BRAIN TUMOR SEGMENTATION

Dissertation submitted to Jawaharlal Nehru University in partial fulfilment of the requirements for the award of the degree of

Master of Technology

In

Computer Science and Technology

By

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Certificate

This is to certify that the dissertation entitled "*Brain Tumor Segmentation*" is being submitted by **Ms. Aditi Priya** to **School of Computer and Systems Sciences, Jawaharlal Nehru University, New Delhi-110067, India** in the partial fulfilment of the requirements for the award of the degree of **Master of Technology in Computer Science and Technology**. This is entirely his own work, carried out in the School of Computer and Systems Sciences under the supervision of **Prof. R. K. Agrawal**. The matter personified in this dissertation has not been submitted for the award of any degree of this or any other university.

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Declaration

I hereby declare that the dissertation entitled **"***Brain Tumor Segmentation***"** in partial fulfilment of the requirements for the degree of **Master of Technology in Computer Science and Technology** submitted to **School of Computer and Systems Sciences, Jawaharlal Nehru University, New Delhi-110067, India** is an authentic record of my own work carried out under the supervision of **Prof. R. K. Agrawal**. The matter personified in this dissertation has not been submitted for the award of any degree of this or any other university.

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Aditi

Abstract

There are many approaches suggested in literature for segmentation of brain tumors. The performance of brain tumor segmentation method improves when information is considered from multiple sequences of magnetic resonance imaging. In this thesis work, a novel method is proposed for segmentation of brain tumor which consists of 3 stages. The first stage utilises a combination of Discrete Wavelet Transform and Principal Component Analysis for image fusion, motivated by the research work of Rajnikanth et. al., in which fusion of images of different modalities is done. In the second stage, Otsu thresholding which is comparably simpler and computationally less intensive than SGO thresholding method is utilized in the current work. Third stage consist of a well- known segmentation technique called Fuzzy-C means segmentation, which overcome limitations of the watershed segmentation. To evaluate the performance of the proposed work, an average similarity score i.e. Dice score is used. Experiments are performed on the BRATS 2013 dataset. Dice score is calculated separately for HGG and LGG dataset and compared its performance with existing methods. The achieved results of the proposed method are promising.

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Chapter 1

1 Introduction

1.1 Overview

The brain is an essential part of every individual, which controls the functionality of other parts of the body. The structure of the human brain is very complex. It consists of mainly three types of tissue which are Cerebrospinal Fluid (CSF), White Matter (WM) and Grey Matter (GM) shown in the Figure 1.1 below:

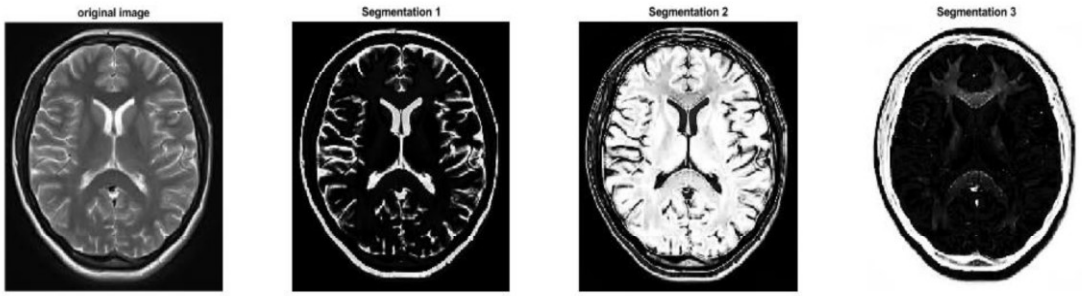

Figure 1. 1: Segmented tissues of T1 MRI image (Adapted from [1]). From left: a. original image, b. CSF, c. white matter, and d. grey matter.

There are millions of individuals diagnosed with brain diseases mainly caused by the growth of abnormal tissues. Brain diseases include Schizophrenia, Glioblastoma, Brain Tumor, Hydrocephalus, Alzheimer, Parkinson, etc. As per survey conducted by World Health Organization (WHO), brain tumor and stroke are considered as the second and third major cause of death in the entire world. Every year, almost 40,000 people are identified with brain tumor in India out of which nearly 20 percent consist of the children [2]. The occurrence of brain tumor has increased by 25 since 1975 and according to National Brain Tumor Foundation (NBTF), the number of people who die because of brain tumors has grown by nearly 300 [3, 4] in the recent years worldwide.

World Health Organization grades brain tumors from I to IV and the grading is based on severity of the disease. Brain Tumors can be further classified as primary and secondary tumors. In primary brain tumors, the cells originate in the brain only and in secondary brain

tumor, the cells spread from some other infected area of body. Tumor is one of the most common brain related diseases. As the tumor grows, the pressure also increases, which causes the patient to feel intense pain, sensory changes and confusion. So, early diagnosis of it helps in the treatment process.

Brain tumor analysis is one of the important areas of medical imaging analysis. With the advancement in technology in medical imaging devices especially MRI, we can easily obtain essential information from body structure images. MRI finds pertinent contrast between different brain tissues and also, depicts the degree and extent of brain tumors.

MRI describes the structures of the brain quite appropriately, however segmentation of medical images is a cumbersome process because of presence of several artifacts like low spatial resolution, inhomogeneity, noise, less contrast, partial volume effect. When, manual segmentation is done, the tumor areas that are present are marked manually, which is an expensive as well as weary task and involves a lot of expertise. To overcome these, automated image segmentation is needed.

Images obtained using MRI are used for analysis and study of brain. Research shows that images obtained using MRI gives precise and better results than other modalities. Most of the current state of art that exists on segmentation of brain tumor utilizes various MRI sequences such T1-weighted (T1), T1-weighted contrast-enhanced (T1c), as T2-weighted (T2), fluid-attenuated inversion recovery (Flair) which will be described shortly as in [5]. Each of these MRI sequences is suitable for different purposes. In automated analysis of brain tumor, different combination of MR sequences is commonly used to obtain better accuracy and results.

The content of water is not present in bones and cerebrospinal fluid, which appear black. Depending on the amount of water in the tissues, blood and soft tissues appearance varies between black and white. Also, the contrast of these tissues depends on the imaging parameters. The contrast in tissues mainly depends on repetition time (TR) and echo time (TE).

1.2 Magnetic Resonance Sequences

There are mostly four MR sequences used known as T1-weighted (T1), contrast enhanced T1 (T1C), T2-weighted (T2), and Fluid-attenuated inversion recovery (FLAIR), and they will be described shortly. These tissues are obtained from MRI machine with the variation of echo time (TE) and repetition time (TR).

1.2.1 T1 -weighted image

When the duration of TR is less, the longitudinal magnetization recovers better in water than with fats. This establishes better discrimination of water from fats. Due to this, CSF and water appear darker and blood and fat appear brighter. Anatomical details are presented better in T1 than T2 but at the time of investigation of brain tumor, they usually do not provide any relevant information. However, when a contrast agent fluid is used, it highlights the blood flow in T1 images. So, the active tumor region and the vessels appear to be hyper-intense and can be easily discriminated from the surrounding tissues. Such images are called (contrast enhanced T1-weighted) T1c images.

1.2.2 T2-weighted image

Longer duration of echo time provides better discriminating power between fats and water than shorter duration of echo time. Due to which, water content tissues appear brighter in T2 images than other modalities.

1.2.3 FLAIR image

This is a MR sequence in which suppression of fluids occurs that is able to cause Cerebrospinal fluid (CSF) suppression in a brain image. Due to which, lesions are easily distinguishable and appear to be hyper-intense as in T2 images and CSF appears to be hypo-intense. This modality is the most commonly used modality in brain images.

Different modalities such as T1, T1C, T2 and FLAIR images with tumor present in them are depicted in Figure 1.2.

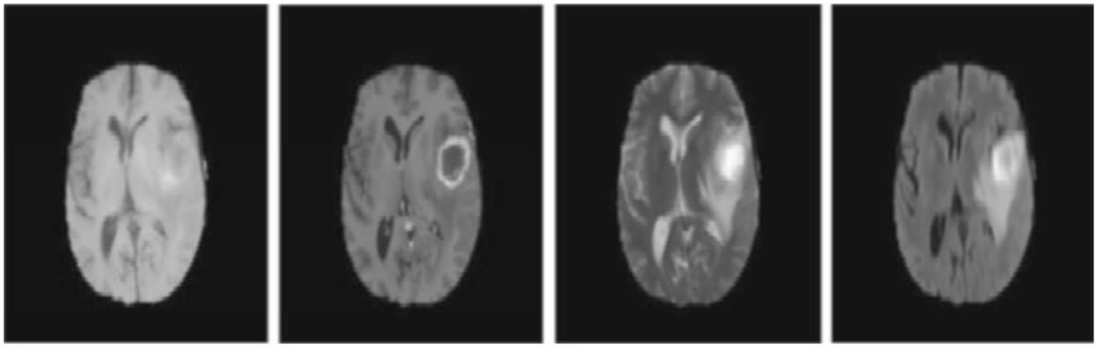

Figure 1. 2: Different modalities with tumors present in them (Adapted from [6]). From left: T1 weighted image, T1c weighted image, T2 weighted image, and FLAIR image. These are obtained using BRATS 2013 dataset

The main aim of automated analysis of brain tumor is to get necessary and relevant information regarding, whether a tumor is present or not, type and location along with its size. The information which we retrieve using clinical imaging can help us in making an early diagnosis and can prevent many future problems related to brain tumor.

Diagnosis of brain tumor, consists of several steps namely pre-processing step, segmentation step, extraction of features step, and classification step. The first step of almost all medical imaging process is usually pre-processing. This is mainly required for removing noise, bias field correction in order to produce better and refined images which can be used for further analysis. Next step is image segmentation, in which an image is partitioned into several homogenous regions, usually based on the various characteristics and attributes of the pixels in the image. It is mainly use to separate foreground objects from background and we will discuss some existing works in brain tumor segmentation proposed in literature in the next section.

1.3 Related Work

This section deals with to review the research works related to segmentation of brain tumor and other tissues surrounding it. Segmentation of medical images is a cumbersome process because of presence of several artifacts like low spatial resolution, in-homogeneity, noise, less contrast, partial volume effect. Manual segmentation of brain tumor areas is an expensive as well as weary task and involves a lot of expertise.

To overcome these, automated image segmentation is needed. The main aim of automated analysis of brain tumor is to get necessary and relevant information regarding, whether a tumor is present or not, type and location along with its size. The information which we retrieve using clinical imaging can help us in making an early diagnosis and can prevent many future problems related to brain tumor. Automatic segmentation of brain tumor is also a cumbersome task because of some unpredictable properties of a brain tumor like size of tumor, it's shape and location.

Since different techniques related to segmentation of brain tumors are based on different image information, a variety of methods are suggested for its implementation and to evaluate the performance.

Cordier et al. [7] proposed an approach known as Patch-based Segmentation in which segmentation is based on similarities that exist between multi-channel patches of training data and multi-channel patches of unknown label of test data. Initially a database is constructed for multi-channel patches that is obtained for training data, in which the label maps are already known. Majority voting scheme is utilized for finding segmentation map for each test patch.

Bauer et al. [8] proposed a method for automatic brain tumor segmentation which is based on tumor growth model and a hybrid of average atlas. Once the pre-processing steps such as bias-field correction, rescaling, denoising etc are completed, then segmentation step is constructed in a conditional random field formulation.

Buendia et al. [9] proposed a method known as GAIN+ which is a better version of originally described grouping artificial immune network developed for automatic segmentation of brain images. This was developed to dynamically allow any number of input samples for training for automatic segmentation of brain tumors.

Geremia et al. [10] proposed a technique known as Spatially Adaptive Random Forests (SARFs) for segmentation of brain tumors in multi-modal MR images. This was developed to surpass the issues that occur in volumetric medical images. It uses 3D image representation and discriminative random forests and for the segmentation purpose, structured labelling is used.

Hamamci et al. [11] proposed a semi-automatic method in which the specific regions of the brain tumor and gross tumor volume are specifically targeted on T1C images. It works on the principle of cellular automata on T1c MR images.

Meir et. al. [12] proposed a brain tumor segmentation as a supervised problem, which is a variant of the work by Bauer et al. in [8]. It consists of mainly three main steps first is the

feature extraction method which gives a pixel-wise feature vector, second step is classification and third step is a subsequent spatial regularization.

Doyle et. al. [13] proposed a method using Variational Expectation-Maximization (EM)and Hidden Markov Fields. This method needs no training and all the parameters that are used are estimated with the help of Variational Expectation-Maximization algorithms with some constraints. To provide stability during optimization, prior probabilities maps are utilized.

Festa et.al. [14] suggested an automated brain tumor segmentation method which uses random decision forests. It consists of three pre-processing steps which includes N4ITK [15] method which is used for bias field correction, ITK [16] which is used for normalizing the intensity scale of each sequence and the final step in which all sequences are cropped to acquire the same volume and each brain voxel is classified using random decision forest.

Reza et. al. [17] proposed a method for brain tissue segmentation which utilizes texture features in brain MR images. Figure 1.3 shows the execution of the proposed method. It consists of mainly four steps. The First step is pre-processing which includes bias field correction, intensity and inhomogeneity correction. The second step is feature extraction in which two set of features are extracted namely texture features which includes fractal PTPSA [18], mBm [19] and classical textons [20] and non-local features and all these features that extracted are fused together. After extracted features are fused together, the third step is classification in which prediction of tissue labels is done using Random Forest classifier.

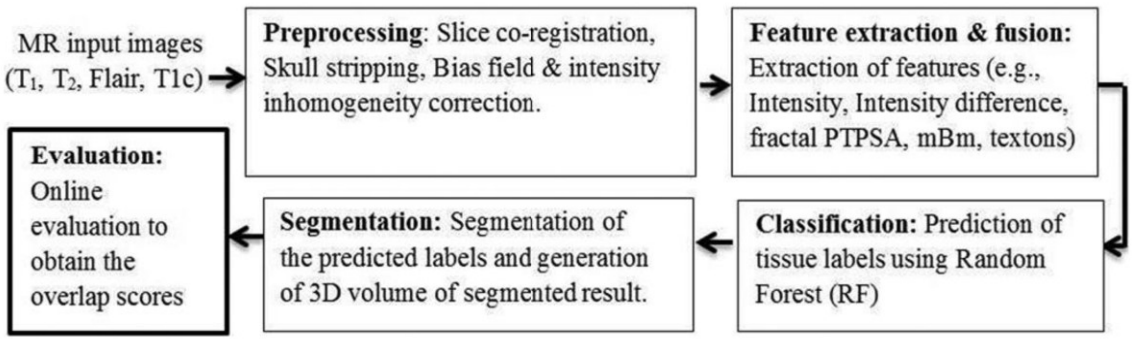

Figure 1. 3: Generic flow diagram of the proposed method

A fully automated method was proposed by Kalaiselvi et al. [21] in which tumor regions were extracted and segmented from multi-sequence MRI images. The proposed work comprised of three steps namely tumor region extraction, tumor region segmentation and postprocessing.

A completely automated method was proposed by Tustison et al. [22] which was based on Random forest. It consisted of expanded feature sets such as geometry, intensity and asymmetry. The asymmetry feature set were excellent in stablishing discriminating properties in this proposed work.

In the research work [23], Rajnikanth et. al. suggested a three-stage process for brain tumor segmentation. In the first stage, the combination of discrete wavelet transforms (DWT) and principal component analysis (PCA) is used for fusion of images modalities. In the stage two, Social Group Optimization (SGO) and Shannon Thresholding Technique is used for obtaining the thresholded image. A well-known technique known as watershed segmentation is used for the segmentation purpose.

In this work, the technique used for thresholding *i.e.,* SGO is a computationally intensive technique and the watershed segmentation method used for segmentation suffers from problem of over-segmentation and also, marker-controlled watershed segmentation requires the initial defining of internal and external markers.

1.4 Motivation

To overcome the problems of the proposed work by Rajnikanth et. al. [23], a three-stage novel method for automatic brain tumor segmentation is proposed to improvise the performance of tumor segmentation. The first stage consists of a combination of DWT (Discrete Wavelet Transform) and PCA (Principal Component Analysis) for image fusion in which fusion of images of different modalities is done. In the second stage, Otsu thresholding which is comparably simpler and computationally less intensive than SGO thresholding method is utilized in the current work. Third stage consist of a well- known segmentation technique called Fuzzy-C means segmentation. All the problems and ambiguities of the watershed segmentation used in the current work are taken care by FCM. The proposed method is computationally less intensive in comparison to the work of Rajnikanth et. al. [23].

The objectives of this work research work are:

- To investigate the related research works to find their shortcomings

- To develop novel brain tumor segmentation method, which is computationally simple and provide better performance
- To evaluate and the performance of the proposed work with existing methods on a publicly available BRATS 2013 dataset.

Rest of the thesis is organized as follows: Chapter 2 presents the proposed work along and its comparison with existing work on a publicly available BRATS 2013 dataset. Finally, Chapter 3 includes Conclusion and Future work.

Chapter 2

2 Proposed Work

2.1 Objective

The objective of the proposed work is to develop fully automated methods that can easily segment brain tumor from 3D MRI images without any user interaction. Even though the user interaction is sometimes needed e.g., for post processing correction, the proposed methods must not involve any user and should be focused on dealing with gliomas of both high grade and low grade. The attention should be paid on improving the segmentation accuracy.

The motivation for the proposed work comes from the existing three step work proposed by Rajnikanth et al. [23]. The three stages are:

- DWT (Discrete Wavelet Transform) and PCA (Principal Component Averaging) combination technique used for image fusion.
- Social Group Optimization (SGO) and Shannon thresholding.
- Watershed segmentation used as the segmentation technique.

In this, the fusion step and the thresholding step together makes the pre-processing stage and the marker-controlled watershed segmentation used here makes the post-processing stage. The first stage involves image fusion in which a fused image is obtained using DWT-PCA combination. This approach is a widely used because it enhances the brain MRI information due to pixel-level grouping of images. The second stage included a tri-level thresholding technique known as SGO and Shannon thresholding which is used for clustering or dividing the brain images into three regions which are background, normal region, and tumor region. The third stage includes a segmentation technique known as marker-controlled watershed segmentation which is used for obtaining the exact tumor region.

A tri-level thresholding technique is utilized in in the proposed work, which is a computationally expensive procedure for calculating the threshold. The watershed segmentation technique that is used in this work suffers from problem of over-segmentation. Also, it requires initial defining of the internal and external markers, which has to be done manually.

To overcome these shortcomings, instead of a tri-level thresholding scheme, a well-known Otsu thresholding method is used which is computationally less expensive. Instead of watershed method, a well-known technique known as Fuzzy C-Means is used as a segmentation technique in the proposed work. The FCM does not suffer from the problem of over-segmentation and do not require any definition of the initial markers which, in turn reduces the overhead.

2.2 Methodology

The proposed work mainly consists of three stages which are shown in Figure 2.1 For the experimental analysis the test images are taken from the BRATS 2013 dataset. In the proposed work, the fusion step and thresholding step together makes the pre-processing stage and the Fuzzy-C Means segmentation makes the post-processing stage. Lastly, the performance evaluation of the proposed work is done by comparison of the tumor portion that is segmented and the ground truth that exists in the BRATS 2013 dataset.

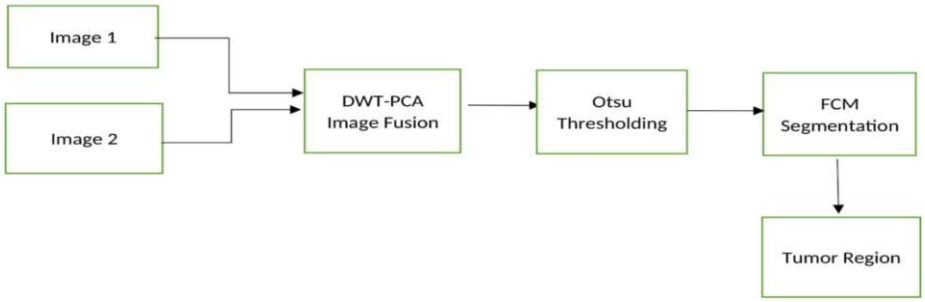

Figure 2. 1: Execution of the proposed work

2.2.1 Image fusion

This is a technique that is used widely to enhance brain MRI information because it groups images on pixel level. In the proposed work, DWT (Discrete Wavelet Transform) and PCA (Principal Component Averaging) combination technique is used for image fusion of different modalities. This combination technique was proposed by Vijayarajan and Muttan [24] for performing fusion of the slices of brain that is obtained with the MRI.

In this method, each 2D-image is first decomposed at level 1 using discrete wavelet transform (DWT) into one 2D-approximation coefficients (A), and three 2D-detailed coefficients of different orientations (Vertical coefficients (V), Horizontal coefficients (H) and Diagonal coefficients (D)). This process may be continued for higher level decomposition for other resolutions.

Figure 2.2 shows 1 level decomposition of a MR slice using DWT. Similarly, we can decompose another MR slice using DWT.

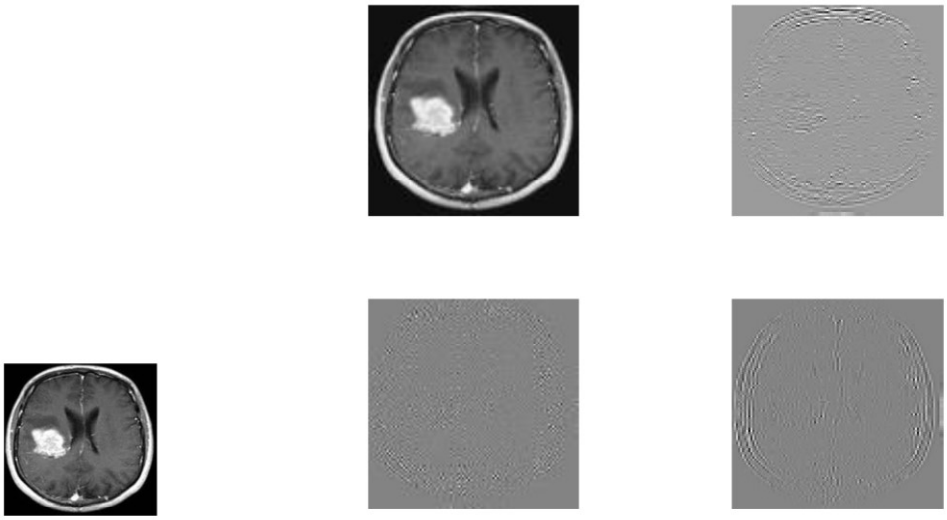

Figure 2. 2: 1 level decomposition of a MR slice using DWT

The principal components are determined using PCA from two source images for each coefficient separately. When two images are used, we obtain two principal components. The first component determines the directional vector along which the variation in data is maximum. Using these two principal component vectors say $v_1^A \; and \; v_2^A$ for a given approximation coefficient, we obtain two normalized components for a given approximation coefficient as:

$$m_1(A^{1,2}) = \frac{v_{11}^A}{v_{11}^A + v_{21}^A} \tag{2.1}$$

$$m_2(A^{1,2}) = \frac{v_{21}^A}{v_{11}^A + v_{21}^A}$$

(2.2)

where say $v_1^A \; and \; v_2^A$ are first and second principal component vectors corresponding to first and second dominant eigenvalues of the covariance matrix $A^{1,2}$of approximation coefficient matrix of two MR sequence.

Similarly, we obtain two normalized components for a horizontal detailed coefficient as:

$$m_1(H^{1,2}) = \frac{v_{11}^H}{v_{11}^H + v_{21}^H}$$

(2.3)

$$m_2(H^{1,2}) = \frac{v_{21}^H}{v_{11}^H + v_{21}^H}$$

(2.4)

Similarly, we obtain two normalized components for a vertical detailed coefficient as:

$$m_1(V^{1,2}) = \frac{v_{11}^V}{v_{11}^V + v_{21}^V}$$

(2.5)

$$m_2(V^{1,2}) = \frac{v_{21}^V}{v_{11}^V + v_{21}^V}$$

(2.6)

Similarly, we obtain two normalized components for a given diagonal detailed coefficient as:

$$m_1(D^{1,2}) = \frac{v_{11}^D}{v_{11}^D + v_{21}^D} \tag{2.7}$$

$$m_2(D^{1,2}) = \frac{v_{21}^D}{v_{11}^D + v_{21}^D}$$

(2.8)

The two normalized principal components are computed using:

$$\mathrm{M}_1(\mathrm{avg}) = \frac{m_1(A^{1,2})+m_1(H^{1,2})+m_1(V^{1,2})+m_1(D^{1,2})}{4} \tag{2.9}$$

$$\mathrm{M}_2(\mathrm{avg}) = \frac{m_2(A^{1,2})+m_2(H^{1,2})+m_2(V^{1,2})+m_2(D^{1,2})}{4} \tag{2.10}$$

Finally, the fused image is obtained by:

$$\mathrm{Fused\_image} = \mathrm{M}_1(\mathrm{avg})I_1 + \mathrm{M}_2(\mathrm{avg})I_2 \tag{2.11}$$

where I_1 and I_2 are two different MR sequence of size $M \times N$, $M_1(avg)$ and $M_2(avg)$ are the first and second normalized principal components of wavelet coefficients of MR image sequences respectively.

2.2.2 Otsu Thresholding

Otsu's method [25] is a well-known method to perform automatic image thresholding. This method returns the optimum value of the global threshold to segregate object from the background in the image. It is computationally simple and inexpensive. It does not need any prior knowledge. This threshold is determined by maximizing between-class intensity variance.

For a K segments, the between-class variance is determined as:

$$\sigma_B^2 = \sum_{j=1}^{K} P_j(\mu_j - \mu_G)^2 \tag{2.12}$$

where $P_j = \sum_{i \in S_j} p_i$

$$\mu_j = \frac{1}{P_j}\sum_{i \in S_j} ip_i \; represents \; the \; mean \; value \; of \; segment \; j$$

$$\mu_G = \sum_{i=1}^{K} P_i \, \mu_i \; represents \; the \; global \; mean \; value \; of \; image$$

The optimum K-1 threshold values $(t_1, t_2, t_3, \ldots, t_{K-1})$ to segment the image in to K partitions are obtained as:

$$\sigma_B^2(t_1, t_2, t_3, \ldots, t_{K-1}) = \max \sigma_B^2 \tag{2.13}$$

2.2.3 FCM Segmentation

In this work, fuzzy c-means clustering [26] is used to perform tumor segmentation. The FCM aims to minimize the objective function which is given by:

$$J = \sum_{j=1}^{c} \sum_{i=1}^{N} \mu_{ij}^{m} \left\| x_i - c_j \right\|^2 \tag{2.14}$$

where c is the total number of clusters, c_j is the centroid of the j^{th} cluster, μ_{ij} is the membership value of the sample x_i in the j^{th} cluster and $\mu_{ij} \in [0,1]$, m is the fuzziness factor and $m \in (1, \infty)$ tells that there is a strict partitioning between all clusters and for a data point. The total sum of membership values for each sample among c clusters is equal to 1 and is given as:

$$\sum_{j=1}^{c} \mu_{ij} = 1 \qquad \forall \quad i = \{1, 2, 3, \ldots, N\} \tag{2.15}$$

The membership and centroids are obtained by solving Lagrange problem corresponding to the objective function under the given constraints. After solving the Lagrange problem, the membership μ_{ij} and the cluster centroid c_j are obtained as:

$$u_{ij} = \frac{1}{\sum_{k=1}^{c} \frac{\left\|x_i - c_j\right\|^{\frac{2}{m-1}}}{\left\|x_i - c_k\right\|}} \tag{2.16}$$

$$c_j = \frac{\sum_i^N \mu_{ij}^m x_i}{\sum_i^N \mu_{ij}^m} \quad \forall\ j = \{1,2,3,\ldots,c\} \tag{2.17}$$

The membership μ_{ij} and the cluster centroid c_j are computed using an iterative optimization of the objective function. This iteration will stop when $\left\{\left\|\mu_{ij^{k+1}} - u_{ij}^k\right\|\right\} < \varepsilon$, where ε is a very small value.

2.3 Performance Evaluation

The performance of proposed work is evaluated by comparing the extracted tumor region with the existing Ground Truth (GT) in the database in terms of dice score. The performance is computed in terms of Dice score [27, 28, 29], a similarity measure, which is computed as:

$$Dice\ (\mathrm{G_i}, \mathrm{S_i}) = 2(\mathrm{G_i} \cap \mathrm{S_i})/|\mathrm{G_i}| \cup |\mathrm{S_i}| \tag{2.18}$$

where G_i is ground truth image, S_i represents segmented image. $|\mathrm{G_i}|\ and\ |\mathrm{S_i}|$ represent the number of pixels in ground truth image and segmented image respectively. Higher value of the dice scores of the given method is considered to be better.

2.4 Results and Discussions

The experimental results of the proposed work are reported and analysed in this section. The proposed work here is performed on 216 × 160 sized brain images. Initially, the experiments are performed with the proposed method without fusion i.e., on a single modality. Few examples of slices of BRATS[1] 2013 dataset for modalities: Flair, T1C, T1 and T2 are shown along with ground truth in Figure 2.3. After the fusion of two slices of two different modalities using the DWT-PCA approach is depicted in Figure 2.4. It can be observed that the image is enhanced and now the different types of tissues and tumor are better visible and

[1] http://www.braintumorsegmentation.org

distinguishable. The output of three stage proposed work on some slices are shown in Figure 2.5 and the brain tumor extracted that is extracted are also shown in Figure 2.5. From Figure 2.5, it can be seen that for extraction of the tumor region the performance of the proposed work without fusion performs good on Flair and T2 modality among all the single modalities experiments that are performed. The performance of proposed work is further improved when two slices from Flair and T2 are fused and the other two stages of the proposed method are applied.

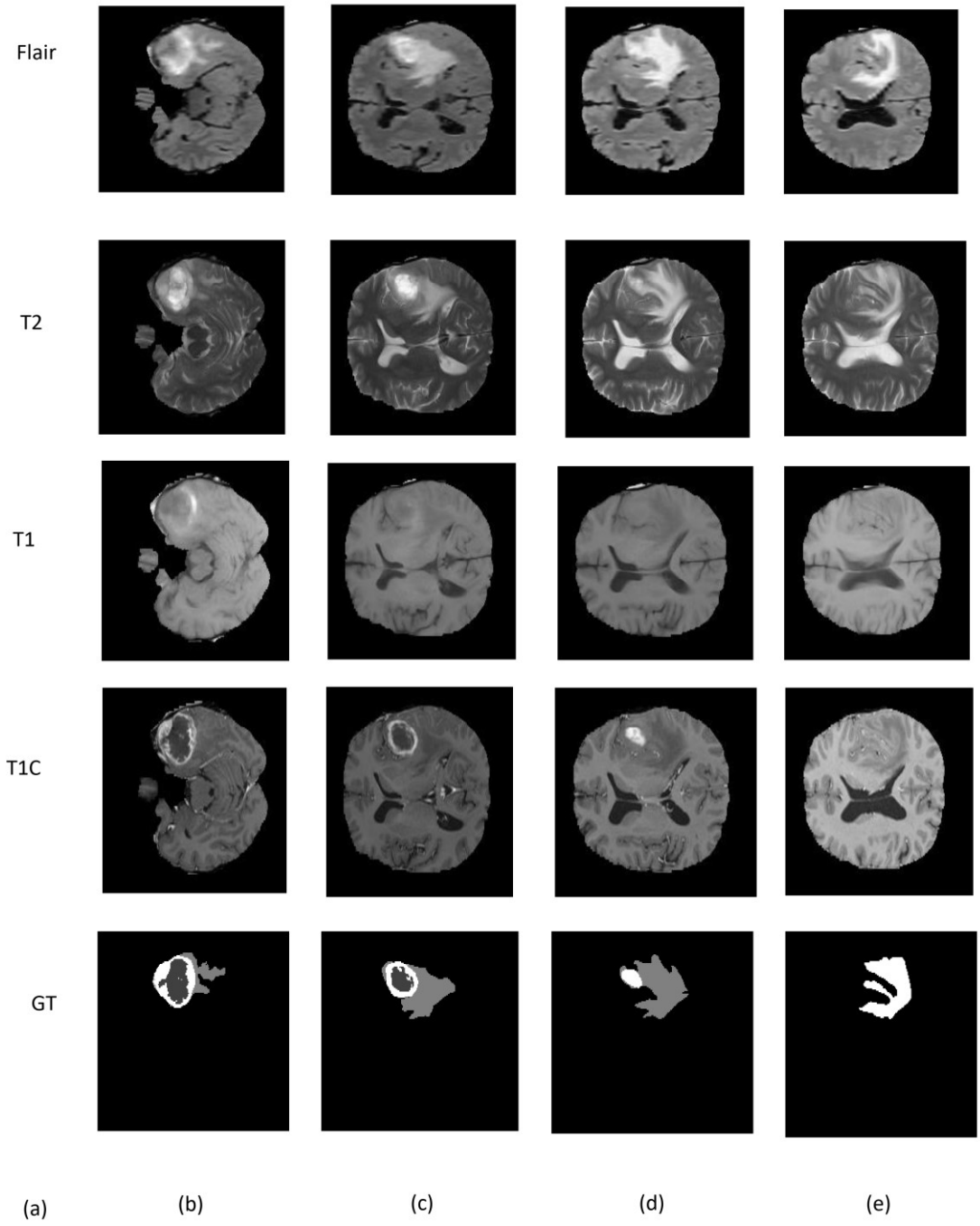

Figure 2. 3: Slices of brain MR image taken from the BRATS 2013 dataset. a. modality, b. slice70, c. slice95, d. slice102, e. slice109

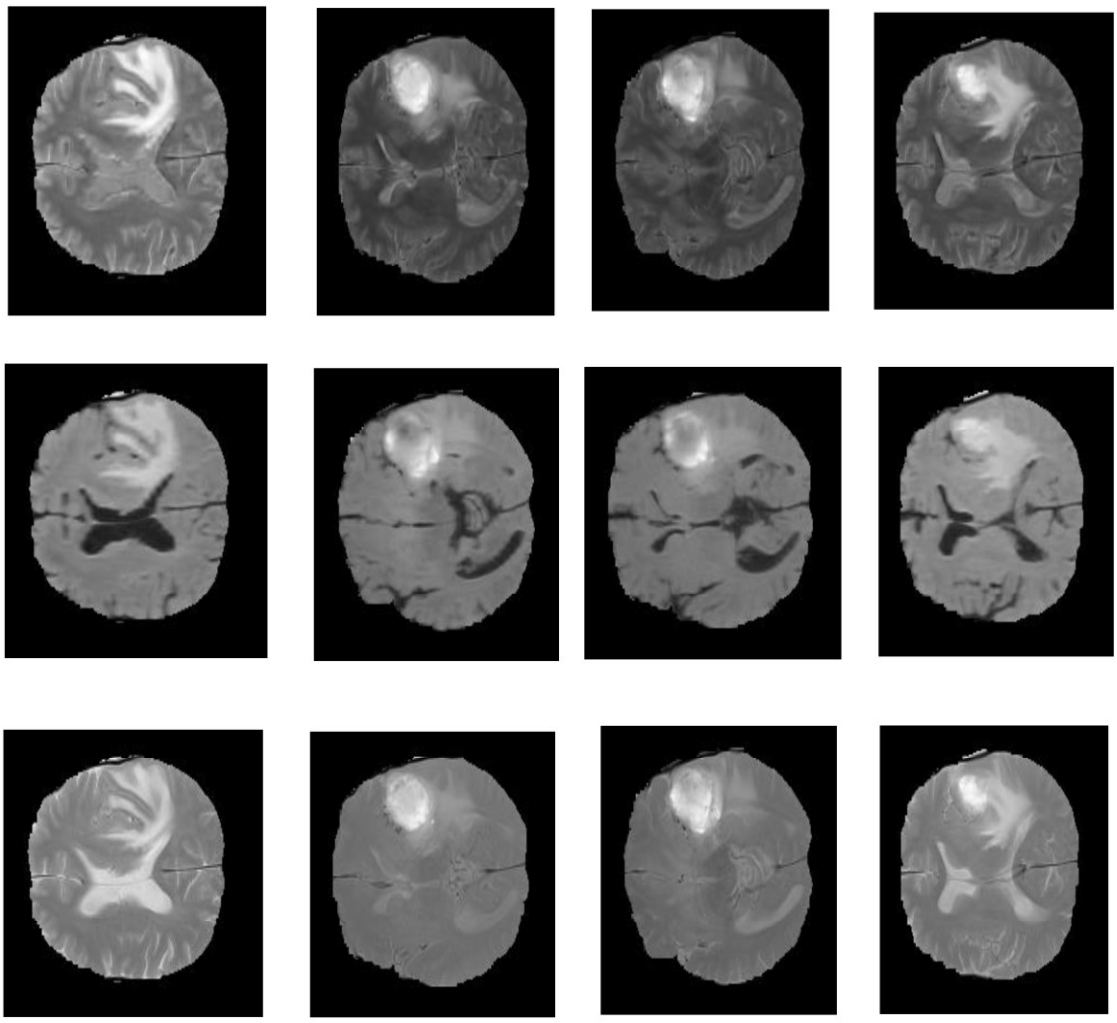

Figure 2. 4 : Fused image of slices taken from BRATS 2013 dataset. a. Images obtained after fusion of two Image modalities, b. slice70, c. slice95, d. slice102, e. slice109

Flair+ T1

T1+ T2

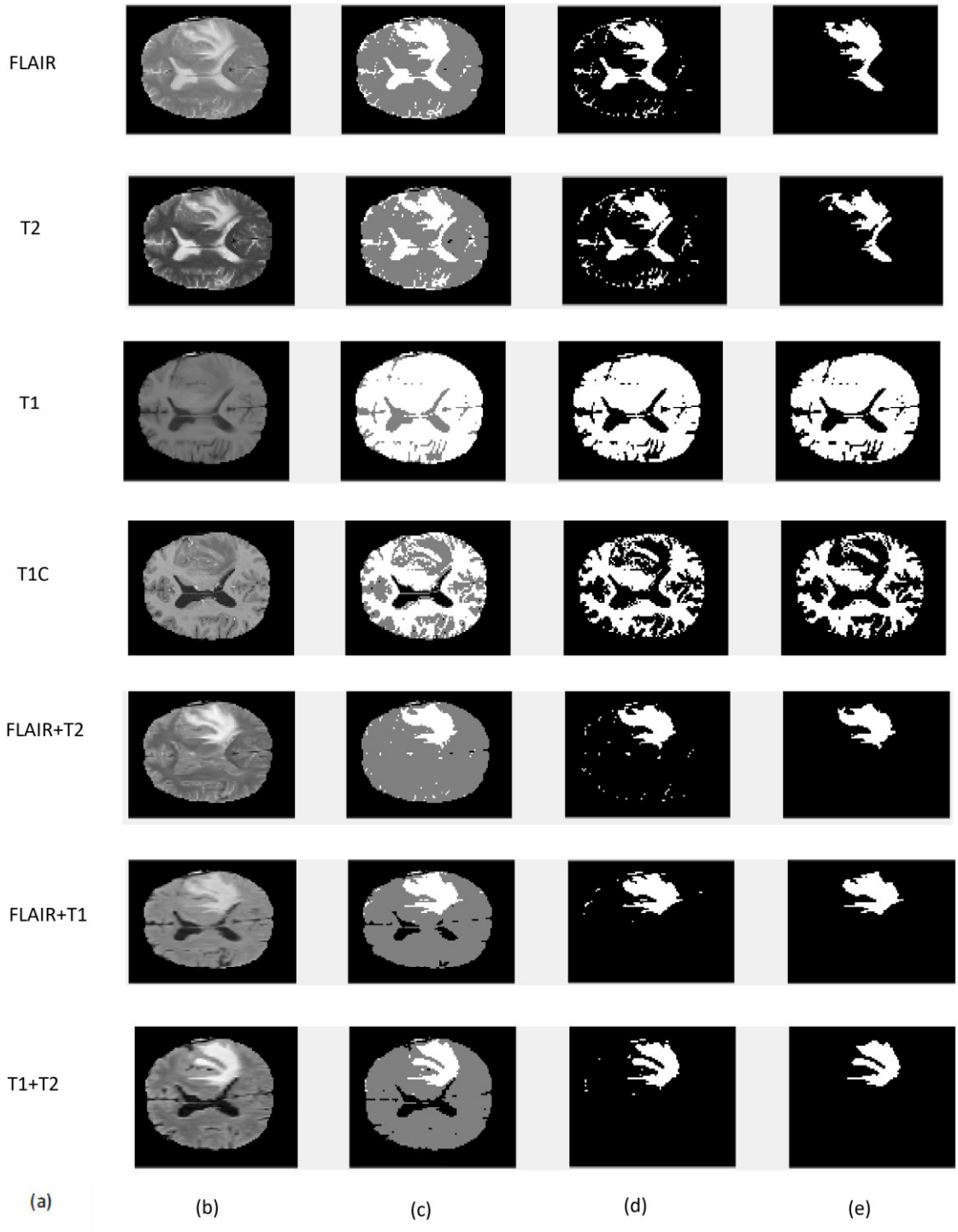

Figure 2. 5 : Results acquired from the proposed work. a. Image modality, b. Source image, c. Thresholded image obtained using Otsu thresholding, d. Segmented image obtained using FCM, e. Extracted brain tumor

Table 2. 1 : Dice similarity score obtained for 20 HGG patients and 10 LGG patients with the BRATS 2013 dataset.

Dataset	Flair	T2	T1	T1C	Flair+T2	Flair+T1	T1+T2
HG1	0.860131	0.748546	0.268871	0.207124	0.843409	0.530999	0.7022
HG2	0.851546	0.43663	0.208714	0.066554	0.787183	0.234297	0.5635
HG3	0.918581	0.790972	0.240384	0.220179	0.895948	0.341	0.7126
HG4	0.890645	0.879969	0.085594	0.029913	0.89397	0.3734	0.4143
HG5	0.414536	0.262476	0.159914	0.162014	0.674818	0.20668	0.3401
HG6	0.883312	0.857701	0.129064	0.136561	0.911794	0.3412	0.3777
HG7	0.581084	.424388	0.242620	0.266492	0.688195	0.2619	0.3653
HG8	0.887686	0.807085	0.142554	0.258983	0.882589	0.4215	0.451
HG9	0.849434	0.766087	0.032597	0.012651	0.859283	0.5442	0.4492
HG10	0.072817	0.03189	0.114010	0.107994	0.554182	0.21054	0.1021
HG11	0.944181	0.908577	0.150123	0.242989	0.946269	0.5253	0.5225
HG12	0.392153	0.281774	0.072575	0.012292	0.536725	0.383	0.1014
HG13	0.239907	0.208791	0.101089	0.11095	0.456983	0.2531	0.2916
HG14	0.831891	0.73678	0.067725	0.215161	0.861291	0.302	0.3417
HG15	0.857794	0.879133	0.133031	0.291619	0.914835	0.5789	0.7482
HG16	0.61812	0.767518	0.047812	0.145397	0.858409	0.4136	0.5515
HG17	0.623761	0.763523	0.348528	0.09614	0.780056	0.5698	0.6923
HG18	0.492393	0.475575	0.224889	0.002859	0.594877	0.3087	0.0107
HG19	0.361764	0.596013	0.356326	0.055356	0.611007	0.4135	0.5658
HG20	0.841004	0.722783	0.060485	0.305838	0.8543	0.7057	0.6365
LG1	0.602445	0.710651	0.368871	0.177511	0.327156	0.2493	0.4011
LG2	0.933491	0.834475	0.268714	0.175169	0.940222	0.5193	0.508
LG3	0.405647	0.611576	0.240384	0.190102	0.708109	0.1947	0.2663
LG4	0.536817	0.8103	0.285594	0.188744	0.857049	0.2974	0.3549
LG5	0.844579	0.681801	0.259914	0.210063	0.237216	0.1695	0.1286
LG6	0.670551	0.911721	0.329064	0.215479	0.937366	0.0511	0.5545
LG7	0.768628	0.572864	0.24262	0.235594	0.819651	0.2581	0.2939
LG8	0.602345	0.552946	0.342554	0.233134	0.637557	0.4343	0.4305
LG9	0.70886	0.534621	0.232597	0.207307	0.479526	0.2948	0.1023

LG10	0.30312	0.691217	0.18401	0.131707	0.7789	0.274278	0.3442

The performance of proposed work is evaluated by comparing the extracted tumor region with the existing GT in the database in terms of dice score. Table 2.1 presents the dice scores obtained for 20 HGG patients and 10 LGG patients with the considered BRATS 2013 image dataset. Table 2.2 includes average dice scores for HGG and LGG for single modality MR volume and fused volume. The best results for HGG and LGG are shown in bold.

Table 2. 2 : Average dice score obtained with the BRATS 2013 dataset

MODALITY	**FLAIR**	**T2**	**T1**	**T1C**	**FLAIR+T2**	**FLAIR+T1**	**T1+T2**
HGG	0.68	0.62	0.31	0.15	**0.78**	0.40	0.45
LGG	0.64	**0.70**	0.25	0.20	0.68	0.27	0.34

From the results that are obtained, it can be seen that the Flair modality provides better dice similarity score for HGG patients as compared to T2, T1C, T1 images and T2 performs better for LGG patients. But the performance of the proposed method using fused Flair + T2 is superior in comparison to other modalities for HGG patients. The performance of the proposed method using fused Flair + T2 is superior to other modalities except T2.

Table 2.3 presents comparison between the proposed work and existing methods. The best results for HGG and LGG are shown in bold. It can be noted from Table 2.3 that the performance of the proposed method is same or better than existing methods for HGG except the method proposed by Kalaiselvi et al. [21]. The performance of the proposed method is better than existing methods for LGG.

Table 2. 3: Comparison of the proposed work with the existing work

	Average Dice Score	
Authors	**HGG**	**LGG**
Bauer et al [8]	0.74	0.49
Buendia et al [9]	0.71	0.19
Cordier et al [7]	0.71	0.60
Geremia et al. [10]	0.65	0.55
Hamamci et al. [11]	0.78	0.55
Meir et al. [12]	0.77	0.46
Doyle et al. [13]	0.78	0.63
Fiesta et al. [14]	0.77	0.24
Reza et al. [17]	0.77	0.52
Kalaiselvi et al. [21]	0.79	0.75
Tustison et al. [22]	0.78	0.68
Proposed	**0.78**	**0.68**

Chapter 3

3 Conclusion and Future Directions

There are many approaches suggested in literature for segmentation of brain tumors. The performance of brain tumor segmentation method improves when information is considered from multiple sequences of magnetic resonance imaging, which needs to be fused appropriately. Motivated by the research work of Rajnikanth et. al., in this thesis, a novel method for automatic brain tumor segmentation which comprises of 3 stages is proposed. The first stage utilises a combination of Discrete Wavelet Transform and Principal Component Analysis for image fusion, in which fusion of images of different modalities is done. In the second stage, Otsu thresholding which is comparably simpler and computationally less intensive than SGO thresholding method is utilized in the current work. Third stage consist of a well- known segmentation technique called Fuzzy-C means segmentation, which overcome limitations of the watershed segmentation. For performance evaluation of the proposed work, an average similarity score i.e. Dice score is used. Experimental analysis is done on the BRATS 2013 dataset. Dice score is calculated separately for HGG and LGG dataset and compared its performance with existing methods. Experimental results reveal that the Flair modality provides better dice similarity score for HGG patients as compared to T2, T1C, T1 images and T2 performs better for LGG patients. But the performance of the proposed method using fused Flair + T2 is superior in comparison to other modalities for HGG patients. The performance of the proposed method using fused Flair + T2 is superior to other modalities except T2. Further comparison with existing methods reveals that the performance of the proposed method is same or better than existing methods for HGG and better than existing methods for LGG. The better performance is achieved because of appropriate fusion of two different MR modalities slices, which brings complimentary information. Also, the thresholding with Otsu method allows FCM to provide better segmentation performance.

In future, we would like to develop other way to fuse MR slices of two or more modalities to further improve performance of brain tumor segmentation. We would validate robustness of the proposed method on MR sequences in presence of noise, in-homogeneity. There is need to investigate the effect of higher-level image decomposition using DWT on the performance of brain tumor segmentation.

References

[1] https://mrimaster.com/PLAN%20BRAIN%20IMAGE%20t1%20tra%20post%20gd.html.

[2] A. Dasgupta, T. Gupta, and R. Jalali, “Indian data on central nervous tumors: A summary of published work,” *South Asian journal of cancer*, vol. 5, no. 3, pp. 147, 2016.

[3] T. Logeswari and M. Karnan, “An improved implementation of brain tumor detection using segmentation based on soft computing,” *Journal of Cancer Research and Experimental Oncology*, vol. 2, no. 1, pp. 006–014, 2010.

[4] Abd-Ellah, Mahmoud Khaled, et al. "Classification of brain tumor MRIs using a kernel support vector machine." *International Conference on Well-Being in the Information Society*. Springer, Cham, 2016.

[5] Armstrong, Terri S., et al. "Imaging techniques in neuro-oncology." *Seminars in oncology nursing*. Vol. 20. No. 4. WB Saunders, 2004.

[6] Saman, S., Jamjala Narayanan, S. Survey on brain tumor segmentation and feature extraction of MR images. *Int J Multimed Info Retr* **8,** 79–99 (2019)

[7] Cordier, Nicolas, et al. "Patch-based segmentation of brain tissues." 2013.

[8] Bauer, Stefan, et al. "Segmentation of brain tumor images based on integrated hierarchical classification and regularization." *MICCAI BraTS Workshop. Nice: Miccai Society*. 2012.

[9] Buendia, Patricia, et al. "A grouping artificial immune network for segmentation of tumor images." *Multimodal Brain Tumor Segmentation* 1 (2013).

[10] Geremia, Ezequiel, Bjoern H. Menze, and Nicholas Ayache. "Spatial decision forests for glioma segmentation in multi-channel MR images." *MICCAI Challenge on Multimodal Brain Tumor Segmentation* 34 (2012).

[11] Hamamci, Andac, and Gozde Unal. "Multimodal brain tumor segmentation using the tumor-cut method on the BraTS dataset." *Proc. MICCAI-BRATS* (2012): 19-23.

[12] Meier, Raphael, et al. "Appearance-and context-sensitive features for brain tumor segmentation." *Proceedings of MICCAI BRATS Challenge* (2014): 020-026.

[13] Doyle, S., et al. "Fully automatic brain tumor segmentation from multiple MR sequences using hidden Markov fields and variational EM." *Procs. NCI-MICCAI BraTS* (2013): 18-22.

[14] Pereira, Sérgio, et al. "Automatic brain tissue segmentation of multi-sequence MR images using random decision forests." *Proceedings of the MICCAI grand challenge on MR brain image segmentation (MRBrainS'13)* (2013).

[15] N. J. Tustison et al., "N4ITK: Improved n3 bias correction," IEEE Trans. Med. Imag., vol. 29, no. 6, pp. 1310–1320, Jun. 2010.

[16] L. G. Nyúl, J. K. Udupa, and X. Zhang, "New variants of a method of MRI scale standardization," *IEEE Trans. Med. Imag.*, vol. 19, no. 2, pp. 143–150, Feb. 2000.

[17] Reza, S., and K. M. Iftekharuddin. "Multi-class abnormal brain tissue segmentation using texture." *Multimodal Brain Tumor Segmentation* 38 (2013).

[18] S. Ahmed, K. M. Iftekharuddin, and A. Vossough, "Efficacy of texture, shape, and intensity feature fusion for posterior-fossa tumor segmentation in MRI," IEEE Trans. Inf. Technol. Biomed., vol. 15, no. 2, pp. 206–213, Feb. 2011.

[19] A. Islam, S. M. S. Reza, and K. M. Iftekharuddin, "Multi-fractal texture estimation for detection and segmentation of brain tumors," IEEE Trans. Biomed. Eng., vol. 60, no. 11, pp. 3204–3215, Nov. 2013.

[20] T. Leung and J. Malik, "Representing and recognizing the visual appearance of materials using three-dimensional textons," Int. J. Comput. Vis., vol. 43, no. 1, pp. 29–44, 2001.

[21] Thiruvenkadam, Kalaiselvi, and Kalaichelvi Nagarajan. "Fully automatic brain tumor extraction and tissue segmentation from multimodal MRI brain images." *International Journal of Imaging Systems and Technology*.

[22] Tustison, Nicholas J., et al. "Optimal symmetric multimodal templates and concatenated random forests for supervised brain tumor segmentation (simplified) with ANTsR." *Neuroinformatics* 13.2 (2015): 209-225.

[23] Rajinikanth, V., et al. "DWT-PCA image fusion technique to improve segmentation accuracy in brain tumor analysis." *Microelectronics, electromagnetics and telecommunications*. Springer, Singapore, 2018. 453-462.

[24] Vijayarajan, R. and Muttan, S: Discrete wavelet transform based principal component averaging fusion for medical images, AEU—International Journal of Electronics and Communications, Vol. 69, No. 6, pp. 896–902 (2015).

[25] Otsu, Nobuyuki. "A threshold selection method from gray-level histograms." *IEEE transactions on systems, man, and cybernetics* 9.1 (1979): 62-66.

[26] M. Balafar, "Fuzzy C-mean based brain MRI segmentation algorithms," *Artificial intelligence review*, vol. 41, no. 3, pp. 441–449, 2014.

[27]. Menze, B., Reyes, M., Leemput, K.V. et al.: The multimodal brain tumor image segmentation benchmark (BRATS). IEEE Transactions on Medical Imaging, Vol. 34, No. 10, pp. 1993–2024 (2015).

[28]. Chaddad, A. and Tanougast, C: Quantitative evaluation of robust skull stripping and tumor detection applied to axial MR images, Brain Informatics, Vol. 3, No. 1, pp. 53–61 (2016). https://doi.org/10.1007/s40708-016-0033-7.

[29]. Rajinikanth, V., Satapathy, S.C., Fernandes, S.L. and Nachiappan, S: Entropy based Segmentation of Tumor from Brain MR Images—A study with Teaching Learning Based Optimization, Pattern Recognition Letters, Vol. 94, pp. 87–94 (2016). https://doi.org/10.1016/ j.patrec.2017.05.028