A Novel Fully Automatic Technique for Liver Tumour Segmentation from CT Scans

Nader H. Abdel-massieh*

Mohiy M. Hadhoud* 

Khalid M. Amin* 

1Faculty of Computers and Information – Menoufia University - Egypt

Abstract — The liver is a common site for the occurrence of tumours. Automatic hepatic lesion segmentation is a crucial step for diagnosis and surgery planning. This paper presents a new fully automatic technique to segment the tumours in liver structure with no interaction from user. Contrast enhancement is applied to the slices of segmented liver, then adding each image to itself to have a white image with some pepper noise and tumours as dark gray spots. After applying Gaussian smoothing, Isodata is used to threshold the tumour in the slice. In order to eliminate erroneous segmentation, discriminative rule based on diagnostic knowledge on liver cancer shape is applied along with a 3-D consistency check is performed based on three-dimensional information that a lesion mass cannot appear in a single slice independently. Tests are performed on abdominal datasets showing promising result.

Index Terms—Tumour detection; Contrast enhancement; Gaussian smoothing; Isodata threshold

I. INTRODUCTION
Cancer is one of the leading causes of death worldwide and in the Region. Liver cancer is more common in developing countries within Africa and East Asia: in some countries, it is the most common cancer type and it is predicted that for 2030 it will enter the top 20 causes of death. Infection with the hepatitis C virus (HCV) is a major public health problem in Egypt. Egypt has the largest epidemic HCV in the world. The recently released Egyptian Demographic Health Survey (EDHS) in 2009 tested a representative sample of the entire country for antibody of HCV. The sample included both urban and rural populations and included all 27 governorates of Egypt. Over 11,000 individuals were tested. The overall prevalence (percentage of people) positive for antibody to HCV was 14.7%. Not everyone remains infected but EDHS reported that 9.8% continue to have HCV RNA. That means almost 10% of the total population are infected and are infectious to other people.

Medical decisions are rarely taken without the use of imaging technology such as Computed tomography (CT). Not only more comfortable and safe for the patient; imaging enables the inspection of the whole body in a non-invasive way and allows views of anatomy and physiology that cannot be obtained by any other way.

To identify tumours from CT slice images, there is a need for segmentation of tumorous lesions. Typically, this has been manually done by trained clinicians. The task is time-consuming, requiring much effort and can be subjective depending on the experience of the clinician.

II. PREVIOUS WORK
Many research groups have developed different approaches for liver and lesion segmentation. Park et al [1] proposed a method that first obtains a segmentation of the liver using intensity histogram transformation and maximum a posteriori classification resulting in a binary mask. After morphological processing of the mask, the tumors are located by defining a statistically optimal gray level threshold within the mask area. Seo proposed a multi-stage automatic hepatic tumour segmentation method [2]. It firstly segments the liver, then; hepatic tumour is segmented by using the optimal threshold value with minimum total probability error. Promising results are shown, even if the approach produce diverse false positives, especially for small tumours. A method by Ciecholewski et al [3] used a contour model to obtain a segmentation of the liver, and then by histogram transformation enhanced the image to find neoplastic lesions at locations of cavities within the healthy liver volume. Jolly et al [4] locates tumours on 2D plains after simple gray level distribution estimation, and the results are combined to obtain final 3D segmentations. Zhao et al. [5] developed a region growing algorithm using intensity distributions of the seed ROI provided by users to delineate liver metastases. They also used specific shape constraints to prevent the region growing from leaking into surrounding tissues. Bourquain et al. [6] used interactive region-growing method for the vessels and tumours. Among other works that used region growing to detect liver lesions [7], In [8], Arakeri et al. proposed an automatic region growing method that incorporates fuzzy c-means clustering algorithm to find the threshold value and modified region growing algorithm to find seed point automatically. Massoptier and Casciaro [9] firstly, segmented the liver by adopting a statistical model-based approach and then apply a wavelet analysis for classifying the tumours. Chen and Metaxas [10] used Markov Random Field (MRF) estimation coupled with Deformable models for the segmentation of tumours. Lu et al. [11] also used the active contour with a manually specified initial contour to obtain the tumour boundary. Shang et al. [12] presented active contour model with an embedded classifier, based on a Gaussian mixture model fitted to the intensity distribution of the medical image to segment liver, vessels and lesions. Jiahua et al. [13] utilized comprehensive the edge detection, the watershed algorithm and region merging approach, while [14] used watershed and active contour algorithms to do volumetric study. Other approaches were presented including Expectation maximization [15] and level set [16-18]. Some approaches added constraints to decrease erroneously segmented tumours like knowledge-based constraints [19].

III. MATERIALS AND METHODS

A. Liver Segmentation
In this paper, the liver structure is firstly segmented from the original CT image to form a new image which only includes the liver region with tumours if existed and a blank background. Segmenting Liver could be done using the novel proposed method [20].
**B. Tumour Detection**

Having segmented the liver structure in the CT image, the next step is to enhancing the contrast of the segmented slices as liver parenchyma and tumour tissue have similar gray levels. For selecting the stretching range, there is a trade-off between reducing the noise in the image and avoiding over-enhancement.

Linear contract stretching is used to increase the difference between liver tissue and tumours. Among several methods of contract stretching, such as Selective histogram equalization, direct stretching with the linear relationship, linear stretching according to the fitting curve and nonlinear stretching with the logarithmic transformation, direct stretching with the linear relationship shows good result [21], which can be performed with formula number (1):

\[
I' = \frac{I'_{\text{max}} - I'_{\text{min}}}{I_{\text{max}} - I_{\text{min}}} (I - I_{\text{min}}) + I'_{\text{min}}
\]  

(1)

where, \(I\) and \(I'\) are the gray levels before and after transformation, respectively. \(I'_{\text{max}}\) and \(I'_{\text{min}}\) are the highest and lowest gray level after transformation, \(I_{\text{max}}\) and \(I_{\text{min}}\) are the maximum and minimum gray level in the liver region before the transformation, respectively.

After finishing with contrast enhancement stage, the difference in gray level between liver and tumour is now clear. The gray levels of liver parenchyma are higher than that of tumour tissue as shown in Fig. 2(b). The following step is to add the enhanced image to itself.

\[
R(i,j) = I'(i,j) + I'(i,j)
\]  

(2)

After contrast enhancement the pixels of liver parenchyma is brighter, in range between 140 and 160, so that when the value of each pixel is added to itself the value of addition will reach 255 and will appear as white. On the other hand, the pixels which represent tumour tissue is dark with gray level in range between 15 to 40, and so when the value of each tumour pixel is added to itself according to formula (2), the result gray level will be between 30 to 80 appearing as dark spots.

The result of addition is image background as well liver tissue that appears as white background with some pepper noise, and tumours that appears as dark spots with range of gray levels. In order to remove the noise and make the region of tumour more homogeneous as in shown Fig. 3(a), Gaussian smoothing is used as in formula (3), where \(x\) is the distance from the origin in the horizontal axis, \(y\) is the distance from the origin in the vertical axis, and \(\sigma\) is the standard deviation of the Gaussian distribution.

\[
G(x,y) = \frac{1}{\sqrt{2\pi}\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}}
\]  

(3)

In order to turn the image into binary with tumour as black blob on white space, Isodata algorithm is used to automatically threshold the image, followed by morphological hole filling, erosion and dilation as shown in Fig. 3(b).
D. 3-D Slices Correction

Another discriminative rule relies on 3-D consistency check is performed based on three-dimensional information that a lesion mass cannot appear in a single slice independently. If a slice has a suspicious tumour and this slice has no interaction with other suspicious tumours in the neighbouring slices, this slice with a suspicious tumour will be considered erroneous and the selected blob will be disregarded, Fig 4(b).

IV. RESULTS

The datasets were acquired from two clinics. We applied the algorithm to 7 datasets (200 2D liver images). They are non-contrast-enhanced and there was no previous assumption about shape, size, location, and intensity range of liver structure or tumour. The algorithm was implemented on java environment, a personal computer using a P4 (3 GHz) processor and a 2GB memory. The proposed hepatic tumour detection method was evaluated by comparing the automatically detected liver volumes to the ground truth, manually traced by experts.

Evaluation of the algorithm was performed by computing four parameters: sensitivity, specificity, accuracy, and error rate as shown in Table 1.

V. DISCUSSION AND FUTURE WORK

In the present study, we describe the steps of our new algorithm to automatically segment tumours in liver structure from CT scans, designed to achieve automatic detection of the liver. The proposed technique has achieved a promising result as shown in Table 1, with 0.8720 sensitivity and 0.9973 specificity.

Dataset number 2 has the highest score; because it contains one big tumour appear in successive slices. Dataset number 1 has the lowest score because segmentation of lesions in some slices was not accurate enough, and so a number of pixels were considered as false positive.

Among other works that aimed at segmenting tumour; In [3] Ciecholewski and Ogiera reported the sensitivity of their method to be 0.7330 its specificity to be 0.8330 , and accuracy to be 0.7830. In [2] Seo reported the sensitivity to be 0.6471, specificity to be 0.9294 , and accuracy to be 0.9118. Seo and Chung [22] reported the sensitivity to be 0.7273, specificity to be 0.9257, and accuracy to be 0.8578.

In more recent study, Pescia et al. [23] used non-linear machine learning techniques and achieved 0.86 sensitivity, 0.80 specificity and when liver vessels were removed before tumour segmentation specificity raised to 0.82. Malai and Sadasivam in [24] used linear vector quantization neural network to automatically extract the liver tumour the result was 0.98 sensitivity and 0.85 specificity.

In the future, we will explore methods to reduce false positive by extracting vessels first, and refine the finally segmented edge of proposed tumour.

ACKNOWLEDGMENT

We thank Dr. Mahmoud Habeeb, MD in Radiology, for his sincere help.
### Table 1: Evaluation of the results based on general segmentation metrics

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Sensitivity (avg/std)</th>
<th>Specificity (avg/std)</th>
<th>Accuracy (avg/std)</th>
<th>Error rate (%) (avg/std)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.8358 / 0.0903</td>
<td>0.9995 / 0.0006</td>
<td>0.9988 / 0.0008</td>
<td>0.0012 / 0.0008</td>
</tr>
<tr>
<td>2</td>
<td>0.8943 / 0.1065</td>
<td>0.9996 / 0.0004</td>
<td>0.9993 / 0.0003</td>
<td>0.0007 / 0.0003</td>
</tr>
<tr>
<td>3</td>
<td>0.8879 / 0.1718</td>
<td>0.9999 / 0.0001</td>
<td>0.9998 / 0.0002</td>
<td>0.0001 / 0.0003</td>
</tr>
<tr>
<td>4</td>
<td>0.8585 / 0.1884</td>
<td>0.9978 / 0.0006</td>
<td>0.9966 / 0.0005</td>
<td>0.0011 / 0.0005</td>
</tr>
<tr>
<td>5</td>
<td>0.8632 / 0.1376</td>
<td>0.9933 / 0.0004</td>
<td>0.9972 / 0.0004</td>
<td>0.0002 / 0.0006</td>
</tr>
<tr>
<td>6</td>
<td>0.8796 / 0.1546</td>
<td>0.9998 / 0.0005</td>
<td>0.9995 / 0.0003</td>
<td>0.0010 / 0.0003</td>
</tr>
<tr>
<td>7</td>
<td>0.8845 / 0.0098</td>
<td>0.9912 / 0.0002</td>
<td>0.9987 / 0.0001</td>
<td>0.0013 / 0.0002</td>
</tr>
<tr>
<td>Average</td>
<td>0.8720 / 0.1227</td>
<td>0.9973 / 0.0004</td>
<td>0.9986 / 0.0004</td>
<td>0.0008 / 0.0004</td>
</tr>
</tbody>
</table>

### References


