

# A Parallel Segmentation of Brain Tumor from Magnetic Resonance Images

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**Abstract**— Medical image segmentation is nowadays at the core of medical image analysis and supports computer-aided diagnosis, surgical planning, intra-operative guidance or postoperative assessment. Large amounts of research efforts have been made in developing effective brain MR (magnetic resonance) image tumor segmentation methods in the past years. However algorithms proposed so far are time consuming because it involves lot of mathematical computations. Also serial segmentation of multiple MRI slices (usually required for 3D visualization) takes exponential time. This results in need for improvement in performance as far as the time complexity is concerned. This paper proposes a methodology that incorporates the K-means clustering and morphological operation for parallel segmentation of multiple MRI slices corresponding to single patient. Segmentation of multiple MRI slices for tumor extraction plays major role in 3D (Three Dimensional) visualization and serves as an input for the same. The proposed framework follows SIMD (Single Instruction Multiple Data) model and since the segmentation of individual slice is independent of each other and can be performed in parallel and multithreading definitely speeds up the entire process. Also the framework does not involve any kind of inter-process communication thus the time is saved here as well.

**Keywords**—Segmentation, MRI, Tumor, K-means, Morphology, SIMD, Multithreading.

## I. INTRODUCTION

A tumor is a mass of tissue that grows out of control of the normal forces that regulates growth. There are several kinds of tumor being identified and diagnosed. Brain tumor is one among them[1]. It is group of abnormal cells that grows inside the brain or around the brain. Tumors can directly destroy all healthy brain cells. It can also indirectly damage healthy cells by crowding other parts of the brain and causing inflammation, brain swelling and pressure within the skull. In order to diagnose tumors the medical experts use different medical imaging techniques such as MRI (magnetic resonance imaging), CT (computed tomography) and PET (positron emission tomography).

MRI technology is one such technology that achieved great success in clinical applications, which made non-invasive examination and diagnosis become a reality[2]. Subsequent developments and clinical applications of other advanced imaging technology, such as CT and PET,

made the medical imaging technology develop even faster. Such imaging techniques present the detailed anatomical structure into multiple 2D (two dimensional) images. But 2D images cannot accurately convey the complexities of human anatomy and interpretation of 2D complex anatomy requires special training. Although radiologists are trained to interpret these images, they often find difficulty in communicating their interpretations to a physician, who may have difficulty in imagining the 3D anatomy. However using image processing tasks like segmentation and visualization, 3D reconstruction of MR images is possible.

3D reconstruction of medical images refers to the generation of a 3D representation of the examined structures from the acquired set of 2D images [3]. The technology of 3D reconstruction of medical images is an effective instrument for doctors to analyze the pathology, which can improve the medical diagnostic accuracy greatly. Image segmentation is an important subtask for 3D reconstruction. Having good segmentations will benefit clinicians and patients as they provide important information for 3-D visualization. Humans have a powerful recognition and visual system that allows them to segment well an image under all kinds of conditions. Contrary to this, segmentation is a very challenging task for computers, and research in this field of computer science is prolific. The large variety of image modalities with associated artifacts, the variability of the structures to segment and the strong demand requirements (e.g., high accuracy, automation) seriously hinder the design of efficient segmentation methods. In this context, the use of interactive and parallel segmentation approaches can expedite tedious parameter tuning and reduce the limitations of segmentation methods and enhance the performance in terms of computational time.

### A. Related Work

Large amounts of research efforts have been made in developing effective brain MR image tumor segmentation methods in the past years, however, such methods have failed to achieve the accuracy level comparable to analysis performed by human experts [4] [5]. Automated detection of tumors, in different images is motivated by the necessity of high accuracy requirements in medical diagnosis [6] [7]. Image segmentation technique plays crucial role in medical imaging by facilitating the delineation of regions of interest [8]. There are numerous

techniques in medical image segmentation depending on the region of interest, among them thresholding is the most basic one[9]. It is based on separating pixels in different classes depending on their gray level [10]. In medical imaging, several variations of this approach incorporating local intensities [11] or connectivity [12] are proposed. The gray level between tumor and muscles is very close, so this technique is difficult to apply. Clustering techniques such as K-means [13] and Fuzzy C-Means [14] are interesting methods which classifies pixels in an extracted features space but they are sensitive to noise. As a result these methods are not directly adapted to noisy MR images. S. Rahmi et al. [15] proposed parallel Fuzzy C-Means for segmentation which involves dividing the computations among the processors and minimizing the need for accessing secondary storage, to enhance the performance and efficiency of image segmentation task as compared to the sequential algorithm. But the major operational drawback of FCM technique is time consuming. The above method also involves network traffic delays so it doesn't enhance the performance much.

Recently, Deformable models [16] and Watershed transform methods [17] are efficient for medical image segmentation. Kai Xiao et al. [18] proposed an approach to extract useful information from the correlation between lateral ventricular deformation and tumor. This algorithm does not yield accurate results in case if the tumor is small in size. Jayadevappa et al. [19] suggested the hybrid approach that uses watershed segmentation approach which usually suffers from the problem of over-segmentation. The other approaches based on graph cut segmentation [20], hidden markov random field[21], ant colony optimization [22] and all the other methods proposed so far compromises computational complexity for achieving higher accuracy. Lot of computations is required for getting the accurate results for the tumor extraction problem. As a result, this paper proposes the multithreaded framework for segmenting multiple MRI images in parallel using combination of K-means and morphological erosion.

This paper describes the proposed work in Section II. The results are discussed in Section III and Section IV concludes the paper.

## II. PROPOSED WORK

The analysis on execution time of traditional serial segmentation algorithm for multiple slices shows that the time taken for execution is directly proportional to the number of slices and increases exponentially as the number of slices increases[9]. The proposed multithreaded framework tries to speed up the processing time by performing enhancement and segmentation of all the MRI images corresponding to individual patient in parallel simultaneously. Here segmentation method uses mathematical morphology based operation called erosion for skull stripping and K-means clustering for tumor extraction. Use of combination of morphological operation and clustering technique for tumor extraction yields accurate results. This framework creates new child thread for each of the MRI slice and all the threads execute the enhancement and segmentation procedure for

individual MRI slices in parallel. Before each of the child thread starts executing, the main thread calculates and populates the values for contrast improvement. Also it finishes all the other computations which are common to all the images, so that redundant computations by each of the child threads can be avoided. The proposed multithreaded framework is shown in Fig.1.

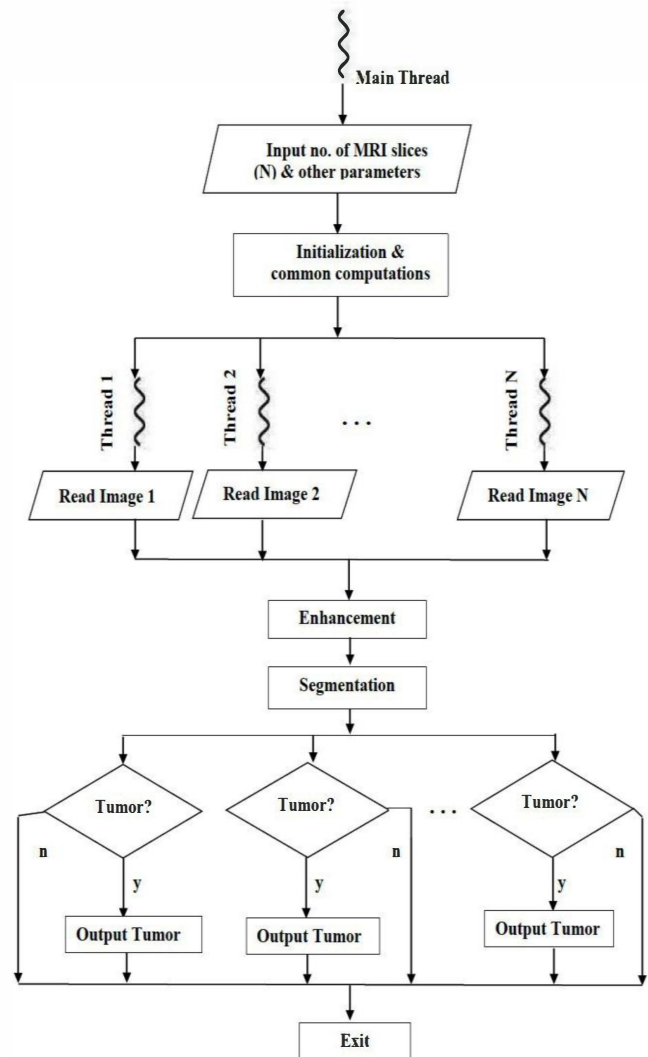


Figure 1. Proposed Multithreaded Framework

Each of the thread executes independently and determine whether tumor exist in the input image or not.If it exist it accurately extracts the tumor in the form of binary image.The enhancement and segmentation procedures are decribed in detail below.

### A. Enhancement

It is very much essential to enhance the quality of MRI images to improve the interpretability or perception of information in images for human viewers, or to provide better input for other automated image processing techniques so that accurate results can be obtained. The following are the enhancement techniques that are used here.

1) *Contrast Improvement*: Here the intensity values in grayscale input image are mapped to new values such that 1% of data is saturated at low and high intensities of input image. This increases the contrast of the output image. The linear mapping of intensity values with  $\gamma$  as 1 is used for the purpose.  $\gamma$  here refers to weight used for mapping intensity values of input to output image. In addition to  $\gamma$ , this mapping also depends on four threshold values that is higher and lower thresholds for input as well as for output (high\_in, low\_in, high\_out, low\_out). The threshold values must be between 0 and 1. The technique maps the intensity values in input image I to new intensity values in output image J such that the values between lower and higher threshold of input should be mapped to values between lower and higher threshold of output [23]. Intensity values below lower and above higher threshold of input are clipped; that is, values below lower threshold of input map to lower threshold of output, and those above higher threshold of input map to higher threshold of output. The mapping is done as given by (3). Here since the mapping is for 256 (0-255) intensity values we pre-calculate the mapping so that each of the threads need not spend its time in calculating it again. This speeds up much of the time also instead of calculating it for each and every pixel of image we calculate the new intensity value for each of the 256 intensity values and then map it to each of the pixels of the image.

$$(1) \quad \text{out} = \text{high\_out} - \text{low\_out}$$

$$(2) \quad \text{in} = \text{high\_in} - \text{low\_in}$$

$$(3) \quad J = \text{low\_out} + \text{out} * ((I - \text{low\_in}) / \text{in})^\gamma$$

2) *Mid-Range Stretch*: This enhancement technique stretches the middle range intensity values and thus highlights or improves the quality of brain tissues and lightens the non-brain tissues present in the MRI image. Since here there is need to segment out the brain tissues, the mid-range stretch techniques yields good results. It takes into consideration the intensity values of brain and non-brain tissues. The intensity values of brain tissues lies in the range of 0.2-0.7 as per literature survey. In order to apply mid-range stretch to an image we need to map each and every pixel of the grayscale image to a value between 0 to 1 just by dividing the intensity value by 255 as shown in (4)

$$(4) \quad X_{ij} = \text{Image}_{ij} / 255$$

where i and j corresponds to row and column index of the image matrix respectively.

Then we need to compute a function  $f(x)$  on the X matrix obtained from (4). The function  $f(x)$  is defined as follows.

$$(5) \quad f(X_{ij}) = \begin{cases} 0.5 * X_{ij} & , X_{ij} < 0.2 \\ 0.1 + 1.5 * (X_{ij} - 0.2) & , 0.2 \leq X_{ij} \text{ and } X_{ij} \leq 0.7 \\ 1 + 0.5 * (X_{ij} - 1) & , X_{ij} > 0.7 \end{cases}$$

After applying the above function mentioned in (5) the grayscale image is converted to an indexed image by using the smallest possible colormap for the image, containing one entry for each unique intensity level in the input image. The output image obtained after applying all this operations is of improved quality and can be used for further processing.

## B. Segmentation

In this case we use K-means clustering technique. Below are the proposed sub-steps that are followed for tumor extraction from enhanced image [9]. Here each of the thread performs the tumor extraction on multiple MRI slices.

1) *Skull Stripping*: Skull stripping is an important pre-processing step in neuroimaging analyses because brain images must typically be skull stripped before other processing algorithms. Following are the steps involved in skull stripping.

a) *Double Thresholding*: This is used to generate the mask. Here we convert the grayscale image to binary image by setting all the pixels in the range  $0.2 * 255 - 0.7 * 255$  to white and the remaining pixels to black as shown in (6). Thus this discards most of the pixels contributing to non-brain tissue. The technique is called double thresholding because it takes into consideration two thresholds upper and lower [11].

$$(6) \quad g(x,y) = \begin{cases} 1 & , 0.2 * 255 \geq f(x,y) \leq 0.7 * 255 \\ 0 & , \text{otherwise} \end{cases}$$

b) *Erosion*: We use erosion on the mask generated on thresholding to remove the skull portion. Here we propose to use disk of radius 3 as structuring element. This structuring element removes all the unwanted pixels contributing to the skull portion of the image. The erosion of the binary image A by the structuring element B is defined by:

$$(7) \quad A \ominus B = \{ z \in E \mid B_z \subseteq A \}$$

where  $B_z$  is the translation of B by the vector z, i.e.

$$(8) \quad B_z = \{ b + z \mid b \in B \}, \forall z \in E$$

c) *Region Filling*: A common use of the Region-fill operation is to fill holes in images. The eroded image obtained will have holes in the brain tissue in case if tumor is present. So in order to get the complete skull strip image including the tumor portion we apply the

region filling algorithm to the generated mask. Here the enclosed or the connected background pixels are converted to foreground pixels to remove the holes present in the eroded image as shown in Fig. 2. The conventional flood fill algorithm is used for this purpose. The skull strip image obtained is shown in Fig. 4.

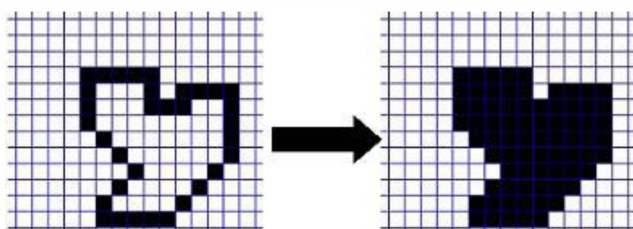


Figure 2. Region Filling

2) *K-means Clustering*: The K-means clustering here separates intensity values,  $X$  into  $K$  clusters. Here the image is partitioned into 3 clusters corresponding to black, gray and white pixels. As an improvement we apply K-means to each and every intensity value i.e. 0-255 instead of applying to each and every pixel in the image [13][14]. K-means clustering algorithm used here can be described as follows:

#### ALGORITHM 2.1: K-MEANS CLUSTERING

*Input*: No. of clusters ( $K=3$ ), Intensity values  $X \in [0-255]$ , Input Image ( $I$ ).

*Output*: Clustered Image

*Procedure*:

1. Select  $K$  cluster centroids  $C_1$  to  $C_k$  randomly, where  $C_i$  corresponds to  $i$ 'th cluster centroid and  $C_i \in [0, 255]$ .
2. Find the distance  $D_{ij}$ , distance of  $X_i$  from  $C_j$  as shown in (10).

$$D_{ij} = |X_i - C_j|, \forall i \in [0-255] \text{ \& } j \in [1-K] \quad (10)$$

$$\text{where } X_i = i, \forall i \in [0-255]$$

3. Compute  $D_i$ , distance of  $X_i$  from closest cluster centroids as in (11).

$$D_i = \min \{D_{ij}, \forall j \in [1-K]\}, \forall i \in [0-255] \quad (11)$$

4. Compute cluster count  $N_j$ , as shown in (12).

$$N_j = \sum (X_i \in C_j) \quad (12)$$

5. Determine the new cluster centroids as shown in (13)

$$C_j = (1/N_j) * \sum X_i, \quad \forall X_i \in C_j \quad (13)$$

6. Go back to step 2 until all centroid are convergent (difference between old and new centroid is above threshold).
7. Assign all pixels of image  $I$  to clusters based on their intensity values.
8. Set pixels based on the threshold as given by (14).

$$I(x,y) = \begin{cases} 1 & , I(x,y) \in C_j, C_j \geq 0.7 * 255 \\ 0 & , \text{otherwise} \end{cases} \quad (14)$$

3) *Tumor Extraction*: The image obtained upon clustering may contain some noise pixels along with the tumor. In order to get rid of this noise and to extract only the tumor from the clustered image connected component labelling algorithm is used here. So to retain only the tumor in the segmented image we keep the maximum connected component and set all other components to black and the result is shown in Fig.4.

### III. EXPERIMENTAL RESULTS

The hybrid approach which uses combination of morphological operation and K-Means clustering yields accurate results for given set of input MRI slices. Sample input containing set of MRI slices corresponding to single patient is shown in the Fig.3. The step by step detailed output for one MRI slice is shown in Fig.4. Also the proposed tumor extraction technique is automatic and carried out without any user intervention. As far as performance enhancement is concerned we can see the improvement in execution time with the increase in number of slices for multithreaded framework. The Fig.5 below show in detail the execution time taken for tumor extraction for varying number of MRI slices. The proposed work is implemented in Java using OpenCV 2.3 libraries and is also implemented in C with OpenMP API for comparison purpose. There is 28% reduction in execution time using Java threads and 88% reduction in execution time with OpenMP. The algorithm works for all the sizes of input MRI images since it suitably crops the area under consideration. The proposed work was tested for MRI images of several tumor patients. The method was able to successfully identify the tumorous images and extract the tumor from the same and was also able to identify the non-tumorous images and print suitable message for the user.

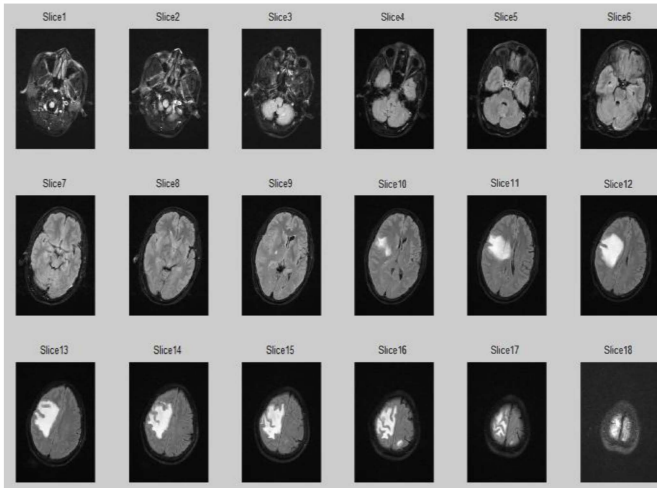


Figure 3. MRI Slices

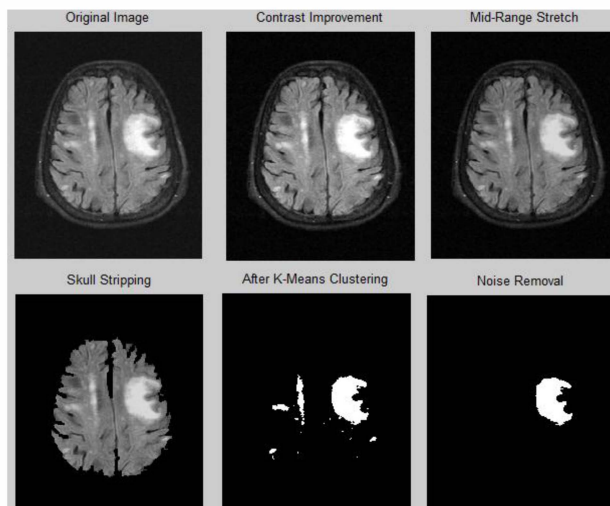


Figure 4. Tumor Extraction

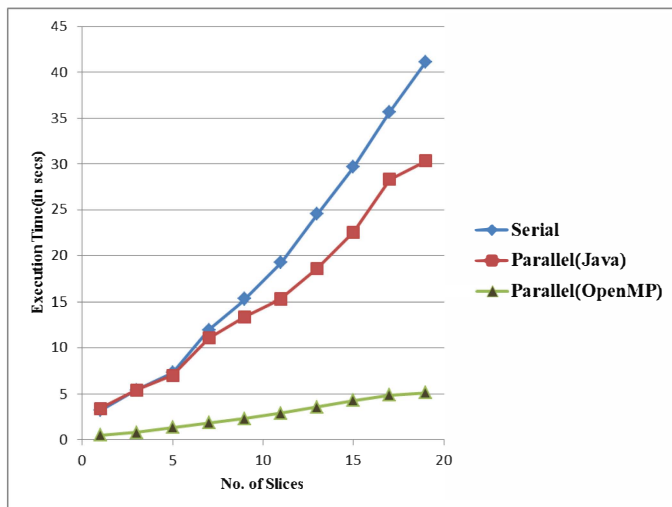


Figure 5. Execution Time Plot

#### IV. CONCLUSION AND FUTURE WORK

The enhancement methods proposed here improved the contrast of the input images drastically and also mid-range stretch enhancement has proved to be beneficial in

obtaining desired quality image which serves as an input for segmentation. The enhanced image was successfully segmented and the tumor was extracted from the multiple slices. Automatic segmentation was performed on the MRI slices without any user intervention and without use of any training data.

The hybrid approach of combining morphological operation and K-means clustering for segmentation gave accurate results and efficiently identified the tumor from the set of MRI slices. The proposed multithreaded framework resulted in improvement of performance in terms of execution time.

This work can be extended to build 3D model using multithreading of the segmented tumor thus incorporating parallelism thereby improving the speed of the time consuming graphical procedures. Also the GPU based framework for segmentation of multiple images simultaneously can also be developed for the tumor extraction.

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