The Detection and Visualization of Brain Tumors on T2-Weighted MRI Images Using Multiparameter Feature Blocks

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Abstract— **The main topic of this paper is to segment brain tumors, their components (edema and necrosis) and internal structures of the brain in 3D MR images. For tumor segmentation we propose a framework that is a combination of region-based and boundary-based paradigms. In this framework, segment the brain using a method adapted for pathological cases and extract some global information on the tumor by symmetry based histogram analysis .The objective of this paper is to present an analytical method to detect lesions or tumors in digitized medical images for 3D visualization. This research opens a new window in the field of image processing by 3D Volume Representation of tumor through the use of Magnetic Resonant Imaging and an integrated software tool called 3D Slicer. The authors developed a tumor detection method using three parameters; edge (*E*), gray (*G*), and contrast (*H*) values. The method proposed here studied the *EGH* parameters in a supervised block of input images. These feature blocks were compared with standardized parameters (derived from normal template block) to detect abnormal occurrences, e.g. image block which contain lesions or tumor cells. The proposed method shows more precision among the others. Processing time is less. This will help the physicians in analyzing the brain tumors accurately and efficiently.**

Keywords— **3D, Brain, Tumor, Segmentation, MRI, Image Registration, and Brain Structures**

I. INTRODUCTION

Tumor is one of the most common brain diseases, so its diagnosis and treatment have a vital importance for more than 400000 persons per year in the world (based on the World Health Organization (WHO) estimates). On the other hand, in recent years, developments in medical imaging techniques allow us to use them in several domains of medicine, for example, computer aided pathologies diagnosis, follow-up of these pathologies, surgical planning, surgical guidance, statistical and time series (longitudinal) analysis .The analysis and study of the brain is of great interest due to its potential for studying early growth patterns and morphologic changes in the cancer process. Recent studies have demonstrated the potential of a decision support system for detecting tumors in medical images, providing radiologists with a second pair of highly trained eyes.

It gives doctors access to additional information present in images that have characteristics generally accepted to be associated with cancer, clusters of bright spots that are suggestive of lesions, patterns suggestive of tissue masses or distortions, and mark regions that have the characteristics of lesions or tumors. Magnetic Resonance Imaging (MRI) techniques are still developing, and recent efforts have been directed primarily at improving image quality and speed of acquisition. MRI provides non-invasive, high quality images of neuro-anatomy and disease processes. Through its ability to detect contrast in the density of soft tissues, MRI is well suited to monitor and evaluate cerebral tumors as they develop and respond or, as the case may be, fail to respond to therapy. There are many sequences that can be used on MRI and the different sequences often provide different contrast between tissues so the most appropriate sequence should be chosen according to disease and what the clinicians want to detect. This paper focuses on analysing T2-weighted MRI images because medical specialists often can diagnose whether a brain tumour exists within a T2-weighted MRI images with sensitivity of 94%. In this paper the tumor type discussed is solid cum cystic brain tumour. For this study T2 and T1 (contrast enhanced) weighted MRI images are used. The primary objective of the research is to present the solid cum cystic tumor in the form that can be easily recognized by any person, 3D representation of the solid cum cystic tumour in which solid and cystic part could by visualized separately in three dimension using surface model making, automatic calculation of the volume of solid and cystic part separately using 3D Slicer.

II. OBJECTIVES

The first aim of this work is to develop a framework for a robust and accurate segmentation of a large class of brain tumors in MR images. Most existing methods are region-based. They have several advantages, but line and edge information in computer vision systems are also important. The proposed method tries to combine region and edge information, thus taking advantage of both approaches while cancelling their drawbacks.

3D contrast enhanced T1-weighted and FLAIR images are the inputs to perform an automatic segmentation of the solid part of tumor and the potential associated edema and necrosis. We first segment the brain to remove non-brain data. However, in pathological cases, standard segmentation methods fail, in particular when the tumor is located very close to the brain surface. Therefore we propose an improved segmentation method, relying on the approximate symmetry plane. Then we developed two new and original methods to detect and initially segment brain tumors. The first one is a fuzzy classification method which combines membership, typicality and neighborhood information. The second one relies on a symmetry-based histogram analysis. The approximate sagittal symmetry plane is first computed, and the tumor is then extracted by comparing the histograms of the two cerebral hemispheres. To refine the initial segmentation, which is not accurate enough, we use edge information. A deformable model constrained by spatial relations is applied for this purpose.

III. METHODOLOGY AND MATERIALS

A. Materials

The required dataset is collected from the DOW University of Health Sciences (Ojha Campus) from GE 1.5 Tesla MRI with the DICOM software. 3cases are studied. The provided data set is consisting of T2, T1 and contrast enhanced T1 images in all the three planes i.e. axial, sagittal and coronal. Each technique has 19 slices for each plane. Dimensions of T2 image is $512 \times 512 \times 15$ and that of contrast enhanced T1 image is $256 \times 256 \times 19$. The platform which is used for the analysis is 3D SLICER version3.6. The method is tested on Microsoft windows XP (Professional), version 2002 with 736MB of RAM.

B. Image enhancement

The methodology involves loading the volumes i.e. all the slices in the axial, sagittal and coronal views directly from the dicom file containing T2 images in the Slicer. Window level preset (WLP) is used to make the cyst and solid appear brighter in their respective T2 and contrast enhanced T1 images as shown in figure and contrast enhanced T1 images as shown in figure a. The figures belong to case1. Figure a: shows the solid appear brighter after WLP for **case1**
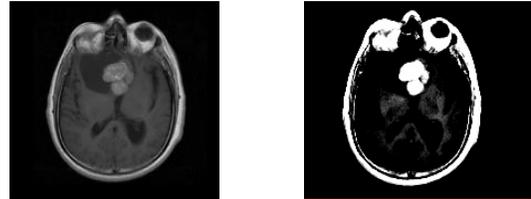

Figure a: shows the solid appear brighter after WLP for case1

C. Segmentation

Amongst various segmentation techniques in 3D slicer label mapping is the best and gives much clear and accurate result. The boundary of the region of interest is traced and the resulting area is labeled automatically. All the slices in which the tumor is visible are label mapped as shown in figure b. The cystic and solid part of tumor is differentiated by the green and red colors respectively.
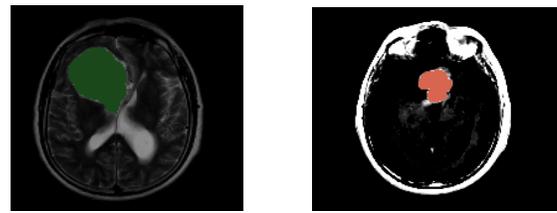

Figure b: shows labeled cyst and solid respectively

D. 3D REPRESENTATION

The Model maker is used to create 3D surface models from labeled image data as shown in figure b. The model maker is a pipeline of algorithms that start from the input label map, creates a binary label map with just the label(s) of interest set to 1, everything else to 0, generates a marching cubes model, runs triangle reduction and triangle smoothing algorithms. The pipeline was optimized for 1mm brain MRI data. Decimation reduces the number of triangles. No decimation is applied in this research as it may reduce the actual volume. However the default value of decimation for 3D slicer is 0.25.
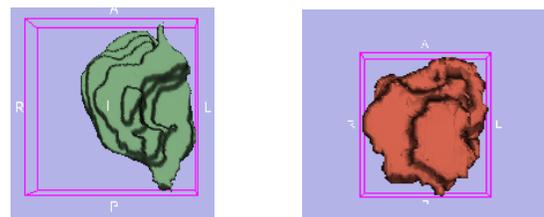

Figure c: This figure shows 3D model of cyst and solid

These models are then loaded in the models module for further processing. This module is used for loading, saving, changing the appearance of, and organizing 3d surface models. Model hierarchies allow you to group together models. When using the Model Maker module, multiple models created from one label map are grouped under a model hierarchy node and as a result we can have a combine view of solid cum cystic tumor.
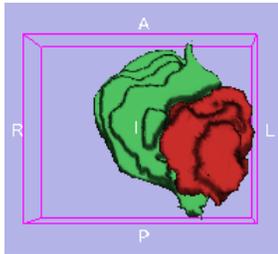

Figure d: 3D view of solid cum cystic tumor

E. Volume Acquisition

A model Hierarchy Tree is organized which allows creating hierarchy nodes, drag and drop models and hierarchies to be part of hierarchies, control color and visibility of models and hierarchies, search, delete, and rename model hierarchies. The model info tab keeps the record of the measurements taken while the model is being made. This will give us the volume which is the result of side by side voxel calculation when the marching cubes algorithm is running. Another feature of this model is the Model Hierarchy Display for a grouped hierarchy of models. Model Display allows adjusting the visualization properties of individual models or model hierarchies. By using this module the tumor obtained is applied to the default VTK of the brain model of the slicer. This indicates the location of the tumor in the brain as in figure e.
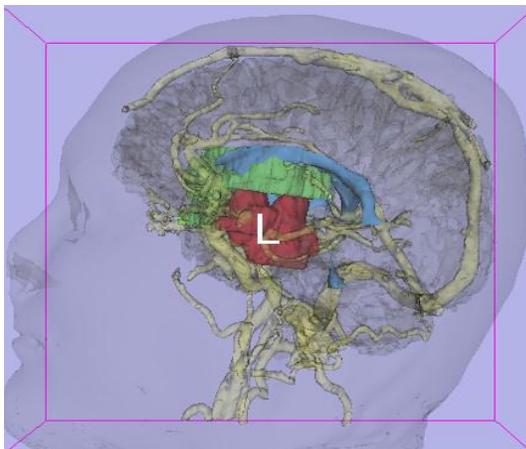

Figure e: shows the left view of brain bearing tumor

IV. RESULTS

The volume of the cyst obtained after segmentation is 69514mm^3and that of solid is 25286mm^3. Since the average volume of the brain is 1341300 mm^3 as per 3D slicer. So for the above case the cystic part is 5.2% of the brain and the solid part is 1.9% of the brain. The above methodology is applied to two other cases and their final results are given below.

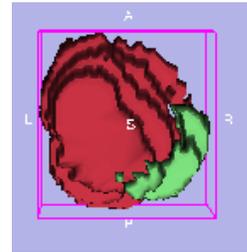Case 2: Volume of the cyst =2914.4mm^3 Volume of the solid=35161mm^3

Figure f: 3D Model for case 2

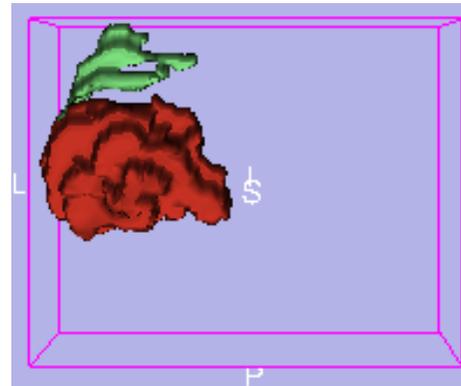Case 3: Volume of the cyst =1063.8 mm^3 Volume of the Solid=10615 mm^3

Figure g: 3D Model for case 3

V. ACCURACY CHECK

In order to make the accuracy check, the results of 3D slicer are matched with the original radiology report. The physicians do not calculate the volume. They only take the measurement between two points on the tumor. For this purpose they choose the slice in which the tumor size is largest. They repeat this procedure for axial, sagittal and coronal views respectively. The error and the relative error (RE) can be calculated between the maximum tumor size as per the radiology report (Lr) and the maximum tumor size according to the segmentation done by the 3D slicer (Ls).

$$Error = Ls - Lr \qquad (1)$$

RE (%) = (Ls-Lr/Lr) ×100   (2)

Accuracy=100-error   (3)

Table I. Accuracy check of the 3D Slicer by maximum length calculation of the readings taken from the radiology report and from the segmented tumor by the Slicer along with their RE% for Case 1. Similarly the above calculations are done for all cases and their average accuracy graph is shown below:

TUMOR TYPE	TUMOR PLANES	Lr	Ls	ERROR	RE%	ACCURACY
SOLID	AXIAL	4.8cm	4.75 cm	0.05	1.04	99.95
	SAGITAL	4.1cm	4.11 cm	0.01	0.244	99.99
	CORONAL	4.1cm	4.06 cm	0.04	0.975	99.96
CYST	AXIAL	6.2cm	6.2cm	0	0	100
	SAGITAL	5.8cm	5.78cm	0.02	0.416	99.98
	CORONAL	5.4cm	5.3cm	0.1	1.85	99.9

Similarly The Above Calculations Are Done For All Cases And Their Average Accuracy Graph Is Shown Below:
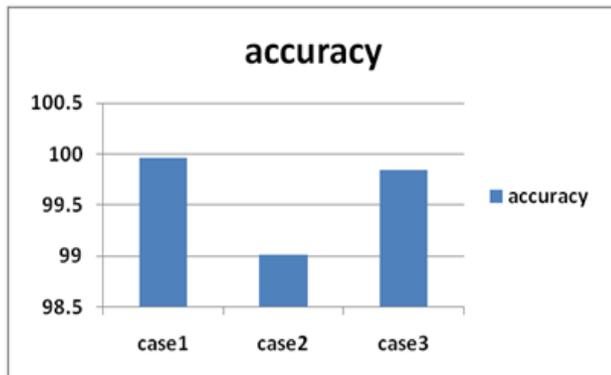
VI. EXPERIMENTAL RESULT

In order to implement this 3D brain tumors and internal brain structures segmentation in MR images efficiently, JAVA program is used. This program could speed up the development of this system because it has facilities to draw forms and to add library easily The proposed method was applied to 10 clinical MRI datasets of various origins and types.

We illustrate the results on four cases, for which manual segmentation of several structures was available, and which exhibit tumors with different shapes, locations, sizes, intensities and contrasts. Evaluation of the segmentation results was performed through quantitative comparisons with manual segmentations, using volume and surface measures. Segmentation results are quantitative evaluations are high accuracy. The voxel size is typically $1 \times 1 \times 1.3$ mm3, so that the average error is less than one voxel. The Hausdorff distance represents the error for the worst point, which explains its higher values. Although the segmented structures are relatively small (about 4000 m3), the volume metrics shows good results. For the similarity index measures, values above 70% are satisfactory. The results show that the segmentation of caudate nuclei is better than thalamus due to their well defined borders. The comparison of the results obtained using the initial segmentation of MPFCM and multiphase level sets illustrates that there is not a large difference between them. But the MPFCM method is faster than the multiphase level sets method.

VII. ACKNOWLEDGMENT

VIII. CONCLUSION

In this paper, we introduced a conceptually simple classification method using multiparameter features on supervised block to computationally classify brain images. Our conclusion is that the proposed method is effectively capable of identifying tumor areas in T2-weighted medical brain images taken under different clinical circumstances and technical conditions, which were able to show high deviations that clearly indicated abnormalities in areas with brain disease. The response time for processing system is 176 milliseconds for each image analysis. Currently we are working towards improving the brain model to include more cases. We expect that the PCB system will become a valuable tool for the study of MRI brain images.

All future efforts will focus on extending this capability to include other types of imaging modalities, e.g. PET/CT (Positron Emission Tomography/Computed Tomography) or PET, into the PCB system through a user-friendly and practical system that will be usable in medical clinics by specialists and medical practitioners. This method gives 99.9% efficiency in segmenting out tumor. After which the 3D volume representation of the tumor can be obtained within few seconds as mentioned above. This will save a lot of time of the surgeons and radiologist providing a much modern technique for brain tumor surgery. As the future work, the validity of procedure can be observed by applying to more cases of same type as well as on other types of tumor. In order to match the results of volume with the original data we need to have such cases in which the whole tumor is sent for biopsy. The 3D analysis and volume calculations can be done by any other software such as SPM and MATLAB. The results can be compared. This will allow error calculations to be done. By 3D modeling of different types of tumors we can see the similarities and differences between them regarding their shapes and structures which will be helpful for the physicians. This can be done with in depth study of different cases of tumor which in turn help the medical professionals in classifying the tumors types on the basis of their volume.

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