

Liver Segmentation and 3D Modeling from Abdominal CT Images

Hong Tai Tran^{*}, A Ran Oh^{*}, In Seop Na^{**}, Soo Hyung Kim^{**}

Abstract

Medical image processing is a compulsory process to diagnose many kinds of disease. Therefore, an automatic algorithm for this task is highly demanded as an important part to construct a computer-aided diagnosis system. In this paper, we introduce an automatic method to segment the liver region from 3D abdominal CT images using Otsu method. First, we choose a 2D slice which has most liver information from the whole 3D image. Secondly, on the chosen slice, we enhanced the image based on its intensity using Otsu method with multiple thresholds and use the threshold to enhance the whole 3D image. Then, we apply a liver mask to mark the candidate liver region. After that, we execute the Otsu method again to segment the liver region from the chosen slice and propagate the result to the whole 3D image. Finally, we apply preprocessing on the frontal side of 3D images to crop only the liver region from the image.

Keywords: Image Processing | Medical Image Processing | Abdominal | Computer Topology

I. INTRODUCTION

From the day X-ray was used in medical application, the segmenting of organs has been manually processed. However, to segment the organ slice by slice manually is a time-consuming task which causes burdens on human resources because you may need many qualified doctors for segmenting and checking X-ray images. Furthermore, an exhausted doctor may make inaccurate diagnoses. Therefore, a system that can segment the liver automatically is an urgent requirement.

There are many challenging factors when developing an automatic or semiautomatic segmentation system for the liver. The first problem is the liver's variation in shape and size which depended on the person. Second, the organs that have similar intensity level can stick closely to each other which, in some cases, are not the real distance

between the organs but because of the viewpoint from a 2D plane. Lastly, if the liver has tumors, those tumor regions will contain different gray level pixels from the normal liver region. In many cases, these tumor regions will not be included in the liver segmented result. The challenging factors are illustrated by Figure 1 where (a), (b) show two variations of liver shape and other organs that have adjacent borders, and (c) show a liver region that contain tumor.

II. RELATED WORK

There are several approaches on segmentation from CT images in [1], [2]. These methods can be divided into some big groups: level-set, region-growing, thresholding and statistical shape model with different pre and post processing operations.

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^{*}Student Member, ^{**}Member: Dept. of Electronics and Computer Engineering, Chonnam National University

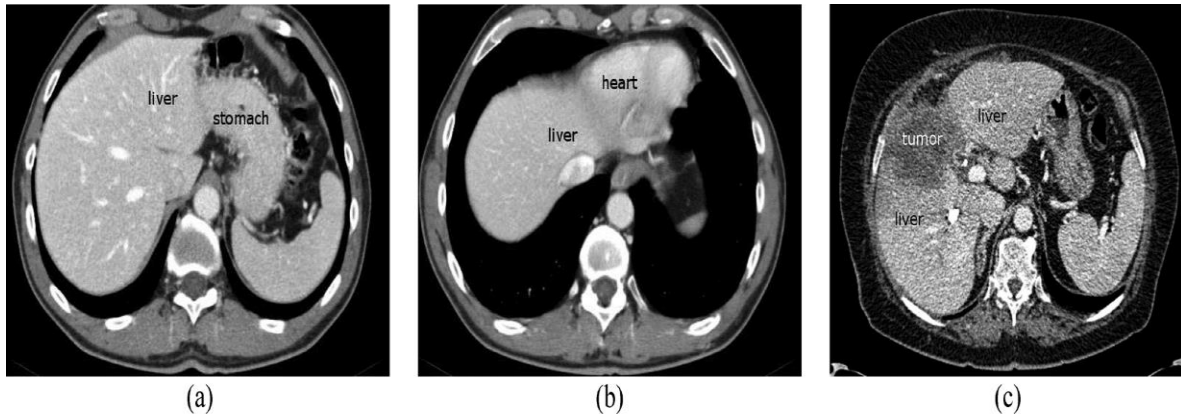


Fig. 1. Segmentation challenging factor[1]

The statistical model approach is good for detecting the liver region but it requires large training sample and knowledge about liver and it cannot work so well when segmenting damaged livers region.

The region-growing approach also has its flaw when requiring initial "seed points" and then determines if the neighbors of these "seed points" pixels should be added to the region based on intensity level which cause some error since the intensity levels of organs is quite similar.

Level-set method takes advantages of its power to handle topology and approach a higher dimension. The problem of the level-set method is that it requires good initial contour which usually obtain manually.

Anter et al. [4] first construct a local liver lesion image. Secondly, they pre-segment the lesion with Otsu method to get the initial contour, finally evolve the active contour with the local C-V level set method to get the final contour of a lesion. The problem is they manually select several points to form a polygon which covers the whole lesion. This method is semi-automatic, which needs human interaction

III. PROPOSED METHOD

Because a 3D abdominal CT image consists of many slices of 2D images, to optimize the processing time, we first find the group of axial slices (Figure 3a) that contain liver region. After that, from that group, we will first apply the segmentation process on the liver slice which has the largest liver region and propagate the result to other slices. In a 2D CT image, there are mainly four intensity intervals from the background (black); abdominal liquid; organ and

abdominal wall; bone (white). Using Otsu method, we find a threshold to take organs from other components. Then, we use a mask made from over 1600 axial images of hand segmented liver (provided by dataset) to mark the region where liver can be. Finally, we take the largest connected component which is the liver. The whole process is described in Figure 2.

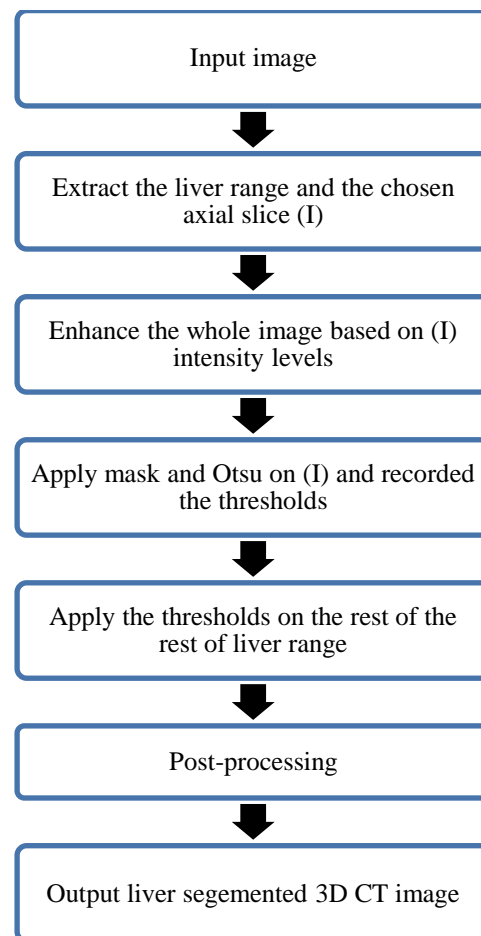


Fig. 2. Proposed flowchart

1. Properties of 3D abdominal CT images

In this paper, we will apply our method to segment whole liver region of 3D abdominal CT images. These 3D images were made from a sequence of scanned images acquired in axial or coronal direction. Then, in most cases, the data sets will be oriented to axial orientation. Each 3D image is a block of voxels, examples for each plane slices are shown in Figure 3.

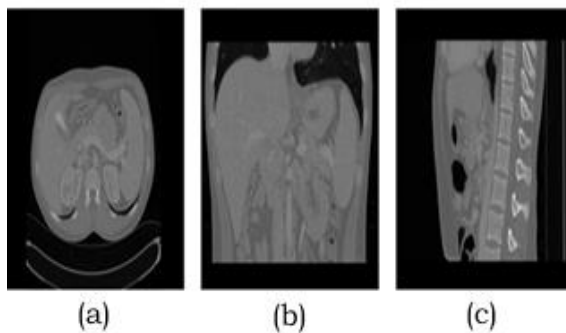


Fig. 3. (a) An axial slice (b) A coronal slice (c) A sagittal slice

2. Extract liver range from coronal side

The purpose of this step is to find all the axial slices which have the liver region and the axial slice that has the largest liver region of them all for our next step of segmentation.

To do this, we start with the middle coronal slice and equalized its histogram. The reason we choose this slice is because, in most cases, this slice will contain enough information about the shape of the liver. Next, we will remove the right-half of the slice because it is the region for other organs (stomach, intestine...) which will cause unnecessary errors for our attracting process. Then, we binarize and erode our image so to remove weak connection region to the liver (which is caused by some organ that is not liver). Lastly, we take the largest connected component in the image and using it to mark the highest and lowest slices of the liver region from y-axis while also find the slice that has the most liver pixels.

The result of this section can be seen in Figure 4; red line (a), green line (b) and blue line (I) are highest, lowest and largest slice mark respectively.

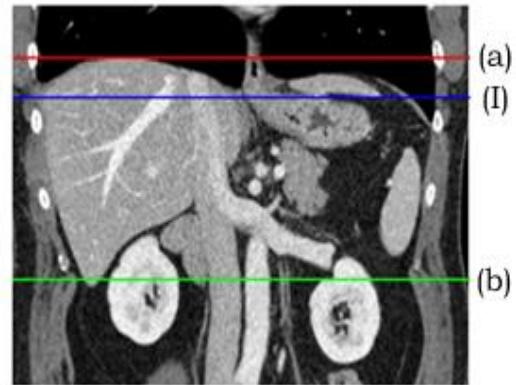


Fig. 4. Liver range (a)–(b) and the chosen slice (I)

3. Segment liver from axial slices

3.1. Automatic enhance 3D CT images

As mentioned above, the intensity similarity is a big obstacle when segmenting the liver from CT images. Hence, to improve the efficiency of Otsu method on liver images, we will first enhance the image to increase the contrast between objects in our image.

Normally, we increase the contrast in each slice to complete this task and then begin the segmentation processes. However, we need to keep the consistency of intensity on every axial slice of the whole 3D images for later propagation process. Because of that, in our approach, we will calculate our enhancing value on chosen liver slices (I) (Figure 5a) and then use the same value to enhance other slices. This process also improves our algorithm accuracy since the slice (I) has more information from liver intensity compared to other axial slices.

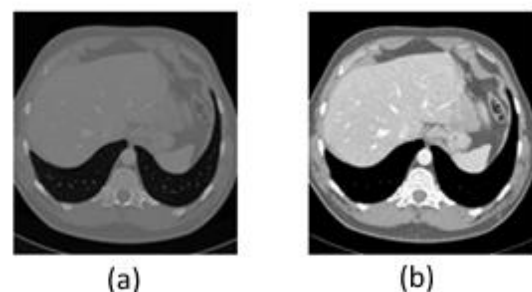


Fig. 5. The original (a) and enhancing result (b)

3.2. Liver Mask.

Since the internal organs in 3D abdominal CT

images have similar intensities and our liver can have various shapes which depended on both the person and the position of our observing axial slice. To effectively segment the liver from other internal organs, we need a way to estimate the liver location on our slices. In our approach, we construct a liver mask from many segmented liver areas provided by the training set from Sliver07 [08]. We calculate from the liver region on every axial slice and record any location that can be liver to make the liver mask (Figure 6).



Fig. 6. Liver Mask

3.3. Apply Otsu on chosen slice (I)

After enhance and apply the mask, in this section, we will describe the process of applying Otsu on the axial slice (I). We choose axial section because in the coronal and sagittal section there are cases where another organ placed in front of the liver while these cases are minimal in axial section.

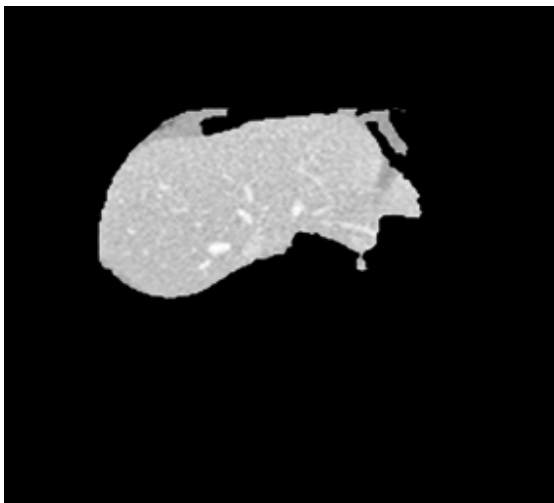


Fig. 7. Final segmentation result on slice (I)

First, we apply two-threshold Otsu on the chosen axial slice (I) and assign the gray level inside those two thresholds to be liver. After that, we will merge the small region because, in some cases, not all liver pixels are inside the threshold. Finally, we remove small connected region near the liver and take only the largest connected component. The final result of this section is the liver region from slice (I) which demonstrated by Figure 7. The thresholds (upper and lower) of Otsu method were also recorded for further processes.

3.4. Propagate result to the whole liver

For other slices that are not (I), first, we apply the mask. Because these slices were enhanced using the same parameter from (I) slices, the lower and upper threshold which is the result of the Otsu method on the chosen (I) slice are also suitable for segmenting the liver region from different intensity region. Then, we apply the same process of merging and choosing the largest connected component. The process is applied slice by slice in axial sides of the images for every slice in the range extracted from the coronal side.

4. Post processing

Since the human liver is a whole big and connected organ, we decide to use the result from 3.3 and modified it by using the coronal side of our image. The post-processing section will fill the hole of our axial slice result on coronal slice perspective then again choose the largest connected region in this coronal side. This process will help us reduce the error from the main process since there are some organs which are connected to the liver from axial sides but not connected to the liver from the coronal perspective and the process also connect some liver region that has been wrongly removed by the main process.

IV. EXPERIMENTAL RESULTS

Our algorithm was applied on liver data set from sliver07 [08], a liver segmentation competition. In this data set, there are some cases where images are skewed or deviated from the center, we will not include these cases and only apply to standard abdominal 3D CT images from the data set. With that condition in mind, we get an acceptable result.

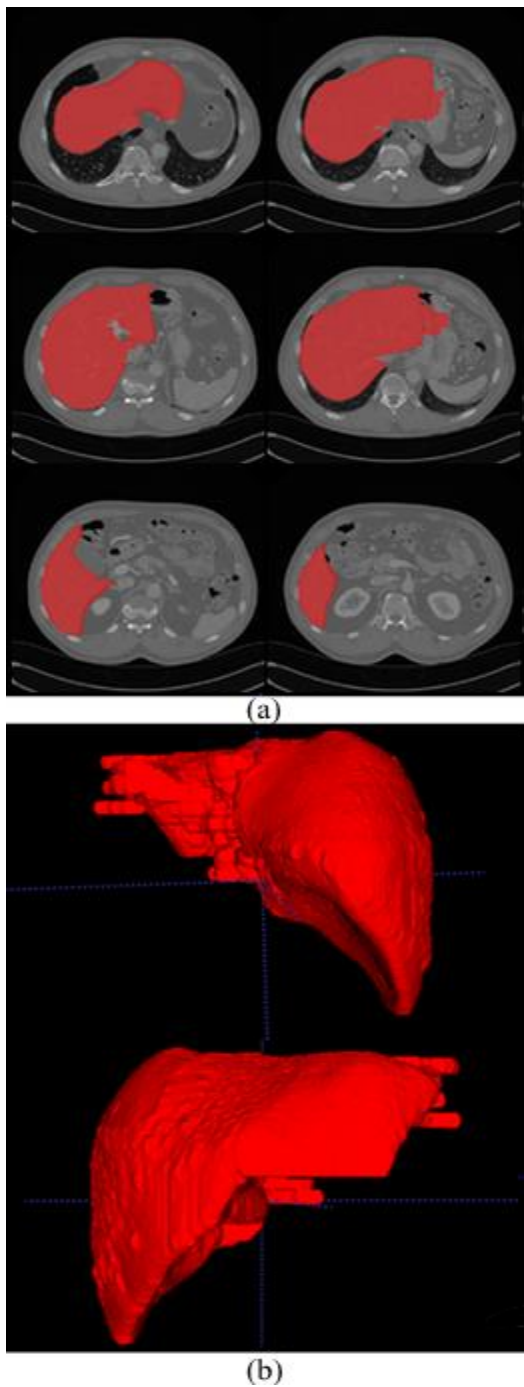


Fig. 8. (a) Segmentation result on coronal slices
(b) 3D model of the whole liver segmentation

Figure 8 shows the result in the top-down orientation of axial side and a 3D model (last two pictures) built using ITK-snap; a free, open source program; from one of the 3D images from sliver07. The 3D model is not necessary to be smooth since the axial slice from actual CT has some distance to each other (the result showed image contain 212 axial slices).

Table 1. Processing time and F-measure

#	Number of slices	Execution time	F-measure
1	183	13s	0.7801
2	64	8s	0.7951
3	79	8s	0.8156
4	212	20s	0.9040
5	111	10s	0.6578
6	251	25s	0.8680
7	228	25s	0.8886
8	210	27s	0.8881
9	191	28s	0.8698
10	151	22s	0.8743
11	121	11s	0.7402
12	245	28s	0.8811
13	335	30s	0.8715
Average		19.6s	0.8334

Table 1 shows the evaluation using F-measures from [7] which obtain when comparing our result to hand segmented result from sliver07. F-measures can be calculated using the following formulas:

$$F = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (1)$$

where

$$\text{Precision} = \frac{\text{TruePositive}}{\text{TruePositive} + \text{FalsePositive}} \quad (2)$$

$$\text{Recall} = \frac{\text{TruePositive}}{\text{TruePositive} + \text{FalseNegative}} \quad (3)$$

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 Authors



Hong-Tai Tran

He received his B.S. degree in Mathematics and Computer Science in Ho Chi Minh City University of Science, in 2014. Since 2015, he has been a Master student at Electronics and Computer Engineering, Chonnam National University, South Korea. His research interests are pattern recognition, machine learning, and medical image processing.



A-Ran Oh

She received her B.S. degree in the school of Computer Statistics from Chosun University, Korea in 2009. Since 2011, she has been a researcher at Department of Computer Science in Chonnam National University, Korea.



In-Seop Na

He received his B.S., M.S. and Ph.D. degree in Computer Science from Chonnam National University, Korea in 1997, 1999 and 2008, respectively. Since 2012, he has been a research professor in Department of Computer Science, Chonnam National University, Korea. His research interests are image processing, pattern recognition, character recognition and digital library.



Soo-Hyung Kim

He received his B.S. degree in Computer Engineering from Seoul National University in 1986, and his M.S. and Ph.D. degrees in Computer Science from Korea Advanced Institute of Science and Technology in 1988 and 1993, respectively. From 1990 to 1996, he was a senior member of research staff in Multimedia Research Center of Samsung Electronics Co., Korea. Since 1997, he has been a professor in the Department of Computer Science, Chonnam National University, Korea. His research interests are pattern recognition, document image processing, medical image processing, and ubiquitous computing