

Automatic Brain Tumor Segmentation from MRI Images Using Region Growing Algorithm

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Abstract: MRI (Magnetic Resonance Imaging) is a technique which helps the physician to visualize the structures of internal organs of human body. Hence segmentation is necessary; it is difficult to identify the boundaries of abnormal regions in the MRI images. Subjective segmentation techniques need high attention with such images and time consuming problems, while objective segmentation techniques facing lots of challenging. However, identification rate accuracy is high. This paper presents a fully automation segmentation technique of MRI brain images. These images are segmented based on selection seed point objectively by improving Region Growing Algorithm. To control region growing process, fixable threshold is selected for each region. The Algorithm has been tested on different normal/abdominal MRI images samples. The results showed that the proposed algorithm is encouraging and efficient of selecting seed point as well as segmenting the MRI images without manual intervention.

Keywords: Image Segmentation, Automatic Region Growing, MRI, Brain Tumor.

1. Introduction

Biologically, brain tumor occurs when abnormal cells are formed in the brain. There are two main types of tumors: malignant tumors and benign tumors. Malignant tumors can be divided into primary tumors that start in the brain, and secondary tumors that have spread from elsewhere, and tumors known as brain metastasis tumors.

Medical image processing is the most challenging area and recently gets extremely attractive by many researchers. Detection a tumor using the brain magnetic resonance imaging (MRI) has become scope for processing medical images.

Image segmentation is one of the most difficult tasks hold an important position in the images that define the quality of the final result. Image segmentation is to divide the image into different regions but keeping the individual characteristics for each segment untouched, taking into consideration the enormous similarities between all segments of neighbouring to add more challenging.

MRI makes it possible to produce different types of tissue contrast by changing the excitation and repetition times, which makes it a very flexible tool for imagining the different desired structures. Due to the nature and appearance of brain tumors, one sequence of MRI is not enough for segmentation the tumor completely, including all the sub-regions. In current clinical routine, it employed different MRI sequences to diagnose and identify parts of the tumor [1]. These sequences are T1-weighted MRI (T1), T1-weighted MRI with contrast enhancement (T1c), T2-weighted MRI (T2) and T2-weighted MRI with fluid-attenuated inversion recovery (T2FLAIR) [2].

T1- weighting is the most widely used sequence for structural analysis. In addition, by using it, the healthy tissue is easily recognized. Improved-contrast images T1-weighted, which provided by patients' intravenous injection of gadolinium-diethylenetriamine pentaacetic acid (Gadollenium- DTPA),

the borders of the tumor looks brighter as the contrast agent accumulates there because of the disabling of the blood-brain barrier in reproduction tumor area. In this sequence, the necrotic and active tumor area can be easily distinguished. In MRI T2-weighted, the region edema, which surrounds the tumor, looks brighter. On the other hand, T2FLAIR (FLAIR) is a special sequence that helps in splitting the region edema from cerebrospinal fluid (CSF) due to suppress the free water signal. Besides it is often specified radiation definition of tumor margins in the clinical context manually by the radiologist on T2 and T1 after gadolinium images of the border between the threshold T2 and T1 over-density variation injuries and improves the surrounding healthy tissue to determine the outer margins of the tumor. Also it is often specified radiological definition of tumor margins in the clinical context manually by the radiologist on T2 and post-gadolinium T1 images of the thresholding borders between the T2 hyper-intense T1 and contrast improved lesions and the surrounding healthy tissue to determine the outer margins of the tumor [3].

Yuvaraj and Ragupathy, (2013) proposed a feature based approach, in which statistical features are extracted in the various selected regions. If the extracted feature matches with the predefined features, then a seed point is fixed in that region [4]. Saad et al., (2012) applied the histogram thresholding technique, to automate the seed selection process [5]. Meenalosini et al., (2012) uses a histogram based approach, in which the histogram analysis is done to compute initial seed point [6]. In an approach proposed by Shan et al., (2008) the seed points are automatically selected on the basis of both textural and spatial features [7]. Singh, P. and Singh, J., (2013) proposed a region extraction approach, which includes dividing image into region of interests (ROI), and extracting the seed points as the centroid of each ROI [8]. This method fails to provide good results, when the foreground and background are merged together, and the regions of interests (ROI) are not efficiently derived. Yashpal, and Gokhale, (2012) proposed an algorithm in which initial seeds are determined using no-edge and smoothness property of the image pixel. If the pixel is not on

the edge and has high similarity to its neighbors, then it is allocated as a seed pixel [9]. The same approach is also applied by Mundhada et al. (2014) for colour image segmentation [10].

The aim of this paper is to provide a mechanism for segmentation of a tumor in the brain using magnetic resonance imaging scanned image data sets.

In this paper, an approach for fully automatic method is proposed, to improve the performance of image segmentation. This method does not involve any human interventions.

The rest of the paper is the region growing algorithm, then the implementation of the algorithm, and its results. The last section is conclusion.

2. Material and Methods

In the proposed approach for a given MRI image, the algorithm is as follows:

Step 1: Compute the grey levels in the image, and sort them in ascending order.

Step 2: Compute the frequency of the grey levels of the image.

Step 3: Assign the first pixel as the first seed point.

Step 4: Merge the pixels to obtain improved seed point,

a) If the merging criteria is fulfilled,

- Replace seed point by the mean of the merged pixels.
- Add frequency of the pixel to the frequency of the seed point.
- Position of the seed point is assigned equal to the initial seed point.

b) Otherwise,

- Assign pixel as the new seed point.

c) Repeat step 4, until all pixels are merged.

Step 5: Sort the final seed points in decreasing order of their occurring frequency.

Step 6: Each seed point starts to grow by searching for Neighbourhood pixels or regions with similar properties that create connected regions. If the grey level of the neighbour pixel is similar to the initial seed then add it to the region, otherwise, the new pixel will be started as a new region until all pixels in the image are belonging to a region.

In the proposed algorithm, a threshold is selected. The similarity is defined as the difference between neighbors' pixel values. Each pixel around a boundary of growing region that have difference less than the threshold will be included in that region, otherwise not.

3. Results and Discussion

Digital Imaging and Communications in Medicine (DICOM) is considered as benchmark database when implementing and testing many MRI segmentation systems.

In this paper the DOCOM, which had been constructed by Doctor Antoine Rosset (CEO and OsiriX company Guru), and Joris Heuberger (CTO and Problem Solver), Many cases from DICOM database are considered to evaluate the performance of the proposed method each patient Database contain 22 slice of T1-weighted MRI images and 22 slice of T2-weighted MRI [11], has been used in our experiments. Some of the 2D slice may not contain any tumor. For acquisition of single slice from the 3D image, MHA read function was used.

A real dataset was also used from Oncology teaching hospital, Medical City, Baghdad, Iraq. each patient Database contain 20-30 slice of T1-weighted MRI images, 20-30 slice of T2-weighted MRI images, axial, sagittal and coronal.

The proposed region growing algorithm for image segmentation was implemented in MATLAB. Several MRI images were tested. The result shows efficient segmentation as shown in Figure 1.

4. Conclusion

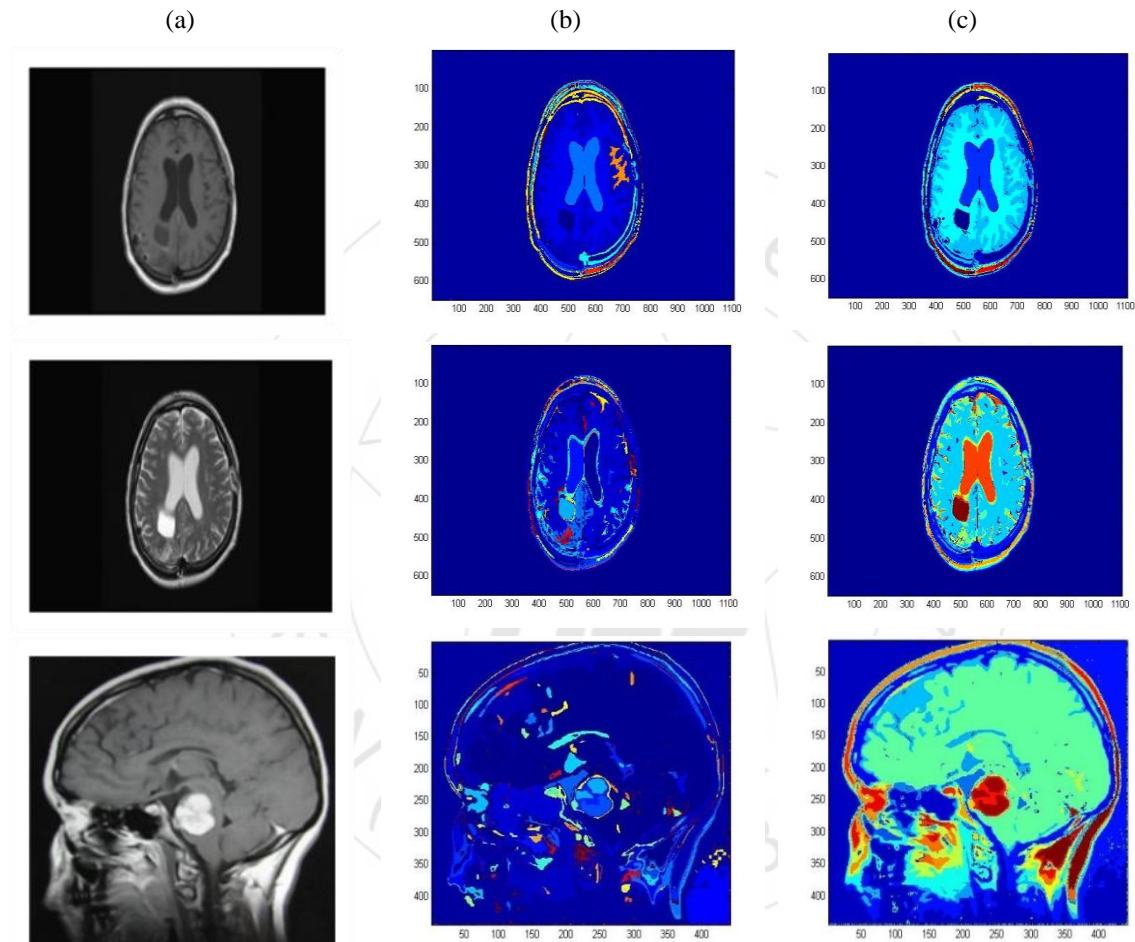
In this paper, an automatic region growing method for automatically segment 2D MRI image is proposed. The implementation results show satisfactory results for image segmentation. This implies that the proposed algorithm can be successfully used to achieve automatic image segmentation, and can be used in various MRI brain images. One of the advantages of this algorithm is not to allow user intervention. The other benefit of this algorithm is clearly that the proposed algorithm able to consuming less execution time.

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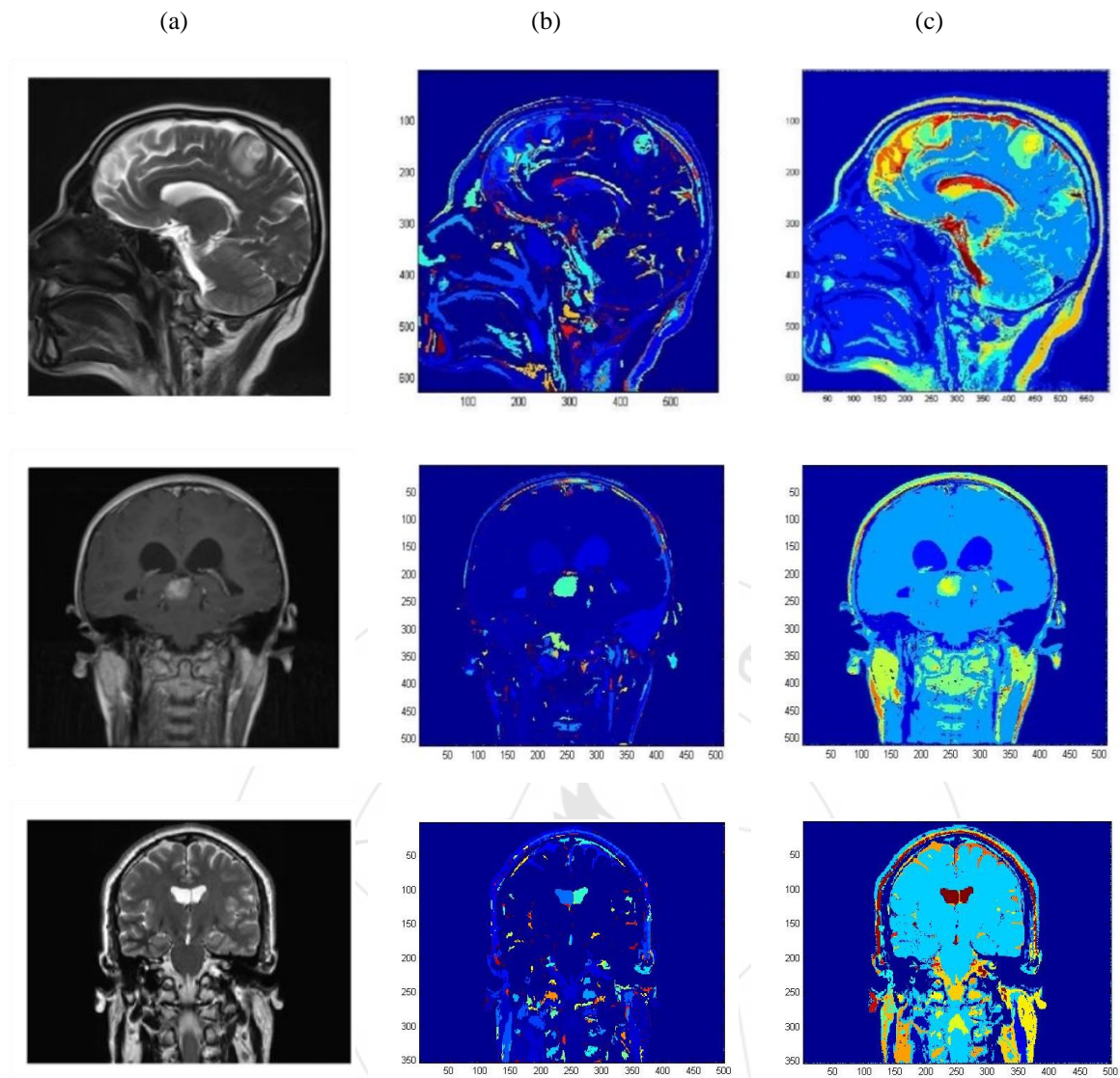


Figure 1: Proposed Segmentation Algorithm Results: (a) Original images (b) Initial segmentation, (c) Final Segmentation.