BRAIN TUMOR VOLUME ESTIMATION OF 3D MAGNETIC RESONANCE IMAGING

Abstract

The greatest treatment for patients is provided by radiologists with the aid of an e-health care system. Patients' chances of survival will rise if early therapy is provided at the appropriate time. Brain tumors are the abnormal development of malignant cells in the brain. There are two types of brain tumors: benign tumors and malignant tumors. The World Health Organization (WHO) recommended grading system is utilized to classify the tumor. Grade I and II tumors are low or benign tumors. Grade III and IV tumors are classified as high or malignant. Many image processing techniques are employed for tumor identification, including picture enhancement, segmentation, edge detection, classification, etc. In this chapter, brain tumors are segmented and the volume of the tumor is estimated for Magnetic Resonance Imaging (MRI) images.

Keywords: tumor; magnetic resonance imaging; features

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I. INTRODUCTION

Brain Tumor is an unwanted growth of cells in the brain.. Moreover, the location of the tumour within the brain has a profound effect on the patient's symptoms, surgical therapeutic options, and the likelihood of obtaining a definitive diagnosis. The location of the tumour in the brain also alters the risk of neurological toxicities that alter the patient's quality of life. At present, brain tumours are detected by imaging only after the onset of neurological symptoms. No early detection strategies are in use, even in individuals known to be at risk for specific types of brain tumours by virtue of their genetic makeup.

Current histopathological classification systems, which are based on the tumours presumed cell of origin, have been in place for nearly a century and were updated by the World Health Organization in 1999. Although it has many researches, still it needs accurate prediction of tumour behaviour in the individual patient. They do guide therapeutic decision-making as precisely as patients and physicians would hope and need. Current imaging techniques provide meticulous anatomical delineation and are the principal tools for establishing that neurological symptoms are the consequence of a brain tumour.

Brain tumor detection is the main procedure for early tumor diagnosis and radiotherapy scheduling. Image segmentation plays a significant role in image processing as it helps in the extraction of suspicious regions from the medical images. Though several brain tumor segmentation methods have been available, proficient tumor segmentation methods are still challenging because brain tumor MRI images exhibit complex characteristics. In addition to tumor heterogeneity, tumor edges can be complex and visually vague. To address this problem, a novel automatic tumor segmentation method is proposed for MRI images.

Brain tumor analysis is done by doctors, but its grading gives different conclusions which may vary according to the expertise of the doctor. The purpose of this research is to model a diagnostic system to assist the radiologists in detecting the brain tumor and to help doctors who are in the initial stages of their career.Medical image segmentation helps in differentiating and visualizing the organs and tissues, for measuring and comparing the size of tissue, provides an idea to plan for surgery and other recovery treatments.

Medical image segmentation is different from usual segmentation method. Medical image segmentation satisfies the needs of clinicians. Segmentation partitions the pixels of an image into significant groups. Normally segmentation is performed based on intensity, texture, color, shape, size, pixel continuity and also based on the model of the object. FCM clustering had been used to create a segmentation method [1]. The performance of this system is assessed based on processing speed, convergence rate, and cluster validity function. Using this suggested Intuitionistic FCM approach, some of the segmented results are misclassified.

Fuzzy neuro-logic segmentation, which enhances segmentation and recognizes distinct brain tissues present for a given MRI data set [2], was created for the segmentation of brain tumors. A novel method has been put forth those experiments with multi-objective spatial FCM on noisy pictures. Automatic cluster detection is performed [3].

Fuzzy clustering is a high-dimensional fuzzy character-based clustering network approach that has been introduced [4]. A unique method that employs neural networks to successfully segment and segregate healthy brain tissues from the tumor area has been developed [5]. Based on the sensitivity, accuracy, and specificity of the KNN classifier, Bayesian classifier, and neural network, the performance of the suggested technique is assessed. The accuracy of the neural network classifier was 83%. Utilizing DWT, another method has been suggested [6]. This method is used to group brain tumors together in a single voxel of the MR slices. The accuracy of this approach is 94.2%.

For the selection of pertinent traits, Kullback-Leibler Divergence (KLD) was developed [7]. MRI images can also be processed using a technique called posterior-fossa tumor clustering. Then, KLD classification is carried out utilizing features that maximize expectation. SVM classifier was used to propose an integrated classification strategy [8]. Dynamic and contrast-enhanced MRIs are effectively classified using SVM classifiers based on texture analysis. The identification of the brain tumor using MRI images has been automated [9].

In this system, segmentation is first carried out using the histogram approach, followed by feature extraction and, ultimately, SVM classifier for classification. This method was created to address concerns with picture noise, bias, and volume effect, as well as image complexity. The local dissimilarity volume served as the foundation for a unique 3D local dissimilarity technique that was described [10]. This method allows for the comparison of two pictures as well as the provision of image localization data. This system's performance is contrasted with that of radiologists' medical methods.

II. PROPOSED METHODOLOGY FOR TUMOR VOLUME CALCULATION

This section talks about the suggested methodology's architecture. Figure 1 depicts the suggested framework architecture. This tumor detection method goes through five stages: pre-processing, feature extraction, segmentation, classification, and volume estimation. The BRATS dataset is used to test the proposed system. It consists of T1, T1c, T2 and Flair sequence. Each image is pre-processed before processing. To extract the features, skew and correlation are employed.

The spatial relationships between the pixels are measured using correlation, whereas skew measures the absence of symmetry between the pixels. After that, the tumor zone is segmented using segmentation. This method uses Self Organizing Map (SOM) for segmentation. The tumor is categorized by the random forest classifier into the proper group (tumor or non-tumor). This chapter uses binary classification for this step. For tumor images, using the volume of ellipsoid formula, which is covered in the subsection, the volume of the tumor area is then approximated.

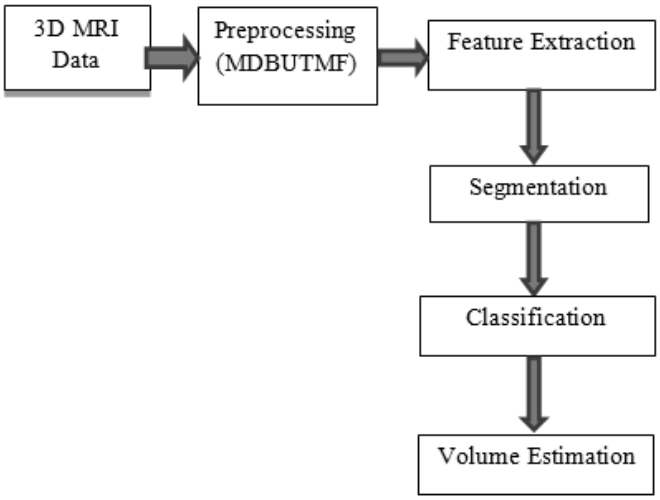
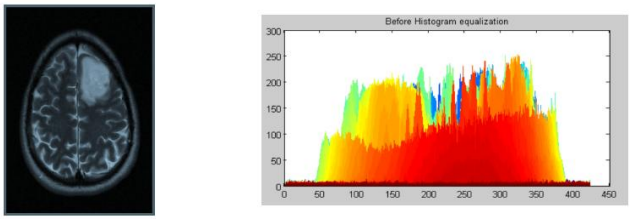


Figure 1: Architecture of the Proposed System

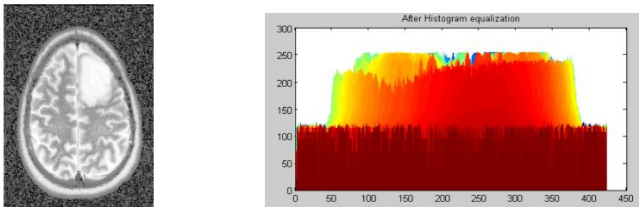
1. **Preprocessing** Preprocessing is used to improve the image by removing noise, distorted, and blurry elements for improved visual quality. The classification and segmentation results benefit from it. The range of the intensity values in brain images is normalized by separating the intensity values to the highest value. The anisotropic diffusion filter is used to enhance the image to noise percentage.

After pre-processing, Modified Decision Based Unsymmetric Trimmed Median Filter (MDBUTMF) is employed on an enhanced MRI for de-noising. This MDBUTMF filter processes the corrupted images by identifying the noise in the image. If the pixel runs between the maximum and minimum values of the gray level, then that pixel remains unchanged. Other pixels are processed by MDBUTMF. The preprocessing method is employed to correct image intensity. In Figures 2 and 3, the histograms of the original and the preprocessed picture are also displayed.



(a) **(b)**

Figure 2: a) Original Image b) Histogram of Original Image



(a) **(b)**

Figure 3: a) Enhanced Image b) Histogram of Enhanced Image

2. **Feature extraction:** The supplied data's dimensions are 240 × 240 x 155. The greatest tumor will be seen on each slice of the selected MRI sequence. For feature extraction, correlation and skew features are used. Skew is a measurement of an absence of symmetry. Tumor size decreases with a larger skew value and increases with a lower skew value. Let f be the image of size r x c, in order to calculate skewness, use the formula

$$\text{Skew} = \frac{1}{\text{rxc}} \frac{\sum f(a,b) - Mean}{SD^2} \qquad (1)$$

To gauge the spatial relationships between the pixels, correlation is employed. In order to calculate correlation, use the formula

$$\text{Correlation} = \frac{1}{\text{rxc}} \sum_{a=0}^{r-1} \sum_{b=0}^{c-1} \frac{(a,b) f(a,b) - Mean}{SD} \qquad (2)$$

Where,

Mean is the average intensity of the image and

SD is the Sum of Difference value.

Value 1 shows the maximum correlation for the correlation trait, whereas value 0 indicates no connection. When the correlation value is higher, the tumor is thought to be malignant, and when it is lower, the tumor is seen to be non-cancerous. The feature values for some of the input images are shown in Table 1 below.

Table 1: Skew and Correlation Feature Values

Input	Skew	Correlation
Image 1	0.0056	0.9912
Image 2	0.0067	0.9865
Image 3	0.0032	0.9943
Image 4	0.0033	0.9734
Image 5	0.0042	0.8976
Image 6	0.0048	0.9433
Image 7	0.0064	0.9233
Image 8	0.0051	0.9356
Image 9	0.0065	0.9568
Image 10	0.0059	0.9786
Image 11	0.0065	0.8954

3. **SOM based segmentation:** In this method, segmentation is accomplished using SOM. Depending on these properties, the SOM is trained to route the picture to the appropriate tissue location. Maps have helped to lessen the size and grouping of comparable regions that are helpful in understanding huge Figure information. Two layers make up SOM. Input nodes make up the first layer. The output nodes in a two-dimensional network make up the following layer. Each unit has a multidimensional test associated with it. Through a small number of clusters, the map attempts to accurately and precisely represent features. At the conclusion of the training procedure, the clusters are transformed into a well-organized grid, allowing for the separation of related groups and undesirable groupings.

   During training, SOM groups the output unit data for the current input feature array. The unit that is closest to the input becomes the Best Matching Unit (BMU), and the weight vectors of this BMU and its nearby units are rearranged. During training in SOM, the weight vector is modified using the Linear Vector Quantization (LVQ) method, which makes use of the tagged data.

   The use of LVQ is justified since it evenly names codebook arrays to group the components of the input array, yet duplicate distributions of samples occur at the group borders. With a small beginning rate of knowledge to boost identification accuracy, it is advised that this step be taken to start studying through the LVQ1 method, which swiftly converts it, and continuing through the LVQ3 procedure. As a result, this method uses LVQ3 after LVQ1 for an execution time of 1000 with 0.5. In the LVQ3 algorithm, this approach uses the window width parameter of 0.2 and the relevant study parameter of 0.3.

4. **Volume estimation:** The amount of space a tumour takes up is measured by its volume. Image volumes are essentially 3D arrays. The majority of tumours have hemispheric and ellipsoid forms, thus it won't be realistic. Therefore, volume of ellipsoid is calculated as

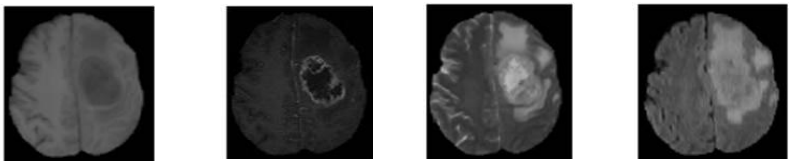
$$Volume = \frac{4n}{3}(a \times b \times c)cm^3 \quad (3)$$

   Which is more accurate.

III. EXPERIMENTAL ANALYSIS

The BRAin Tumor Segmentation (BRATS) 2015 dataset is used to evaluate the suggested methodology [11]. Training and Testing datasets are its two subsets. The training dataset is one of these subsets and is open to everybody. You may get it from the website (BRATS 2015 site). 220 Higher Grade Glioma (HGG) cases total, of which 146 are training cases and 74 are test cases, make up the training dataset. Images from the training dataset include ground truth values. The annotated five labels are as follows: 0 for everything else, 1 for necrosis, 2 for edema, 3 for non-enhancing tumour, 4 for enhancing tumour.

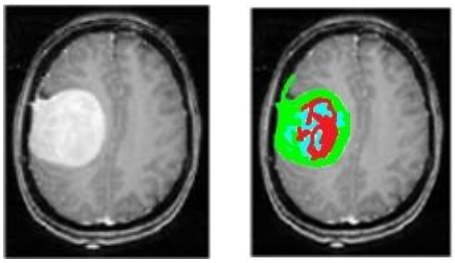
The evaluation is done for the enhancing tumour (only the enhancing tumour region is regarded positive, everything else is deemed negative), the core (necrosis, enhancing tumour, and non-enhancing tumour taken as a class that is positive), and the whole tumour (all tumour structures lumped together as the positive class). Hence we have only two classes: tumor and non-tumor. Figure 4 displays the first four MRI sequence input slices for a specific patient.



(a) (b) (c) (d)

Figure 4: Input images (a) T1 (b) T1c (c) T2 (d) Flair Weighted Image

Figure 5 shows the segmentation results for sample brain image where tumor occurs in border portion.



(a) (b)

Figure 5: (a) Input Brain Image with Tumor in Border (b) Segmented Image

The automated volume estimating approach is quicker than the manual one. For patients with both low-grade and high-grade brain tumors, this suggested system offers an alternate option to the manual approach for assessing tumor sizes. The results of testing all the patient data are provided in Table 2 for 11 patients. Table 2 shows how the tumor volume changes based on the sagittal, axial, and coronal planes.

Table 2: Results of Tumor Volume Depending on Axial, Coronal and Sagittal Plane

Input	**Axial($cm^{3)}$**	**Coronal($cm^{3)}$**	**Sagittal($cm^{3)}$**
Image 1	58.56	56.23	55.34
Image 2	49.13	47.24	46.35
Image 3	42.56	41.34	40.56
Image 4	50.32	49.12	48.89
Image 5	53.86	51.65	50.54
Image 6	48.56	47.43	45.34
Image 7	55.45	54.55	52.66
Image 8	57.55	55.45	54.65
Image 9	54.76	53.67	52.32
Image 10	59.57	58.56	57.12
Image 11	56.43	54.44	53.23

Frontal plane is another name for the coronal plane. Horizontal cuts are produced in the coronal plane, as if slicing an item. The right and left sides of the brain are separated by the sagittal plane. Right angles are sliced in the brain to create an axial plane segment.

The majority of the tumor segments have ellipsoid shapes. The smooth form without any lobulations was described as the ellipsoid shape, which closely resembles the oval or circle shape. Disease free survival and overall survival rates are calculated to evaluate the performance of the proposed method. Results depending on tumor configuration are shown in Table 3.

Table 3: Results based on Tumor Configuration

S.No	Tumor Configuration	Proposed Method Based on Ellipsoid Category
1	No. of. Patients (%)	100
2	Overall Volume of Tumor (%)	30.23
3	Disease Free Survival (%)	75.54
4	Overall Survival (%)	85.6

By adding together all the tumor regions in each slice of the T1, T2, T1C, and Flair images, a 3D volume is often computed. But our suggested solution does not require this. Therefore, the suggested approach determines the tumor's volume more quickly than the manual method and the current method. Based on the data for each patient's tumor volume, disease-free survival was calculated.

IV. CONCLUSION

The chapter attempts to give a helpful contributing strategy for tumor diagnosis and volume estimation. Processing the additional pixels in the multi sequence 3D MRI data takes longer. The suggested technique, however, merges the several MRI sequences of a single patient into a single MRI data in order to produce quicker computing with less. The CSLBP, Mean, Skew, and Correlation features are extracted from each level of the MRI data and provided to the SVM classifier via the suggested approach. So that the classification and segmentation results for the tumor region produced by the suggested technique are more accurate. It is difficult to estimate the amount of the tumor area from a large volume of 3D MRI data. According to the suggested technique, the projected disease-free survival rate is 75.54%. The volume estimation of low and high grade gliomas serves as the foundation for disease-free survival. Comparing the suggested approach to the current method and the manual method, the volume produced is reduced by 10% to 11%.

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