

Enchondroma tumor Detection

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Abstract: Medical Image Processing is one of the most challenging topics in research areas. This paper proposes an approach to detect enchondroma tumor in MR images. Enchondroma is a solitary, benign, intramedullary cartilage tumor that is usually located in the short tubular bones of the hands and the feet, the distal femur, the proximal humerus, and other bones. A proposed approach integrates some pre-processing techniques such as the average filter and the bilateral filter in order to remove noise and to smooth images. This will increase the quality of the image so that they are suitable for segmentation as well as morphological operations that will be used to eliminate false segments. Used to our approach in this paper. We used Matlab software with Graphical User Interface to develop an application that will detect and segment enchondroma precisely from the sequence of MR images. This application will discard the images which do not have a tumor in the final result.

Keywords: Enchondroma, MRI images, Image Processing, Matlab and Segmentation.

I. INTRODUCTION

An enchondroma is a benign tumor found in bone marrow. Enchondroma is in common a benign bone tumor is made of cartilage. The originator of enchondroma is unknown. The usual bones that might be threatened are the bones of the hands and feet. However, other bones like femur, humerus, or tibia might be threatened also. The studies show that enchondroma is most common in middle age people [1]. Diagnosis of enchondroma is done by imaging with CT scan, x-ray or MRI. The MR imaging technique is the best because it has a higher resolution. Magnetic resonance imaging (MRI) is a non-invasive medical system used to show 2D images of the body. This technique is based on a process that uses highly charged magnetic fields to make images of the inside of the body [2]. Currently, MR has more than one methodology to classify images; these are atlas methods, shape methods, variation segmentation, fuzzy methods, and others. New technologies of MRI are T1 weighted, T2 weighted, and Proton density weighted images. All that processed by multi-spectral analysis which integrate fuzzy images[3]. A significant goal in most medical imaging systems is to show the area of interest. By using Matlab in this project, an algorithm has been set to detect Enchondroma. Here we detect the abnormality, segment the tumor and clarify the area of the tumor in the bone. The algorithm has been set to read several MR images for patients in sequence. The next step is preprocessing image for smoothing the image and removing the noise. This is done by choosing between the average filter and bilateral filter. After preprocessing step, the user can start the segmentation process. At this stage the program will eliminate all images except images with abnormalities. At the final stage the program will show the border of the tumor in the original image. All that will be done by using the Graphic User Interface (GUI) in Matlab [4]. The algorithm has been tested on several of human body MRI database of enchondroma images. In this paper is structured as follows: section 2 shows a flowchart that clarifies the sequence of our approach generally. Section 3 explains the preprocessing step. Section 4 explains segmentation methods that detect

enchondroma, which are based on Thresholding segmentation and morphological operation. Section 5 shows the experimental results so that we can evaluate the performance of the proposed approach and the conclusion is in section 6.

II. METHODOLOGY

Figure 1 shows the application flowchart generally. The details will be in the next section.

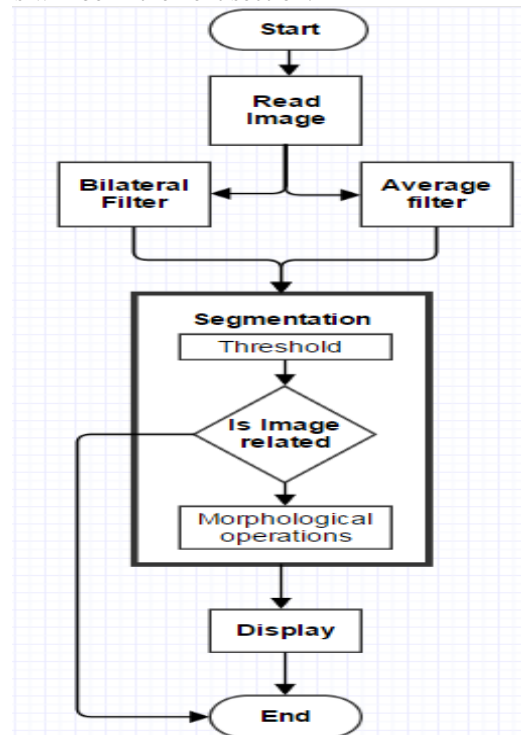


Fig. 1. Flowchart of our approach to detect enchondroma

A. Database

Database that has been used was taken from Radiopaedia.org [5, 6]. We chose T1 and STIR protocols which give enchondroma in a bright range because other MRI images protocols show enchondroma in dark range [7]. The application is designed for MR images which show enchondroma in bright intensities.

III. PREPROCESSING

A. Initial

We used the Matlab application with Graphical User Interface (GUI) to enable users to perform interactive tasks. In the first step, the user has to write the name of the folder which contains the series of MRI images.

These images will be stored in an array in order to deal with them easily in the next processing steps [8]. The images then will be converted into grayscale images. Finally, the grayscale will also be converted to double [9], which has a default range [0 1]. The result of the initial step will be shown in Figure 2.

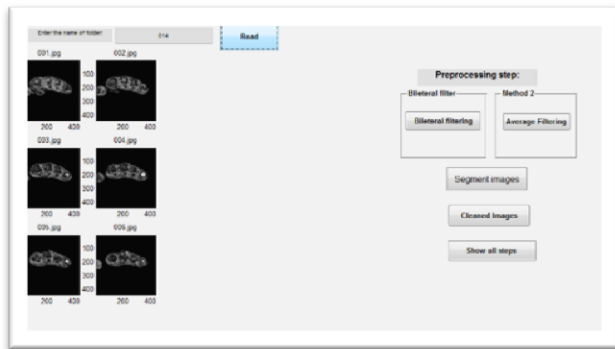


Fig. 2. Initial Process: read Images, converted to grayscale, then, converted to double

B. Preprocessing

Preprocessing is a primary step, which aims to improve the quality of images by removing noise, reducing artefacts, and increasing contrast to make the segmentation step precise [10]. There are several preprocessing techniques such as image adjustment, histogram equalization, and filtering etc. Filtering is one of the most important preprocessing techniques because it reduces noise, sharpens the edges of an object, preserves the edges, and smooth defective images created by the MR imaging system.

We chose the average filter and bilateral filter (Figure 2. a and b) to perform the preprocessing [11]. The user has to choose between them. The average filter (Figure 2.a) is a simple method for smoothing the images, and reducing the variance neighbors of the intensities by replacing each pixel value by an average of the surrounding pixels [1]. So, the average filter gives effective results for smoothing the images especially in the area of the enchondroma tumor as shown are figure 3.a.

Another technique that has been selected is the bilateral filter [12]. The bilateral filter (Figure 2.b) is a non-linear, used for smoothing the images, reducing noise, and preserving the edges.

The output of pixel value is computed by weighted average of intensities from nearby pixels. This weight is based on a Gaussian distribution [13]. The weights depend on intensities and spatial distance [14].

The disadvantage of this filter is the time it takes to process. For this reason, the application gives user two choices for this the step.

Figure 3.b displays the image after filtering by bilateral filter.

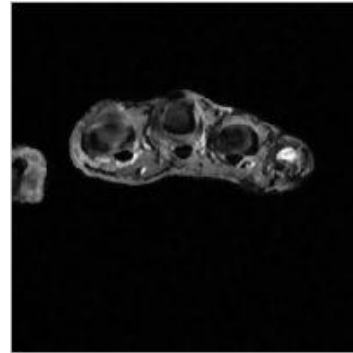


Fig. 3.a. Average filter

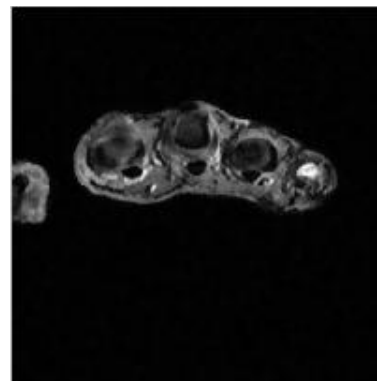


Fig. 3.b. Bilateral filter

C. Segmentation

Segmentation is the process of dividing the image into distinct regions, showing objects or features of interest. In this stage, we used two methods of segmentation: thresholding segmentation and morphological operation. Thresholding is the most common technique, which divides image into a binary image [15]. It is very effective with images that have high levels of contrast. So, the enchondroma tumor pixel values are in bright range. The threshold value (level) based on maximum pixel value in image as follows [16]:

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If max>0.8 then
    T= max*0.7
Else if max <0.6 %

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This means this image tends to be in dark range, so it is not related

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    T=0.6
Else
    T= max * 0.6

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Therefore,

$$bw(x,y) = \begin{cases} 1 & \text{if } I(x,y) > T \\ 0 & \text{otherwise} \end{cases}$$

Figure 4.a shows the result of thresholding segmentation of an image enhanced by average filter and figure 4.b shows the result of thresholding segmentation enhanced by bilateral filter.

Thresholding segmentation alone is not enough because in most cases the images have artefacts or false segments. So, Erosion operator is used to eliminate or decrease small objects [15]. Then, dilation is used to expand regions and edges [17]. Figure 5 shows the result of using this morphological opening.

Moreover, enchondroma usually cannot be located in the margin of the MR images. So, any centroid of any object in the images is located in the margin will be removed. Finally, the application will check which images have a tumor or which images are not related. If all the pixel values of the binary image are equal to zero (dark), then, this image does not contain an enchondroma tumor or the image is not related, so, it will be discarded from the array and only the images which have objects will remain.



Fig. 4.a. Segmented image by thresholding for image enhanced by Average filter



Fig. 4.b. Segmented image by thresholding for image enhanced by Bilateral filter

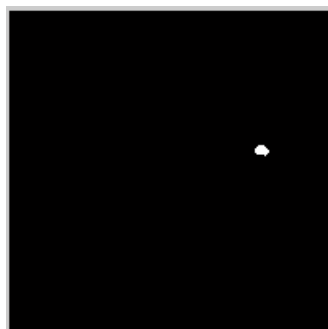


Fig. 5. Final result of the processing

IV. EXPERIMENTAL RESULTS

The work was tested on 5 cases of MR images. Each case varies from 6 to 20 images [5,6]. Table 1 displays the result of each case. But the accuracy was 91.3% for image which have enchondroma, but the problem was that some images are displayed in final result as related to disease which is a drawback. The challenge in enchondroma tumor detection is that enchondroma can be found in many places inside human bones [18]. However, no uniform structure of the area can be found in these places like a brain tumor or kidney stone. Figure 6 and 7 show all steps for some MR images. Figure 7 is false segmentation because enchondroma has the same density of cartilage is

shown in the image [19]. This false segment cannot be removed by morphological operation because it is big.

TABLE 1: EXPERIMENTAL RESULTS

Case #	# images	# images have tumor	Correct segmentation	Incorrect segmentation
1	6	4	4	0
2	11	6	5	2
3	20	8	7	3
4	8	5	5	2
5	1	0	0	1
Total	46	23	21	8

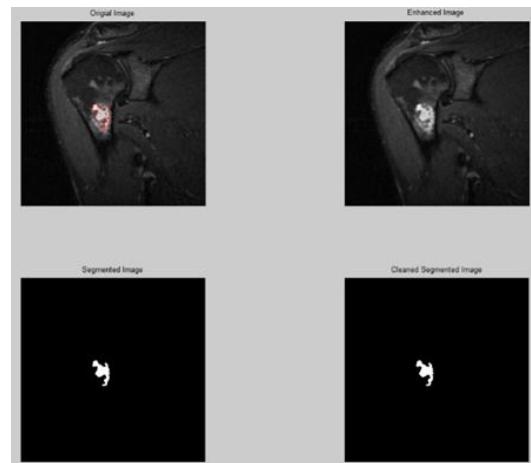


Fig. 6. Case 1 shows all steps of segmentation

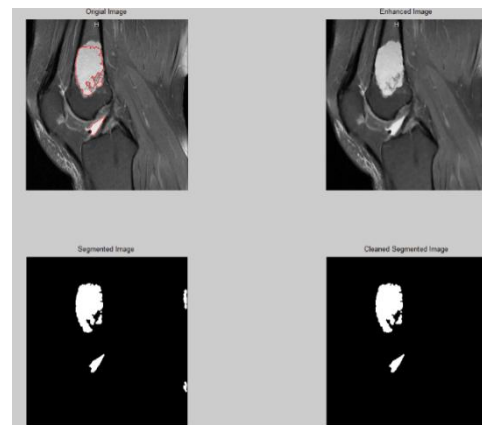


Fig. 7. case 2 shows all steps of the segmentation

V. CONCLUSION

Enchondroma is a mysterious disease affecting the bones. And it's a worthy topic to be used in this topic. That cannot be done without depending on enchondroma perfect database. Therefore, the detection of enchondroma from MR images and takes away the images that do not have a tumor or an unrelated image requires two main steps. In the preprocessing step, average filter and bilateral filter smooth the area of interest and remove noise. We combined thresholding segmentation and morphological operations to get precise segmentation. In addition, the objects which are found in the margin area of the image

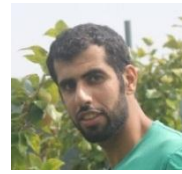
will be removed by finding the centroid of each object. We developed an application to assess the performance of the proposed method.

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BIOGRAPHY

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