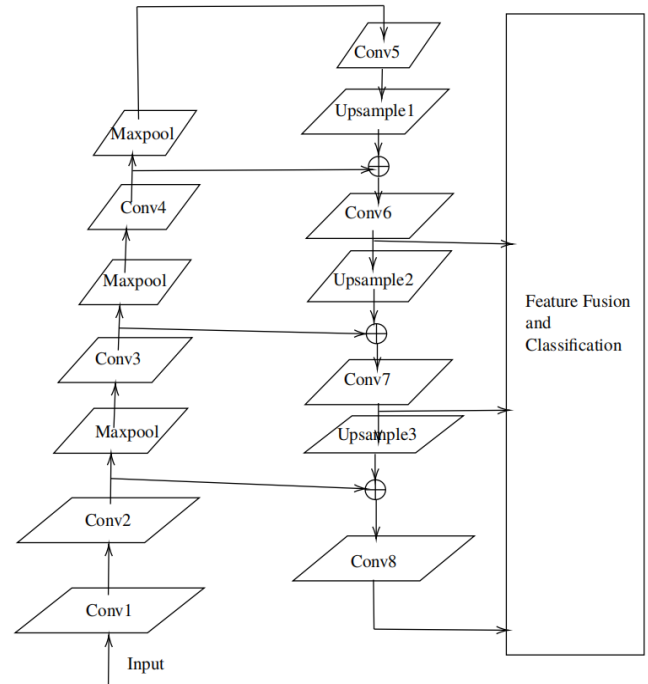


Fig - 8 : Multi Scale Convolutional Layers.

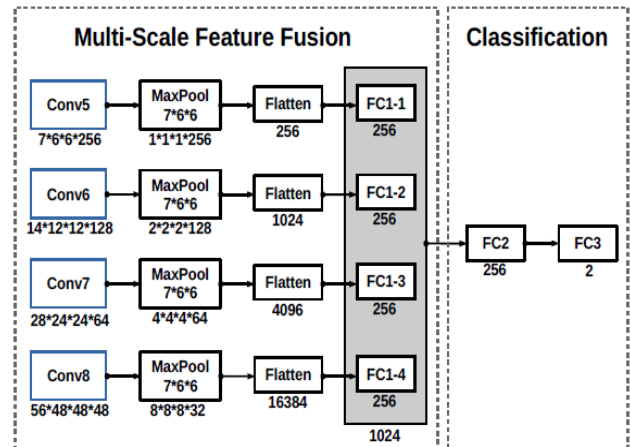


Fig - 9: Multi Scale Feature Fusion and Classification blocks.

4. RESULTS AND DISCUSSIONS

The proposed system of glioma classification has been implemented and the system performance is compared with state of the art biomedical image based classification techniques. The system has been implemented using Google Colab and GPU based system.

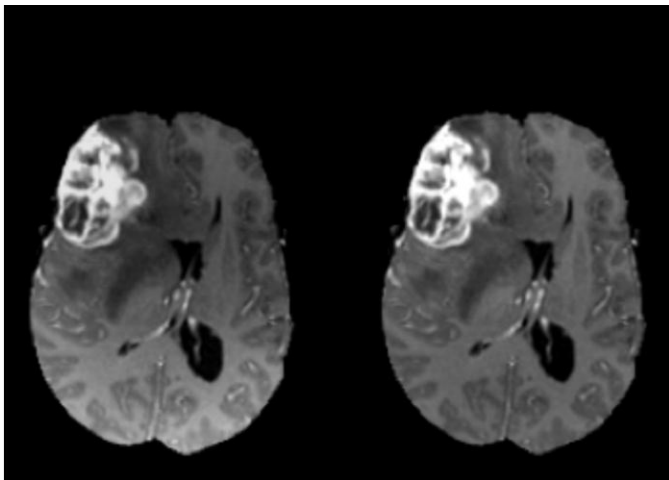


Fig - 10: Brain MRI slice (left) and Bias Field Corrected Brain MRI Slice (right) using N4ITK Bias Field Correction.

The BraTS 2018 dataset is a preprocessed dataset in which skull - stripping and co - registration has already been carried out for the four modalities of MRI scans of each patient along with the segmentation files. It consists of 3D models of the brain MRI. For bias field correction across the MRI scans taken from different institutions, N4ITK bias field correction is employed. This has enabled to normalize the field bias across the different MR images from different MR Imaging machines.

The 3D ESPNet considered all the four types of MR sequences for the tumor segmentation. The segmentation is carried out by tuning the hyper parameters based upon the mean Intersection Over Union (mIOU) on the withheld validation set. The loss function considered for training the ESPNet for segmentation is mean Intersection over Union (mIOU). Data augmentation was used to increase the dataset for Low Grade Glioma by random flipping and scaling. The segmentation enabled us to produce an improved dice score for the whole tumor section compared to the unprocessed approach. The tumor core and enhancing tumor had comparable dice scores compared to the unprocessed approach as shown in Table I. The performance of the segmentation system applied to the BraTS 2018 Validation set which is evaluated by CBICA Image Processing Portal is studied in Table II. The system has comparable results with the original system with slight improvement in the dice scores. The segmented slice is shown in Fig. 11 where the Whole Tumor (Green), Tumor Core (Red) and Enhancing Tumor (Yellow) is marked respectively

Table - 1: 3D ESPNet based brain tumor Segmentation performance comparison.

Segmented Region	Mean Dice Score	
	Raw Database	Preprocessed Database
Whole Tumor	0.850	0.9215
Tumor Core	0.782	0.8891
Enhancing Tumor	0.665	0.7083

Table - 2: Results obtained on the BraTS 2018 online validation set of the proposed system.

Segmented region	Dice Score	Sensitivity	Specificity
Whole Tumor	0.891(0.883) *	0.942(0.93)	0.99(0.99)
Enhanced Tumor	0.737(0.731)	0.821(0.803)	0.9985(0.997)
Tumor Core	0.811(0.804)	0.829(0.810)	0.997(0.997)

*Results for the 3D ESPNet without preprocessing shown in paranthesis.

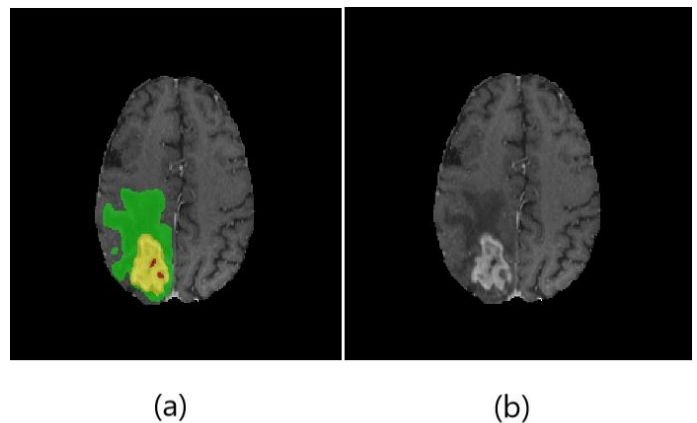


Fig - 11: Segmentation results on BraTS 2018 Validation set. (a) Segmentation output (b) Original slice of High Grade Glioma.

The multi scale 3D CNN based glioma classification is directly carried out on the BraTS 2018 database and the accuracy is boosted from 89.47 % to 91.27 % by utilizing the preprocessing technique of bias field correction for improving the brain MRI. The tumor masks were directly provided from the ground truth files for training phase. For the testing phase, the segmentations from the 3D ESPNet were provided and the ground truth segmentations were provided for testing for comparative study with the state of the art methods of brain tumor classification. The glioma grading is carried out using the T1 Contrast Enhanced sequence of the MRIs alone since it enables to clearly visualize the enhancing tumor region in the glioma that differentiates the high grade and low grade gliomas.

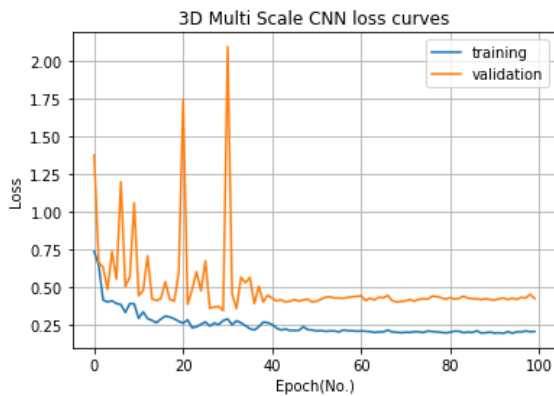


Fig - 12 : Performance Comparison of the 3D Multi Scale CNN Classification Network based on loss.

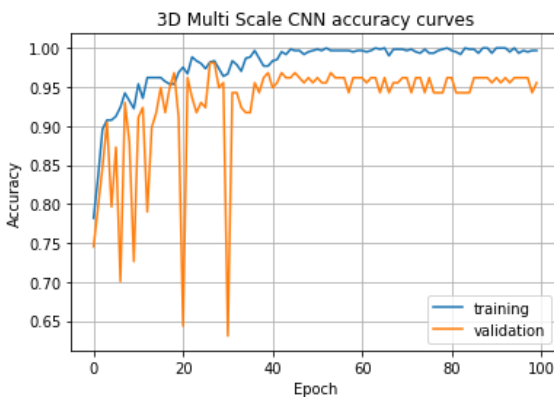


Fig - 13 : Performance comparison of 3D Multi Scale CNN Classification network based on training accuracy.

The accuracy and loss comparison curves are provided in Fig.12 and Fig.13 respectively. They show that the system is trained without over fitting. The training accuracy is greater than the testing accuracy by 0.05 and the training loss and validation loss also differ correspondingly which implies that the training is carried out without overfitting occurring in the system. The preprocessing stage has increased the accuracy of prediction as shown in Table III.

Table - 3: Results for the Multi Scale 3D CNN based Glioma Classification Network.

Accuracy(%)	BraTS 2018	BraTS 2018(preprocessed)
Training accuracy	98.61	99.8
Validation Accuracy	94.74	95.54
Test Accuracy	89.47	94.27

Table - 4: Comparison study of various Brain Tumor Classification Systems.

Authors	Glioma classes(Methods)	Accuracy(%)
Chenjie	HGG/LGG(3D CNN)	89.47
Varghese Alex	HGG/LGG(2D ResNet-50)	79.00
Proposed	HGG/LGG(3D CNN)	91.21(80.86)#

Classification accuracy for the proposed system on segmented regions from 3D ESPNet given in parentheses.

It would be desirable to compare with other state-of-the-art glioma classification methods, however, this appears to be difficult in this case. There are two barriers: (a) there are only a few reported works on glioma classification probably due to the lack of many medical datasets and (b) most of the reported works have been applied to different datasets and also classified different sub-classes or categories of gliomas. The classification result is compared with that of a number of other classification systems based on various other methods and using databases considering different types of gliomas (Table IV). The proposed system has comparatively better classification accuracy as compared to the other implementations for glioma classification.

5. CONCLUSION

The 3D ESPNet is an object segmentation framework that provides a comparatively better and accurate performance compared to the state of the art networks with reduced complexity. The proposed system is efficient in accuracy and runtime. The segmentation phase performed by 3D ESPNet provides accurate segmentation of the glioma regions for further processing. The Multi Scale 3D CNN based classification network enables the classification of the gliomas into High Grade and Low Grade Gliomas. The work is carried out by using the BraTS 2018 database. Hence, the generalization of the system might require more training samples which can be collected from medical research institutions. Altogether the proposed system is an automatic brain tumor classification system that is efficient in output accuracy and run-time for testing phase. The proposed system can be utilized for the detection and classification of other brain tumors after training with the required amount of the suitable database.

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BIOGRAPHIES



Aneeta Christopher

She did her B.Tech in Electronics and Communication engineering from Amal jyothi College of Engineering Kanjirapally. She later on completed her M.Tech in Signal Processing from College of Engineering Trivandrum. Her research areas are Signal Processing, Biomedical Image Processing and Deep Neural Networks.



Dr. Sreelatha G

She received her B. Tech. in Applied Electronics and Instrumentation Engineering from College of Engineering Trivandrum in 1996, M. Tech. in Electronic Design and Technology from Indian Institute of Science, Bangalore in 2006 and Ph. D. from Department of Electronics & Communication Engineering, National Institute of Technology Calicut, Kerala in 2017. She is currently the Technical Officer in College of Engineering Trivandrum. Her research areas are Signal Processing, Image Processing and Medical Image Processing. Published three peer reviewed journal papers and four conference papers in Medical Image Processing. Major contributions are in the area of DNA damage analysis.