



A Review: Thresholding, Segmentation and Surface Area Identification

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Abstract-- We present a new method of segmenting the brain mass for volumetric analysis of brain and surface area calculation of grey and white matter in dynamic contrast magnetic resonance images. Our goal is to provide a useful tool to clinicians which help to identify abnormal gray and white matter concentration of brain and also calculate the respective surface area. We trained our system against the standard values of volume and gyrification index. The calculated values compared against the normal values. It is anticipated that in the future the system can be integrated into clinical workflow so that become routine available to help clinicians make objective interpretations of treatment. The system is inexpensive, user friendly and easy to deploy.

Keywords: segmentation, volumetric analysis, gyrification index, thresholding

I. INTRODUCTION

Imaging now plays a significant role in the assessment and regulation of therapies in oncology. One of the most important subject in the processing MR image is segmentation, especially extraction of the brain regions, which is part of the decision of urgent operation on brain. This type of medical operations need speed up process with maximum accuracy. Accurate brain tissue segmentation of MR (Magnetic Resonance) images has been one of the most important research areas for several years. It is important to have an accurate segmentation of different brain tissue types for various applications such as radiotherapy planning, image guided interventions, surgical planning by using Electroencephalography (EEG) or Functional Magnetic Resonance Imaging (fMRI) information and brain disease studies such as Alzheimer and Multiple sclerosis (MS). However, all the mentioned applications are crucially dependent on the level of accuracy of brain tissue segmentation. Thus, this is important to choose the best algorithm to reach the most accurate tissue segmentation. Majority of the systems just segment the brain and give the volumes but there is no approach to verify whether this volume is in normal or abnormal range. In this study, brain is segmented by using k-means algorithm. A combination of global, adaptive thresholding techniques and at the next stage morphological operations were used for preprocessing. The study was built to prevent wasting time, to provide very significant savings in material and the most important thing is that it would allow to determine the disease in adolescent terms. The data for the thesis is first form of the digitalized MRI images and the output are comparison results between the subjects who are healthy and have disease suspect.

In this work, we reported an interactive system developed for estimating the contrast enhancement in brain MRI for volumetric tumor segmentation and quantification. The system has an intuitive interface and easy to use for nontechnical clinicians. The functions of the system are implemented by following the actual work flows in the clinician's desktop. The rest of the paper is organized in the following way: in section 2 we present our work flow and segmentation methods and volumetric analysis is explained in section 3. In section 4 our results are presented.

II. IMPLEMENTATION

We briefly introduce the system design principles and then the main functions in the following two subsections.

Design principles:

To meet the objective of presenting a practically useful and affordable tool in clinical setting, we follow four principles:

- (1) Volumetric based measurements;
- (2) Develop an interactive system rather than fully automated system. We believe that at this stage it is unwise to exclude clinician's intelligence from a practical tumor segmentation system; hence, necessary input from clinical doctor's medical knowledge (e.g. region of interest (ROI) selection, editing/pruning, verification, etc.) becomes a reliable manner in reality;
- (3) We choose to make the system functionally specific in the volumetric brain segmentation evaluation other than integrating too many other-system-afforded functions in order to keep the system clean and to enable an easy navigation to the end-users;
- (4) We chose the combination of SPM⁸ and FreeSurfer [9] plus FSL [8] as the developing platforms. SPM and FSL are open source packages for medical imaging processing and visualization. FreeSurfer is used to implement the user

interface. We have made a stand-alone install package for the system and it is easy to deploy. The system is also possible to be open-source so that it can continue to be enhanced by more developers and users.

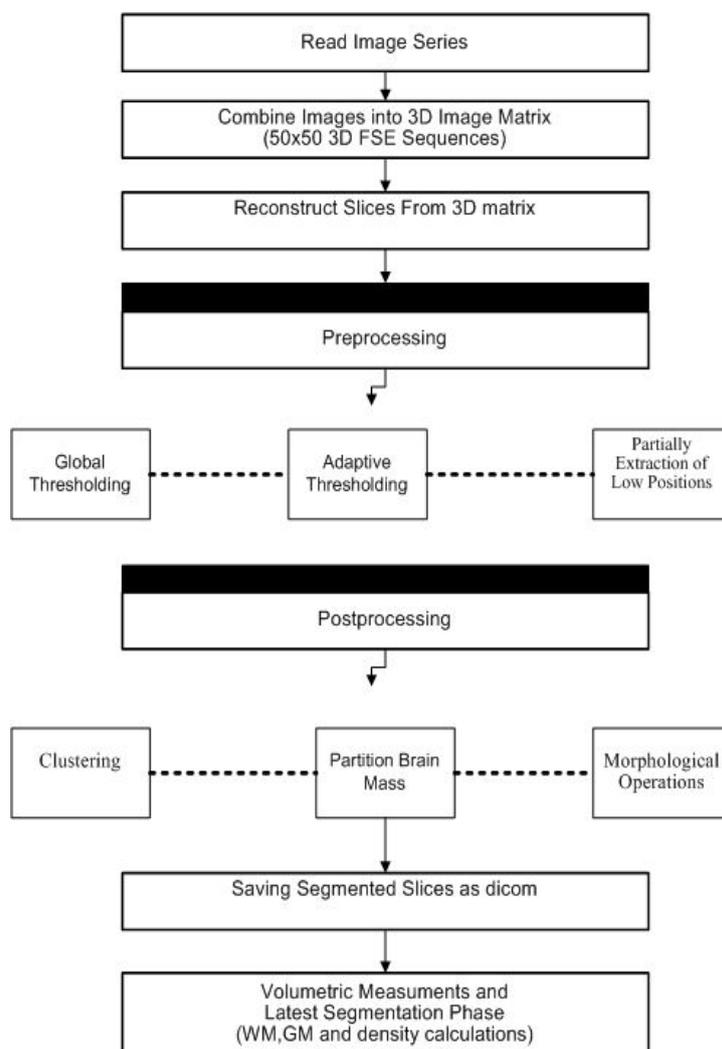


Fig. 1: Flowchart of the developed system.

2.2 Main functions:

Fig. 1 shows the overall flowchart of the developed system. The typical functional flow of the developed system follows in 9 steps.

1. Read DICOM Files

This process involves different steps. For dicom loading multiply file selection is enabled and the program try to produce a whole volume for image analysis. Investigations is supported in the case of dicom and the header informations in this structure are the specific pieces of metadata are used (e.g. pixel spacing,flip angle, the size, number of bytes, class of data, the size of the pixels).

2. Exploring the Data

The next step in the algorithm is to explore the 3D data. The purpose of this step is to consider the images which are relevant to the general interest of the subject. In this stage histograms are preferred and it was kept the right to choose to view an individual slice by entering the slice number. These 9 individual 2D images can be viewed in grayscale.

3. Segmentation

In this section of the program, the purpose is to segment out the area, or data of interest.

(i) For the first segmentation step, global and adaptive thresholding techniques were used depend on the general characteristic of the 3D image data background.

(ii) The next step in the segmentation portion of this program is some manual thresholding to remove unwanted portions of the image data; low levels like Cerebral Spinal Fluid.

(iii) K-means algorithm was used to segment brain mass to extract other tissues. K value was 3.

(iv) To supply if there are any small wisps of soft tissue in the image, erosion operation was used with structuring element with 7x7 neighbourhood .

- (v) Obtained brain mass is isolated. To grow back the brain mass which was reduced previously with the erosion, dilation operation was used again with structuring element with 7x7 neighbourhood .
- (vi) To catch the connected regions brain region was labelled. This operation also supplied to control the boundaries.
- (vii) Last segmentation step is choosing significant labeled resulting image slices from the 3D data set superimposed on original image was evaluated.

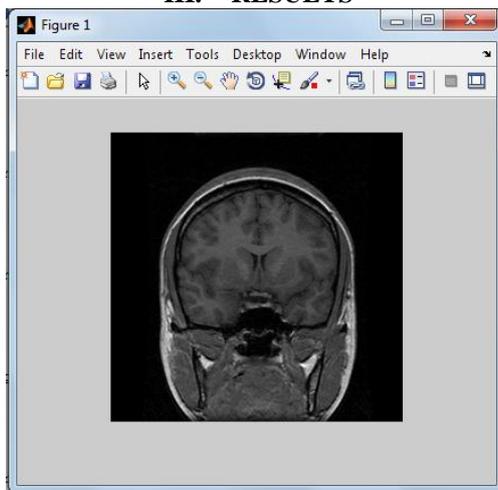
4. Volumetric Measurements After Segmentation

Obtained segmented slices are saved. In file saving only the most important header information is transferred which defines the volume. Segmentation slices saved as given standard parameters like pixel spacing and slice thickness. These slices combined again to 3D matrix and with k-means 3 portions for WM, GM and background were found. Parameter for k value was 3. Density calculations, proportioning volumetric measurements to brain volume, gray fraction and white fraction were obtained. Information about pixel size and slice thickness were used during these calculations.

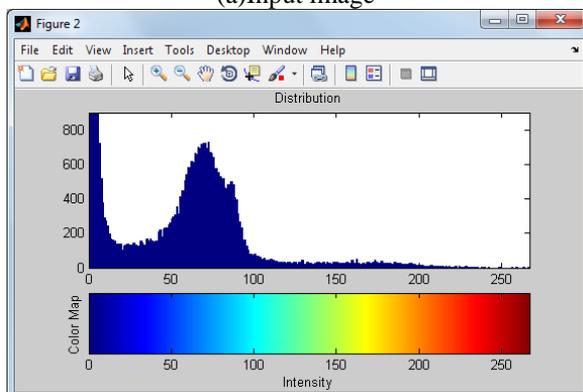
5. Comparison

Finally the calculated grey matter and white matter volume is compared to the standard normal values , the system compare the two values and find normality and abnormality of brain.

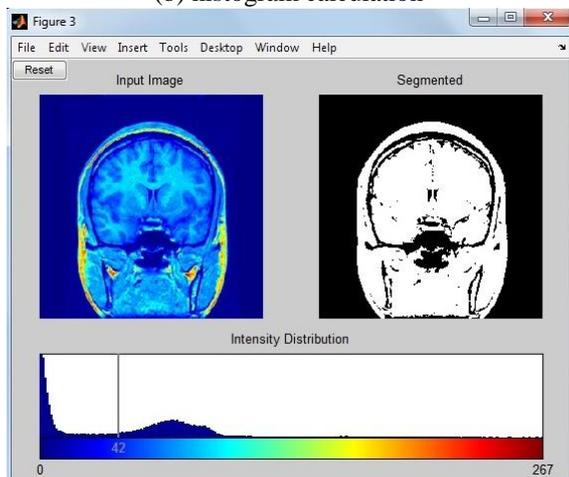
III. RESULTS



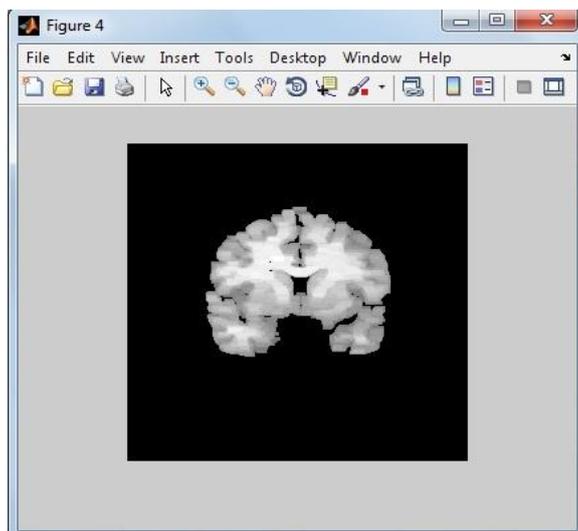
(a) Input image



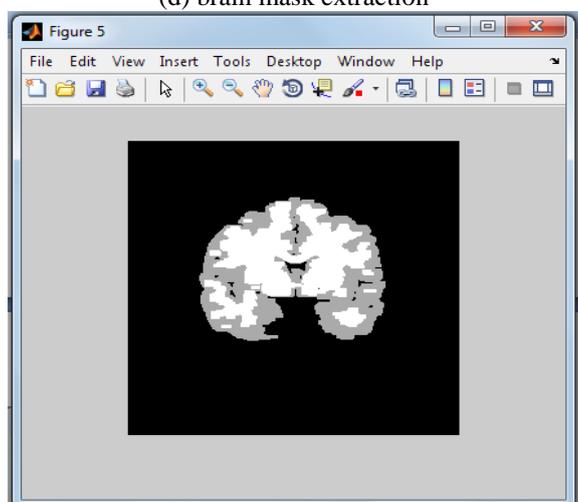
(b) histogram calculation



(c) intensity distribution



(d) brain mask extraction



(e) segmented image

DISCUSSION

In this work we developed a dedicated interactive segmentation system for brain volumetric quantification in dynamic contrast MRI. The system is featured by the seamless combination of effective computer vision techniques and interactive clinical knowledge input from clinicians. It therefore maximizes the benefits of both the computing capacity and clinical intelligence. We demonstrate how the system is effective and efficient to serve as a useful assistant at the end of radiologists and oncologists. The quantitative data yielded by the system can be created in a patient file and automatically compiled as part of a relational database. It is anticipated that such a tool will be useful for neuroscientists to make more objective interpretations of treatment interventions and natural history of disease to best meet patient needs. The system has been preliminarily evaluated using example cases. Further validation by using a large dataset and multiple users will be important in future work to thoroughly test the system's performance in terms of the inter- and intra-reader variability.

IV. CONCLUSION

We introduce a new software system to the community as a practical tool for clinical usage for quantitative and volumetric tumor assessment. The system is inexpensive, friendly in user interface, easy to deploy and integrate with PACS, and possible to be open-source. It holds a great potential to become routine available in future clinical workflow.

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