A Novel Fully Automatic Technique for Liver Tumor Segmentation from CT Scans with knowledge-based constraints

Nader H. Abdel-massieh, Mohiy M. Hadhoud, Khalid M. Amin
Faculty of Computers and Information
Menoufia University
Shibin Elkom, Menoufia, Egypt
nader.hana@ci.menofia.edu.eg, mmhadhoud@yahoo.com, kh.amin.0.0@gmail.com

***Abstract*—The liver is a common site for the occurrence of tumors. Automatic hepatic lesion segmentation is a crucial step for diagnosis and surgery planning. This paper presents a new fully automatic technique to segment the tumors 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 tumors as dark gray spots. After applying Gaussian smoothing, Isodata is used to threshold the tumor in the slice. In order to eliminate erroneous segmentation a discriminative rule based on diagnostic knowledge on liver cancer shape is applied. Finally, 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. Using MICCAI 2008 segmentation evaluation metrics, the novel proposed technique achieved 80.19 as a total score.**

Keywords-tumor 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 tumors 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 tumor segmentation method [2]. It firstly segments the liver, then; hepatic tumor 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 tumors. 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 tumors 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 tumors. 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 tumors. Chen and Metaxas [10] used Markov Random Field (MRF) estimation coupled with Deformable models for the segmentation of tumors. Lu et al. [11] also used the active contour with a manually specified initial

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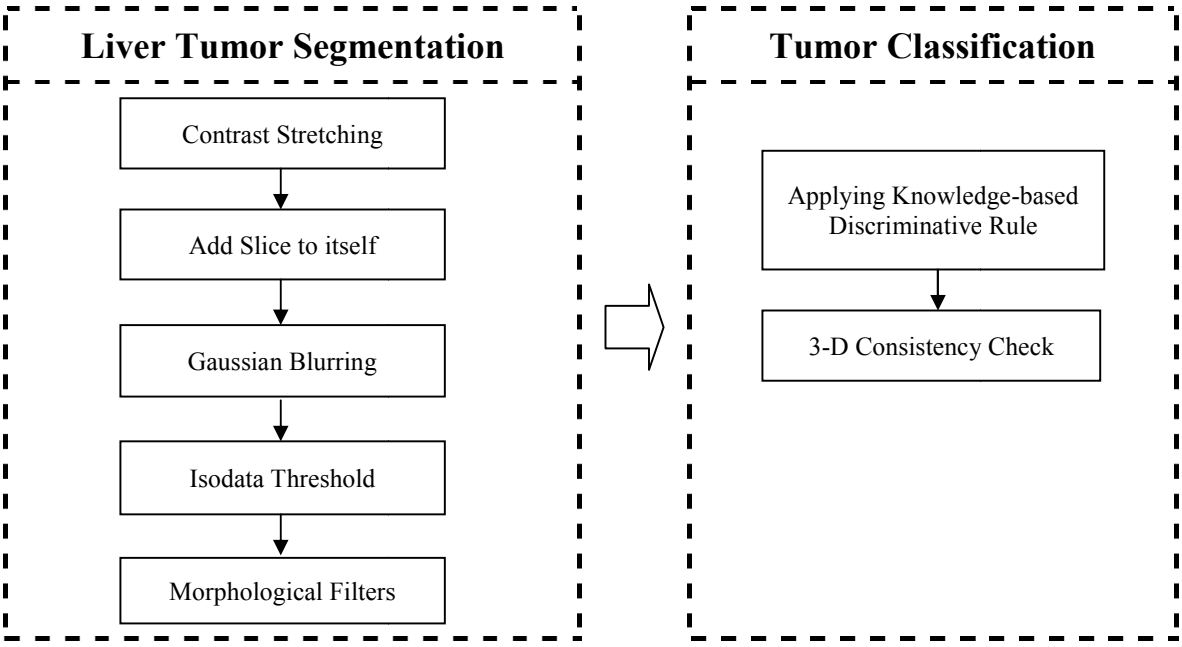


Figure 1. Block diagram of the proposed automatic technique for liver tumor detection

contour to obtain the tumor 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. Jianhua 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 tumors like knowledge-based constraints [19].

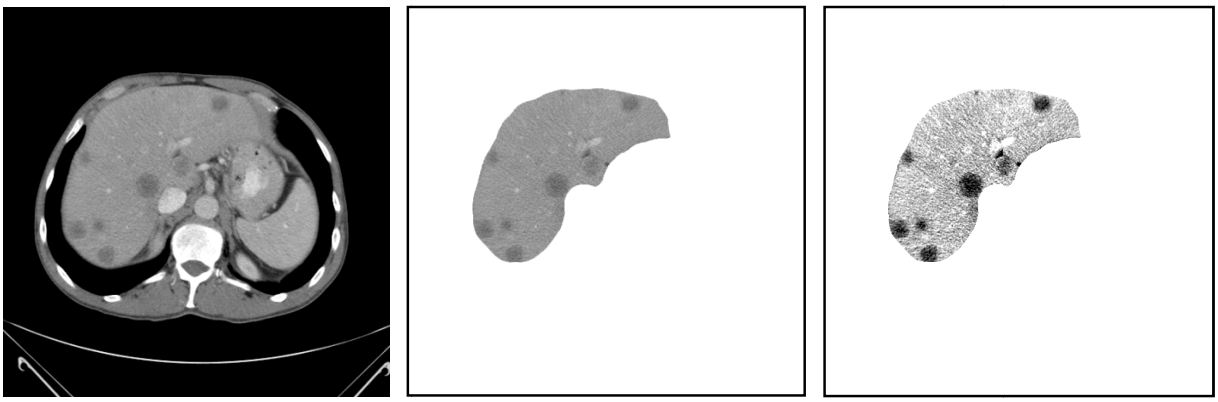
III. MATERIALS AND METHODS

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 tumors if existed and a blank background. Liver segmentation could be done manually, semi-automatically or automatically [20].

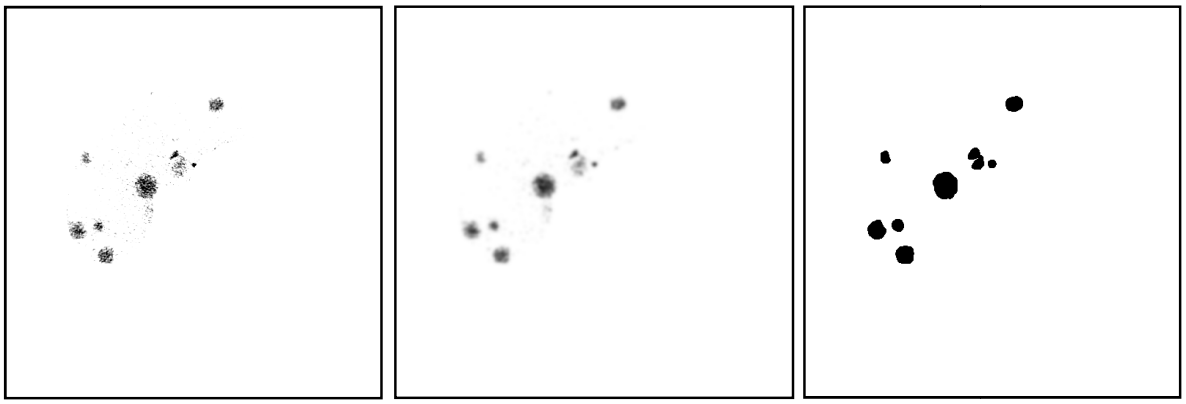
B. Tumor Detection

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 tumor tissue have similar gray levels.



(a) (b) (c)

Figure 2. (a) Original CT slice, (b) Segmented liver structure with tumors, (c) Contrast enhanced CT slice



(a) (b) (c)

Figure 3. (a) Result of adding contrast enhanced image to itself, (b) Gaussian smoothing to Addition Result, (c) Isodata threshold

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 tumors. 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):

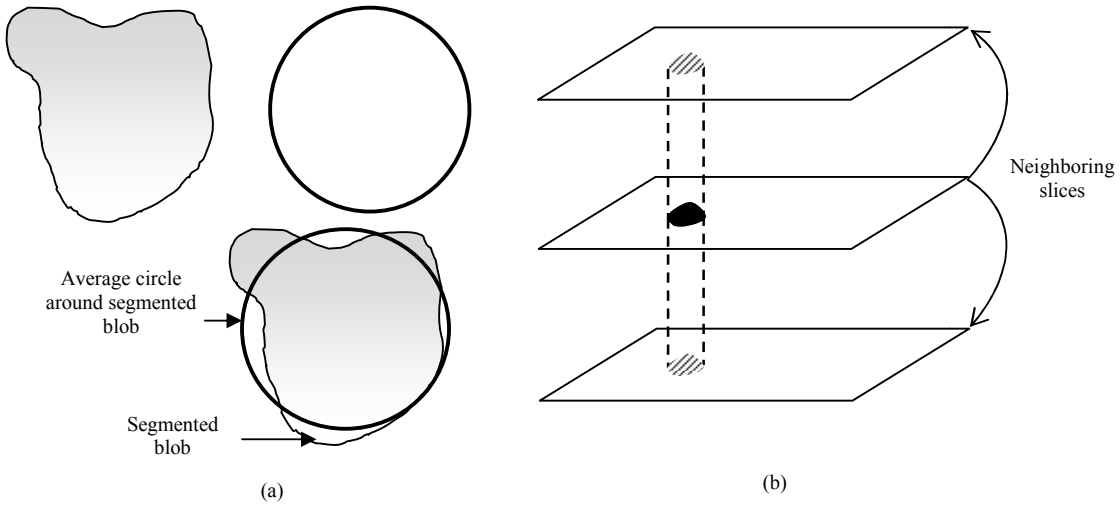
$$I' = \frac{I'_{max} - I'_{min}}{I_{max} - I_{min}} (I - I_{min}) + I'_{min} \qquad (1)$$

where, I and I' are the gray levels before and after transformation, respectively. I'_{max} and I'_{min} are the highest and lowest gray level after transformation, I_{max} and I_{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 tumor is now clear. The gray levels of liver parenchyma are higher than that of tumor tissue as shown in Fig. 2(c). The following step is to add the enhanced image to itself.

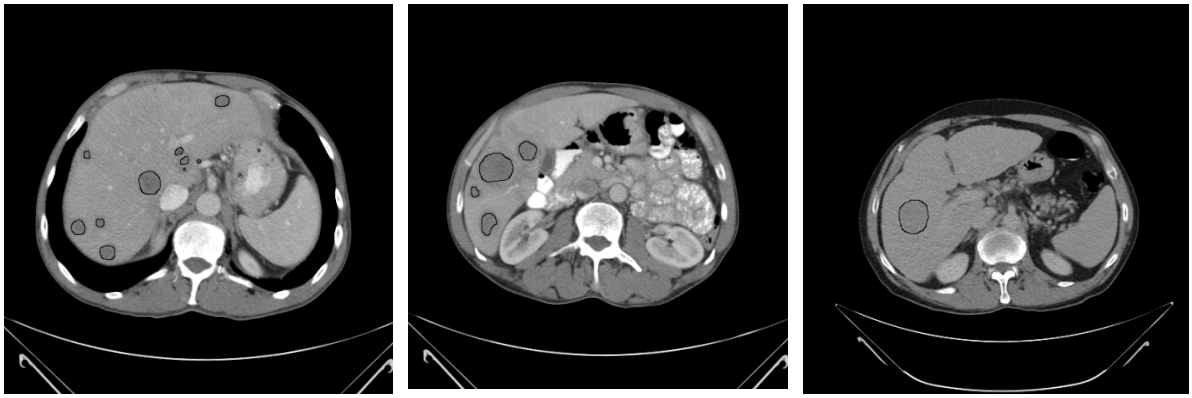
$$R(i,j) = I'(i,j) + I'(i,j) \qquad (2)$$

After contrast enhancement the pixels of liver parenchyma are brighter than before, 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 tumor tissue are dark with gray level in range from 15 to 40, and so when the value of each tumor pixel is added to itself according to formula (2), the result gray level will be range from 30 to 80 appearing as dark spots as shown in Fig. 3(a).



(a) (b)

Figure 4. (a) knowledge-based circularity rule, (b) 3D consistency check with neighboring slices



(a) (b) (c)

Figure 5. Examples of detection results, regions surrounded by the black line are the cancer lesions

The result of addition is image background as well liver tissue that appears as white background with some pepper noise, and tumors that appears as dark spots with range of gray levels. In order to remove the noise and make the region of tumor more homogeneous as in shown Fig. 3(b), 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 σ is the standard deviation of the Gaussian distribution.

$$G(x,y) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (3)$$

In order to turn the image into binary with tumor 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(c).

C. Tumor Classification

The final stage is to eliminate the erroneous segmented tumors. In order to differentiate between a true segmented tumor and CT image defects, a discriminative rule is applied based on medical knowledge that lesion forms a circle-like mass. The circularity of the segmented mass can be defined as in formula number (4):

$$\text{Circularity} = \frac{\text{area of intersection between blob and circle}}{\text{area of formed circle}} \quad (4)$$

The area of the segmented blob is calculated, and then a circle with the same area of the blob is formed. We want to center the circle inside the blob so that all or majority of the circle will be inside the segmented blob. Although there are some algorithms used to detect the center of a blob, yet the irregular shape of blobs may cause misleading result. A simple but effective technique is used; we centred the circle on each pixel of the blob and calculate the intersection between the circle and the blob, we scan with the circle till we get the largest intersection area; hence the center of the blob is obtained. If the circularity is more than 85%, the segmented blob will be considered as circle-like shape and so it is probably a tumor, as shown in Fig 4(a).

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 tumor and this slice has no interaction with other suspicious tumors in the neighbouring slices, this slice with a suspicious tumor will be considered erroneous and the selected blob will be disregarded, Fig 4(b).

TABLE I EVALUATION OF THE RESULTS BASED ON GENERAL SEGMENTATION METRICS

Dataset	Overlap Error %	Score	Volume Difference %	Score	Avg. Dist.	Score	RMS Dist.	Score	Max. Dist.	Score	Total Score
Dataset 1	17.00	86.86	11.15	88.43	0.47	88.35	1.31	81.83	17.00	57.50	78.64
Dataset 2	15.10	88.33	10.18	89.44	1.01	74.84	1.17	83.72	6.24	84.39	82.82
Dataset 3	19.18	85.00	18.74	80.56	1.16	70.98	1.21	83.14	8.19	79.52	79.66
Dataset 4	28.24	78.18	22.02	77.16	0.92	77.10	1.15	83.96	8.54	78.64	80.26
Dataset 5	31.06	76.00	16.00	83.40	1.01	74.81	1.27	82.36	9.40	76.51	77.42
Dataset 6	21.85	83.00	19.33	79.95	0.83	79.36	1.32	81.61	11.83	70.43	78.60
Dataset 7	13.60	89.00	8.92	90.74	0.37	90.68	1.05	85.46	13.60	66.00	82.79
Average	**20.86**	**83.77**	**15.19**	**84.24**	**0.82**	**79.45**	**1.21**	**83.15**	**10.69**	**73.28**	**80.19**

TABLE II. THE AVERAGE RESULTS OF PREVIOUS WORKS THAT USED SAME METRICS

Dataset	Overlap Error %	Score	Volume Difference %	Score	Avg. Dist.	Score	RMS Dist.	Score	Max. Dist.	Score	Total Score
Wong et al. [22]	39.4	70	24.2	75	2.2	49	3.02	59	12.69	68	64
Choudhary et al. [23]	32.14	75	22.58	77	1.77	56	2.40	67	9.29	77	70
Taieb et al. [24]	39.48	70	44.36	57	2.19	45	2.90	60	9.94	75	61
Schmidt et al. [25]	52.95	59	80.02	51	3.91	31	5.19	38	16.28	59	48
Nugroho et al. [26]	31.21	76	15.76	84	1.75	58	2.56	65	11.73	71	71
Shimizu et al. [27]	28.98	72	18.28	73	1.81	49	2.35	61	7.78	73	65
Stawiaski et al. [28]	29,49	77	23,87	78	1,50	62	2,07	71	8,29	79	73
Häme [29]	47.33	64	111.11	56	5.4	34	7.87	40	25.07	50	48
Moltz et al. [30]	30.55	76	25.32	74	1.55	61	2.20	69	9.13	77	72
Smeets et al. [17]	34.58	73	17.79	82	2.01	52	2.67	63	10.09	75	69
Zhou et al. [31]	30.02	77	19.31	80	1.52	62	2.18	70	10.52	74	72
Qi et al. [32]	42.10	68	43.01	62	2.76	37	3.94	52	16.93	63	56

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 tumor. The algorithm was implemented on java environment, a personal computer using a P4 (3 GHz) processor and a 2GB memory. The proposed hepatic tumor detection method was evaluated by comparing the automatically detected liver volumes to the ground truth, manually traced by experts.

Several metrics have been commonly used to evaluate the quality of segmentation. Evaluation of the algorithm was performed by comparing our segmentation results to the ground-truth using five metrics along with a scoring system[33]: 1) volumetric overlap; 2) relative absolute volume difference; 3) average symmetric absolute surface distance; 4) symmetric RMS surface distance, and; 5) maximum symmetric absolute surface distance. These five metrics were used during the liver tumor segmentation competition which was part of the workshop "3D Segmentation in the Clinic: A Grand Challenge II" at Medical Image Computing and Computer Assisted Intervention 2008 conference [34]. Table 1 shows the result of the proposed method applied on the acquired datasets.

V. DISCUSSION AND FUTURE WORKS

In the present study, we describe the steps of our new algorithm to automatically segment tumors 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. Comparing with the averages of other pervious works in table 2, the result shows that the algorithm achieves accurate detection for liver tumor with total score 79.

Datasets number 2 and 7 have the highest score; because both contains one big tumor appear in successive slices as shown in Fig. 5(c).

Dataset number 4 also has high score but not as datasets number 2 and 7, that is because although it also contains one tumor appear in successive slices, but this tumor is small; hence any difference between the manual and the automatic segmentation will be reflected as a noticeable variation in scoring of overlap error and volume difference.

Dataset number 5 contains multiple lesions spread over all the slices of the dataset as shown in Fig. 5(a), the total score is lower than the average score because of a false positive; that is considering a dark artifact in liver structure as a tumor; this artifact appears in two slices not sequential.

In the future, we will explore methods to reduce false positive cases by excluding possible artifacts that could be detected as tumors.

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