

Segmentation of Brain Tumor using Slic with Tumor Volume Identification

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Abstract— Intracranial tumor or brain tumor is an unusual mass of tissue where brain cells multiply and increase wildly. They are potentially life threatening. Despite the fact that brain tumors can happen at any age, it is most common in children aged 3 to 12 and grownups 40 to 70 years of age. Brain tumor segmentation is as yet a difficult field due to the complex features of the brain MR images. In this paper, we propose a computerized method for detection of brain tumor and further calculating the depth of the tumor detected. The proposed system uses Simple Linear Iterative Clustering (SLIC) for segmentation, Discrete Wavelet Transform (DWT) and Principle Component Analysis(PCA) for feature reduction, Gray Level Co-occurrence Matrices(GLCM) for feature extraction and classification using Random Forest. Further the depth is calculated using 3D Geometrical Metrics.

Keywords— Brain Tumor, Random Forest, SLIC, Volume Analysis

I. INTRODUCTION

A brain tumor happens when anomalous cells structure inside the brain. Benign tumors (non-cancerous) and malignant tumors (cancerous) are two main types of tumors. Cancerous tumors are classified as Metastatic and Primary tumors. Primary brain tumors originate from the brain tissues itself or the brain's surrounding tissues. Metastatic brain tumors emerge somewhere else in the body, and relocate to the brain. meningiomas and astrocytomas such as glioblastomas are the most common types of primary tumors in adults. Some examples of Benign tumors includes chordomas, Craniopharyngiomas, Gangliocytomas, Pituitary adenomas. Examples of Malignant brain tumors include Astrocytomas, Glioblastoma multiforme (GBM), Medulloblastomas, Oligodendrogliomas. The occurrence of brain tumors has expanded over the time and varies as per sexual orientation, age, race etc. Because of the tumor's diffuse development, the resection is a tough task.

Medical image segmentation for discovery of brain tumor from the Magnetic Resonance images or from other medical imaging modalities is a significant procedure for choosing right treatment at the opportune time on the grounds that the prior the location, the quicker the treatment can be begun. In this quick staged world, an automated framework for brain tumor identification and classification can save time. With respect to the instance of brain tumor, segmenting a tumor out of brain isn't a simple process. Subsequent to segmenting a tumor out of the brain we can discover various parameters identified with tumor. In order to calculate the volume of the tumor needs to

be represented in 3D. Various works done for volume analysis of brain tumor is discussed in the next section. Manual tracing of tumor boundaries is a traditional technique which is more time-consuming [1].

This study aims for a computerized system for segmentation and detection of brain tumors. Further calculating the depth of the tumor. The research paper is organized as follows: Section 2 describes the related works literature survey, Section 3 describes the proposed technique, Section 4 presents the results and discussion and finally Section 5 describes the conclusion and future scope.

II. RELATED WORKS

A concise portrayal of the work done by various researchers are given underneath:

Ayesha Amir Siddiqi et al[2] proposed a technique for the 3D representation of brain tumor using 3D slicer which is a software for 3D visualization. In this work, brain tumor from 2D images is segmented and then it is converted to 3D for model analysis and calculation of volume. Label Mapping segmentation is used for segmenting the tumor, which involves segmentation of both cystic and solid part of tumor. Surface Model Making technique is used for creating 3D surface models from labelled datas. The volume of the tumor can be calculated with the help of a Model Hierarchy Tree, which can be used for creating models and all the operations related to model hierarchies. The visualization properties of model hierarchies can be done using Model Hierarchy Display. This work claims 99.9 % efficiency in segmentation of tumor.

Abdulfattah A Aboaba et al[3] proposed an algorithm for finding the mensuration of irregular closed space ie irregular shapes, thus tumor volume. This is done using Iterative Spatial Sectoring algorithm. Flowchart of the methodology and the algorithm for the area determination of irregular shapes are presented in the paper. This technique combines the knowledge of basic geometry and integral calculus. The irregular shape can be divided into sectors of different radii, then the area of individual sectors are calculated. It is program code based so it will continue until there is no difference between successive iterations. This work claims that the proposed technique is superior to existing methods.

Fabian Balsiger [4] presented a technique for brain tumor volume calculation. This work is mainly focused on Glioblastoma brain tumor. Active Contour segmentation method is used to segment the tumors. Delaunay Triangulation is used for rendering volume from tumor contours. This work

used two data sets, both having seven pre-operative MR sequences. Amira software is used for tumor model visualization and volume calculation evaluation.

Hossam M Moftah et al[5] presented a method for brain tumor estimation. In this work, 2D brain images are clustered using K-means clustering algorithm. Feature extraction is done followed by 3D tumor volume identification and visualization. Finally the object area of each slice is calculated to compute the volume. Volume measurement algorithm is described in the paper. Patch Object function in MATLAB is used for visualizing 3D objects. The results show high accuracy in tumor volume estimation.

Hayder Saad Abdulbaqi[6] presented a novel approach for improved segmentation of brain tumor CT images by using Hidden Markov Random Field-Expectation Maximization(HMRF-EM) and Threshold method. The volume of brain tumor is calculated by voxel space and 2D image estimation. Guassian smoothing is used on image before applying HMRF-EM algorithm, as preprocessing part. K-means clustering and Canny edge detection are also used prior to applying EM algorithm. On the resultant, threshold method is applied for getting final segmentation. The pixel numbers in tumor region and the area volume value can be determined by voxel space. The proposed method is compared manual method Mango program. This work claims 94% accuracy in segmentation.

III. METHODOLOGY PROPOSED

The presented framework is intended for the exact recognition of brain tumor, by segmentation and classification of typical and atypical brain MRI's. Volume analysis of the detected tumor may be a challenging task, this work aims precise analysis of tumor volume. The first step is Slicing 3D image into 2D image, 2D Image preprocessing(Resizing, Enhancement) is done, Segmentation is done using Simple Linear Iterative Clustering(SLIC), Dimension reduction using Discrete Wavelet Transform(DWT) and Principle Component Analysis(PCA), Feature Extraction using Gray-Level Co-occurrence Matrix(GLCM), Classification using Random Forest, From 3D segmented image Depth measurement for tumor is calculated using 3D geometrical metrics.

A. Preprocessing steps

Tumor images got from the BRATS clinical dataset were 3D images. The first preprocessing step was the conversion of these 3D to 2D images. The 3D data is input, then resize the volume data. Extract the 2d slices from the 3d data with iterative slicing in each axis say xy on z axis, yz on x axis and so on. xy, yz and xz are the three planes these 2D slices are formed to. Extracting the volume content into matrix of image width and height. The number of slices depends on the depth. Reshape each slices. Substitute 1s to global thresholds and 0s to all other values to generate a binary image from 2D gray scale image. Save the extracted slices in different folders say xy yz & xz for different orientations. Read the 2d dataset iteratively with respect to each orientation say xy firstly. Resize the each 2d slices xy dataset. Apply morphological operation to the resized binary image. Fill holes in dilated image to clearly threshold the pixel region. Use Number of Non-Zero matrix elements (nnz) along with a relational operator to calculate number of matrix elements meeting the given condition.

Spatial fuzzy clustering is applied. Obtains a threshold centre from the cluster. Checks the threshold centre not empty. Then proceeds to segmentation.

B. Simple Linear Iterative Clustering

The idea of the superpixel, which is a little gathering of pixels having similar color, was presented in [7]. SLIC superpixel method [8] is used to generate superpixels. Its an adaptation superpixel generation of k-means clustering method. SLIC performs a nearby grouping of pixels in the 5-D space characterized by the L, A, B estimations of CIELAB color space and the xy pixel coordinates[9]. Its strategy is used to partition the images into patches with roughly comparable size. SLIC has a couple of variables which are adjustable to be tuned by managing the balance between them and boundary adherence. It is difficult to perform image segmentation productively on typical pixel-wise image representation since the quantity of pixels is excessively extensive even in a typical image[10]. The number of superpixels are controlled by the parameter k. The input image is divided into k grid like blocks, each having cluster center. Iterative distance limited clustering is done until result converges. And finally the resultant superpixels have regular size. The pixels are grouped based on their intensity and spatial distance metrics. The spatial distance between the ith pixel and the jth pixel is denoted by d_s and can be obtained by –

$$d_s = \sqrt{(x_j - x_i)^2 + (y_j - y_i)^2} \quad (1)$$

where the pixel location coordinates are x and y. The intensity distance d_c between the two pixels is given by:

$$d_c = \sqrt{(I_j - I_i)^2} \quad (2)$$

where I_i and I_j are the ith and the jth pixel's normalized intensity values.

The overall distance measure which is a combination of spatial and intensity distances can be obtained with:

$$D = \sqrt{d_c^2 + \left(\frac{d_s}{m}\right)^2} \quad (3)$$

where m accounts for the flexibility of boundaries of superpixel and is also a compactness coefficient. High m value produces compact segments and a lower value produce boundaries which are more flexible.

C. Dimension Reduction

Feature extraction from brain MRI can be done using DWT. Discrete Wavelet Transform (DWT) coefficients subset captures all the desired features of the MR images. Feature extraction is utilized for gathering tumor portion's feature variable in case of a tumorous image. Principal component analysis (PCA) [11] is used for reducing data dimensions. It recognizes standards in data to be distinguished and communicated by accentuating their similitudes and contrasts. PCA enables a huge number of variables to be overridden with less variables using a linear relation between the variables. This is of most extreme advantage in the automated framework where the variables might or might not be prepared to do any instinctive human interpretation. PCA formulation can also be used as a digital image compression algorithm

with a low level of loss. The helpful components utilized in our modernized framework are Mean, Standard Deviation, Entropy, Variance, Smoothness, Kurtosis and Skewness.

D. Feature Selection

Feature extraction can be done utilizing GLCM. Gray-Level Co-occurrence Matrix (GLCM) is mainly used in medical images to extract the textural features. Neighboring pixel's pixel intensity level is the main focus of GLCM [12]. This technique always accounts for the specific position of pixel relative to other pixel. For the direction of data given for 0° , 45° , 90° , 180° matrices of GLCM was constructed by using the d values as 1,2,3 and 4 [13]. Contrast, Correlation, Energy and Homogeneity are calculated.

E. Classification

Random Forest is used for the classification purpose. Its an ensemble algorithm which combines more than one algorithms of same or different kind for classifying objects. The Random Forest is a meta estimator that fits various choice tree classifiers on different sub-tests of the dataset and utilizations averaging to improve the accuracy and commands over-fitting. Fundamental parameters to Random Forest Classifier can be absolute number of trees to be produced and decision tree related parameters like minimum split, split criteria and so on. Features are trained and tested using Random Forest method. Here its used for the prediction of tumor from 2D features whether it matches with test data.

F. Depth Measurement

Depth measurement for tumor is done using 3D Geometrical Metrics. now for calculating depth of tumor we firstly find the iterative count each tumor slices, then with respect of number of 2d tumor slices projected to actual depth of volume image along z corresponds to depth of tumor in xy projection.

IV. RESULTS

The brain tumor identification from a MRI is a complex process hence automated systems are developed to detect the exact tumor position in a brain MRI. In this paper we develop a novel technique for the tumor segmentation and classification in brain MRI. The proposed approach for the brain MRI classification is implemented in the working platform of Matlab 2018a. The following result demonstrate and evaluate the performance of the proposed system, applied to brain MRI.

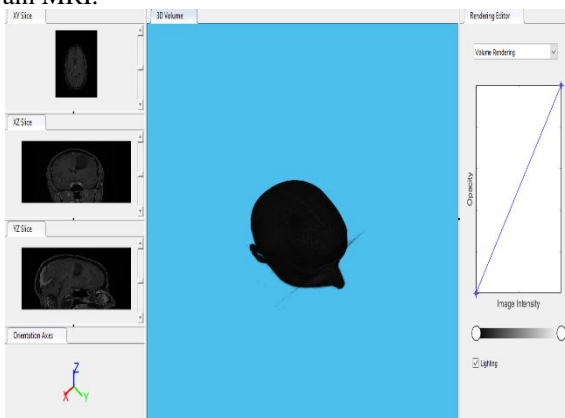


Fig 1: Volume viewer render editor

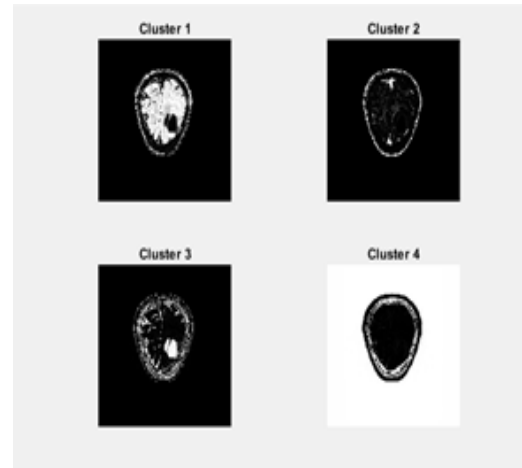


Fig 2: Clustering

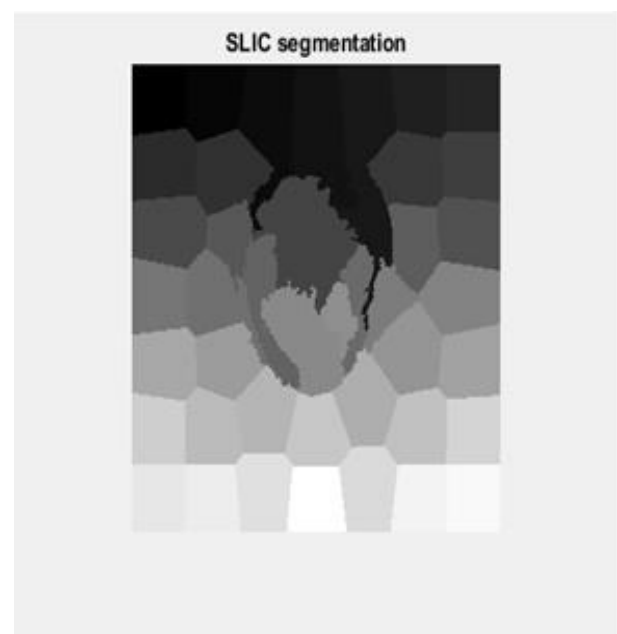


Fig 3: SLIC Segmentation

As shown in the fig 1, MRI slices in XY, YZ, and XZ planes are obtained, once a 3D MRI image is given as input.

As shown in Fig 2. Spatial fuzzy clustering is applied. Simple Iterative Linear Clustering is used to segment the tumor and it is shown in Fig 3. Color mapping is used to differentiate the regions, so as to segment the tumor portion of the brain more conveniently.

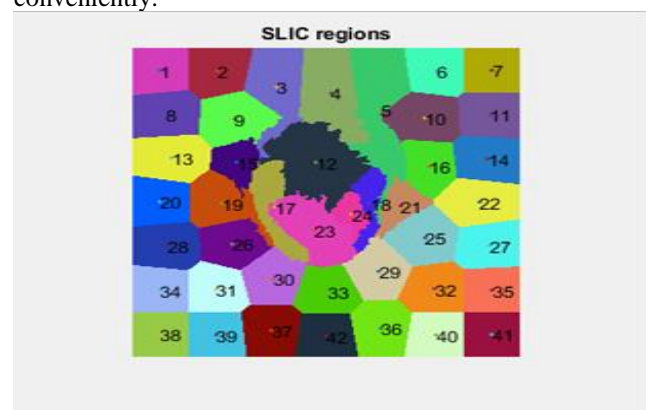


Fig 4: SLIC Regions

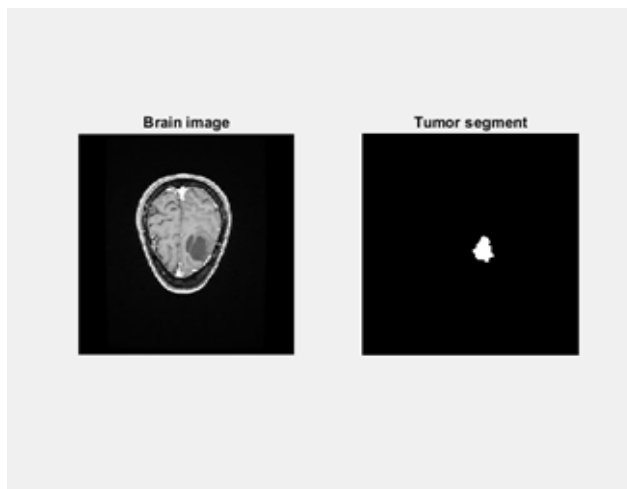


Fig 5: Tumor segment extracted

The 3D input image of brain MRI is converted to 2D slices in XY, YZ and XZ planes. Each of these slices undergo the process of segmentation, feature extraction and classification for the detection of tumor portion. Once the tumor is detected the volume of the tumor is analyzed. The depth of the tumor is calculated. As it is known 3D segmentation is not as easy as 2D images and it's a difficult and challenging task to work on a 3D image.

The input image is an mnc file. The 3D image is then sliced in XY, YZ and XZ planes. Each of these slices undergo the process of segmentation and the above mentioned processes to obtain the depth of the tumor.

Here we have given the results of images processed in XY plane. Starting with the volume viewer clustering followed by SLIC segmentation, SLIC region mapping, tumor extracted portion and tumor in 3D view. The values of GLCM features are obtained accurately and the tumor depth is also calculated finally. Here, the depth calculation of ten images are given in Table I.

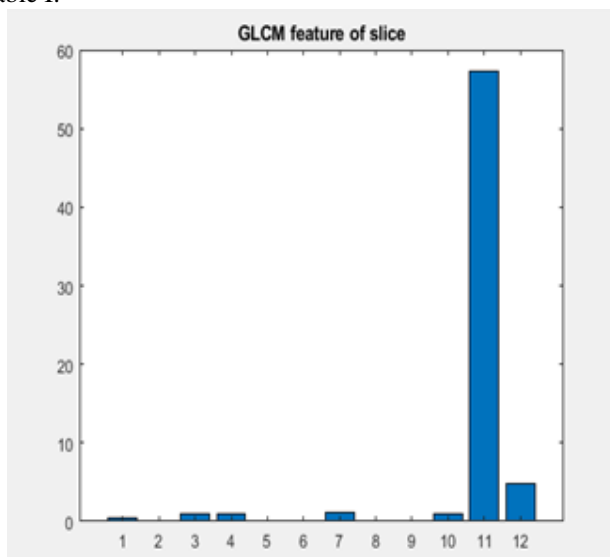


Fig 6: GLCM Features of the slice

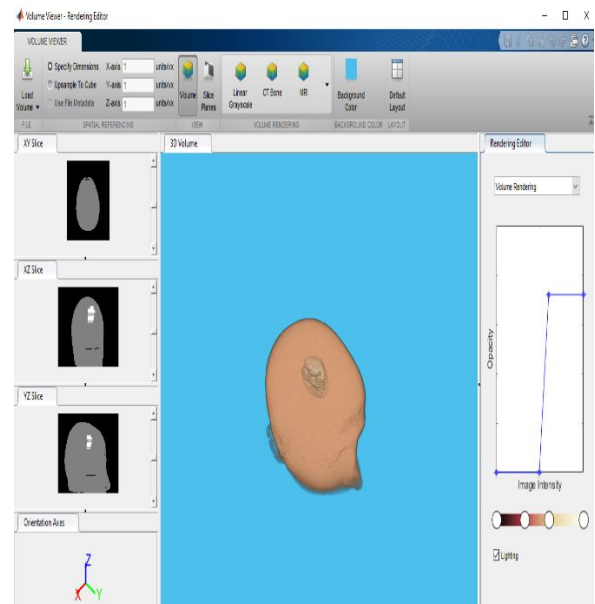


Fig 7: Detected tumor in volume viewer

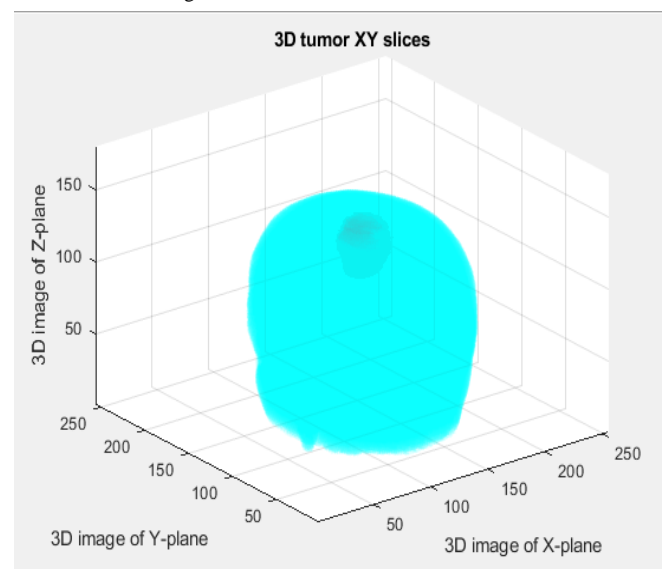


Fig 8: Detected tumor in 3D view

TABLE 1: Percentage Of Volume Obtained

Images	Depth of Tumor (%)
Image 1	14.44
Image 2	11.09
Image 3	18.43
Image 4	10.03
Image 5	23.99
Image 6	18.44
Image 7	30.1
Image 8	25.0
Image 9	20.1
Image 10	13.55

V. CONCLUSIONS

Brain tumor is most treatable and curable if caught at the initial stages of the infection. This finds extreme pressure on the cerebrum, causing an increased intracranial pressure and can cause lasting brain harm and in the long run demise. The proposed system made by segmenting the MRI with Simple Linear Iterative Clustering and classifying cancerous brain tumors automatically by the Random Forest classifier, which uses the statistical texture features extracted by GLCM. Depth analysis of the tumor is a major challenging part, which has been successfully calculated here. This computerized framework could be additionally utilized for the segmentation of pictures with distinctive obsessive condition, types and disease status.

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