

Automatic Segmentation of Liver and Tumor for CAD of Liver

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Abstract— Computer aided diagnosis of liver tumors from abdominal Computer Tomography (CT) images requires segmentation and analysis of tumor. Automatic segmentation of tumor from CT images is difficult, due to the size, shape, position and presence of other objects with the same intensity present in the image. Therefore, it is necessary to segment the liver first so that tumor can then be segmented accurately from it. Liver and tumor segmentation can be performed on the CT image manually or semi automatically. In this paper, an approach for automatic segmentation of liver and tumor from CT images mainly used for computer-aided diagnosis of liver is proposed. The method uses region-growing, facilitated by pre and post processing functions for automatic segmentation of liver and Alternative Fuzzy C-Means (AFCM) algorithm for tumor segmentation. The effectiveness of the algorithm is evaluated by comparing automatic segmentation results to the manual segmentation results. Quantitative comparison shows a close correlation between the automatic and manual as well as high spatial overlap between the regions-of-interest (ROIs) generated by the two methods.

Index Terms—Computer Aided Diagnosis, Liver segmentation, Tumor Segmentation, Region Growing, Alternative FCM

I. INTRODUCTION

Liver diseases are considered life threatening and occur without pre-warning. Liver tumors are abnormal growths on the liver and can be benign or malignant. Benign tumors do not really cause harm to the health while malignant tumors can be fatal [1]. Computer Aided Diagnosis (CAD) which is based on computerized analysis of medical images, is used by radiologists as a “second opinion” in detecting tumors, assessing the extent of disease, and making diagnostic decisions. CAD for liver diseases consists of liver and

suspected region (tumor) segmentation, texture feature analysis and disease classification [2], [3]. Of all the steps, segmentation of liver and tumor is very important. For accurate tumor segmentation, the segmentation of liver from abdominal CT images is very essential. Automatic liver segmentation from CT images is an extremely challenging task, because of variations in shape, presence of neighboring structures with similar intensity, the variability of structures in the abdomen in general, the presence of tumors on boundaries and other abnormalities, the contrast material in the liver and variations in scanning protocols.

Several approaches have been used for segmentation of liver from CT image datasets. Some of them are semi-automatic and some of them are fully automatic. Semi-automatic methods require user intervention to outline the region of interest before leaving to the computer for processing. The various methods used for liver segmentation are, Intensity based threshold and Multimodal thresholds [4]-[7], Statistical based model discrimination of the liver [8]-[9], the Level-set family [10]-[11], Active contour [12], Snake model [13]-[14] and Fuzzy C Means (FCM) clustering [15] are widely used for tumor segmentation. Most of these methods are time consuming and could not respond identically to different patients. They usually produce over segmentation and also give unsatisfied results for the slices with fuzzy liver boundary. The lesion segmentation is inaccurate for different volume and shapes.

Therefore, to address the above problems and for an efficient CAD of liver diseases, an automatic liver and tumor segmentation algorithm from abdominal CT image is proposed. The algorithm uses the combination of intensity analysis, region-growing, pre and post processing steps for automatic segmentation of liver

and Alternative FCM clustering for automatic lesion segmentation.

The rest of this paper is organized as follow. Section II describes the automatic segmentation of liver. Section III describes the automatic segmentation of tumor, Section IV presents the results along with the discussion and finally Section V concludes the work.

II. AUTOMATIC LIVER SEGMENTATION

A. Preprocessing

For accurate and fast liver segmentation the abdominal CT image is pre-processed. The granular noise present in the CT slice image is reduced by convolving with a median filter via 3×3 pixel square kernel across the entire image. The prior knowledge of the liver on abdominal CT image such as shape, location, and intensity value is used to identify the useful area of the image for fast and accurate liver segmentation. Based on the prior knowledge of location, the right bottom region of the image is discarded as this region normally does not contain the liver. This reduces the search area and computational efforts for identifying the initial liver boundary. The histogram of the CT image is drawn and analyzed. In the histogram, the highest pitch, excluding the background and bone values represent the middle intensity of the liver region. The rough estimation of the minimal and maximal intensity of liver pixels is calculated from the histogram, which makes it possible to locate any region inside the liver automatically. The liver pixels within the intensity range estimated are extracted and the resulting image is called the simplified image. The histogram of the abdominal CT image with the liver area marked is shown in "Fig. 1,".

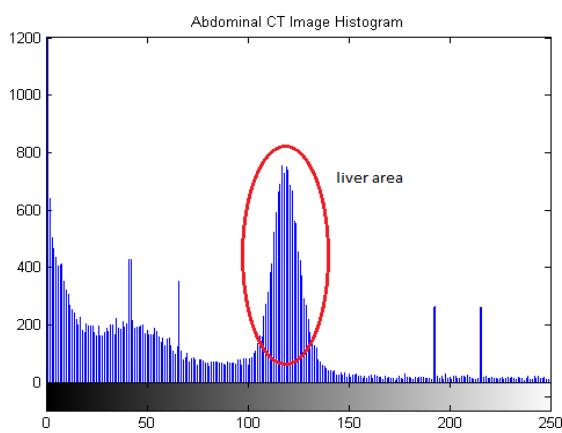


Figure 1. Histogram of Abdominal CT image.

The simplified liver likelihood region usually consists of several other structures, with the intensity similar to the intensity of the liver. These small structures are removed by morphological erosion. A sphere with large radius is used for erosion since the liver has the largest compact volume in the abdomen. The largest connected region of the eroded image is

considered for region growing segmentation. Although, the size of this region may vary among different cases, this method provides a reliable set of liver pixels in all cases.

B. Region Growing

Region Growing (RG) groups the pixels or sub regions into larger regions based on some predefined criteria. [16]- [18]. The basic approach is to start with a seed point and from this grow regions by appending the neighboring pixels to each seed point that have properties similar to the seed. Based on this rationale, region growing can be processed by choosing the right "seed" point, selecting a set of similarity criteria and setting up a stopping rule. Region growing methods often give very good segmentations. "Fig. 2," shows the region growing process from a seed point.

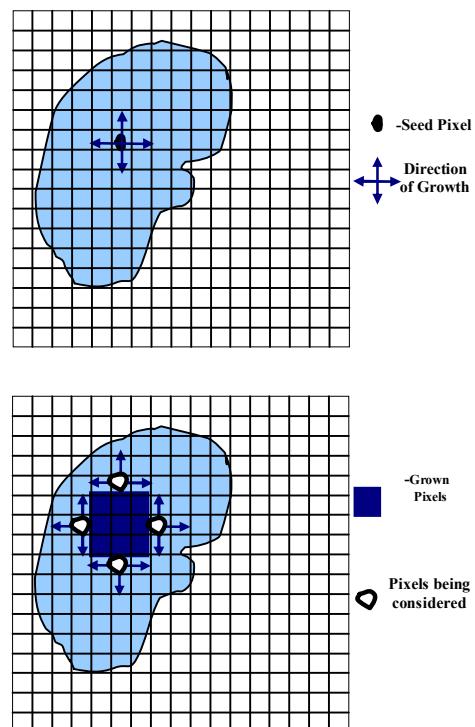


Figure 2. Region Growing.

A seed point is the starting point for region growing and hence its selection is very important for the final result. If a seed point is selected outside the region of interest, the final segmentation would be incorrect. Most of the region growing methods require the seed point to be selected manually in advance. In order to make the region growing segmentation fully automatic, it is necessary to develop an automatic and accurate seed point selection method. For this, a novel method of finding the seed point is proposed in this work. The centroid of the largest connected region of the eroded image is determined and the coordinates of the centroid point acts as the initial seed point for region growing. If the centroid falls on tumor or any other dark objects, then the region growing may not be accurate because,

the intensity of the seed point will not lie in the intensity range of the liver. So, if the seed point has an intensity value outside the intensity range of the liver, a pixel with minimum distance from the centroid, having intensity within the above range is selected as the seed point.

The region growing process for liver segmentation starts from the seed point thus selected. The 4-connected neighborhoods of the seed point region are determined. The similarity measure of each neighborhood pixel with the seed point region is calculated. The similarity measure $\delta(x)$ is the difference between the pixel's gray level value and the mean intensity of the region grown as in equation (1).

$$\delta(x) = |g(x) - \text{mean}[g(y)]| \quad (1)$$

where $g(x)$ is the gray level value of the current pixel and $\text{mean}(g(y))$ is the mean of the already grown region. The pixel with the minimum distance measured this way is added to the grown region. This process continues iteratively by comparing all unallocated neighboring adjacent pixels of the grown region using the similarity measure. This process stops when the intensity difference between region mean and new pixel becomes larger than a certain threshold (τ). The threshold value is selected as minimal as possible.

C. Post Processing

The region growing result may contain holes and connected neighbor tissues. The morphological operations can be used to remove certain unwanted regions that are inevitably present in the segmentation results after using the region growing algorithm. Binary morphological operations have been proved capable of deleting small disconnected regions, filling cavities and smoothening the region-of-interest. It should be ensured that the structuring element chosen does not eliminate too many desirable objects, or retain too many undesirable ones. Sometimes it might be difficult to fulfill these conditions. Here a circular element with radius 3 is used which is selected as a compromise between the noise suppression performance and preservation of details. The larger the radius of the element, the more will be the noise suppressed and the more details are lost and hence the former structuring element is used. The opening procedure serves to smoothen the contours of the object, break narrow isthmuses, and eliminate thin protrusions and small objects. The resulting image is complemented and multiplied with the original CT image to get the segmented liver.

III. TUMOR SEGMENTATION

The segmentation of tumor involves partitioning the image space into different cluster regions with similar intensity image values. The FCM clustering algorithm has been widely used and applied in tumor

segmentation. However, the FCM algorithm is not very effective with noisy or outlying points and with clusters of different volume and unequal sample sizes. To overcome these problems, an alternative FCM clustering algorithm [19] is used. AFCM replaces the Euclidean metric $d^2(x, y) = \|x-y\|^2$ used in FCM by a new distance function defined in equation (2) as,

$$d^2(x, y) = 1 - \exp(-\beta \|x - y\|^2) \quad (2)$$

AFCM is a segmentation algorithm that is based on clustering similar pixels in an iterative way, where the cluster centers are adjusted for all iterations. Let the vector $X = (x_1, x_2 \dots x_n)$ be the segmented liver image which is to be partitioned in to c clusters. An objective function measures the overall dissimilarity within the clusters. By minimizing the objective function the optimal partition is obtained. The AFCM algorithm minimizes the objective function for the partitioning or segmentation of X and is given below,

$$J_{AFCM}(\mu, a) = \sum_{i=1}^c \sum_{j=1}^n (\mu_{ij})^m \{1 - \exp(-\beta \|x_j - a_i\|^2)\}$$

where n is the number of samples in the vector X , c is the number of clusters ($1 \leq c \leq n$), μ_{ij} is the element of the partition matrix U of size $(c \times n)$ containing the membership, m is a constant that defines the degree of fuzziness of the resulting partitions and β is a parameter greater than zero

The objective function can reach global minimum when pixels nearby the centroid of corresponding clusters are assigned higher membership values, while lower membership values are assigned to pixels away from the centroid. Here, the membership value is proportional to the probability that a pixel belongs to a specific cluster which is dependent only on the distance between the image pixel and each independent cluster center. The membership functions and the cluster centers are updated by

$$a_i = \frac{\sum_{j=1}^n (\mu_{ij})^m \exp(-\beta \|x_j - a_i\|^2) x_j}{\sum_{j=1}^n (\mu_{ij})^m \exp(-\beta \|x_j - a_i\|^2)} \quad (3)$$

$$\mu_{ij} = \frac{[1/(1 - \exp(-\beta \|x_j - a_i\|^2))]^{1/(m-1)}}{\sum_{k=1}^c [1/(1 - \exp(-\beta \|x_j - a_k\|^2))]^{1/(m-1)}} \quad (4)$$

where $i=1 \dots c$; $j=1 \dots n$, the parameter β can be estimated by the inverse of the sample variance as

$$\beta = \left(\sum_{j=1}^n \|x_j - \bar{x}\|^2 / n \right)^{-1}, \bar{x} = \sum_{j=1}^n x_j / n \quad (5)$$

The clustering initialization procedure aims to establish good starting point for the clustering centers. In this work the initial clustering centers are computed using the equation (6), which is used to fix up the cluster center for standard FCM algorithm.

$$a_i = \frac{\sum_{j=1}^n (\mu_{ij})^m x_j}{\sum_{j=1}^n (\mu_{ij})^m}, \quad i=1, \dots, c \quad (6)$$

The AFCM Algorithm is given below:

- S1: Fix $m > 1$ and $2 \leq c \leq n$. Set $k = 1$.
 Give any fixed $\epsilon > 0$ and an initial fuzzy C-partition $\mu^0 = \{\mu_1^{(0)}, \dots, \mu_c^{(0)}\}$.
 S2: Estimate parameter β using (5).
 S3: Compute the initial center $a^{(k-1)}$ using (6);
 S4: Compute $a^{(k)}$ with $\mu^{(k-1)}$ and $a^{(k-1)}$ using (3)
 S5: Update μ^k with $a^{(k)}$ using (4).
 S6: Compare μ^k to $\mu^{(k-1)}$ is a convenient norm
 $\|\mu^k - \mu^{(k-1)}\|$
 IF $\|\mu^k - \mu^{(k-1)}\| < \epsilon$, THEN stop
 ELSE $k=k+1$ and return to S4.

The tumor is segmented from the segmented liver using AFCM method. The value of m chosen is 2 because; the updated fuzzy membership value is proportional to the square of the inverse distance from a specific segment location to each cluster's centroid. The value of $\epsilon=0.0001$ and the number of clusters $c=3$.

The pixels of the tumor image are divided into three clusters according to intensity. The pixels in the background (low intensity) are included in the first cluster. The second cluster includes pixels in the tumor region (medium intensity). The pixels in the liver region other than tumor (high intensity) are included in the third cluster.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

The experiment was performed on several samples with various shapes and irregular texture of several patients. All of the used samples are of size 512×512 and slice thickness of 5mm. The process of liver and tumor segmentation from the abdominal CT images for two different patients is shown in "Fig. 3" and "Fig. 4". "Fig. 3A" and "Fig. 4A" show the simplified image created by analyzing the histogram. It is seen that many other structures and tissues are removed in the simplified image. However, the unconnected or small tissues remain. To eliminate these objects and retain the liver region, the morphological erosion is performed. The centroid of the liver region is found and the position of the centroid on the eroded image is shown with a red hair cross in "Fig. 3B" and "Fig. 4B".

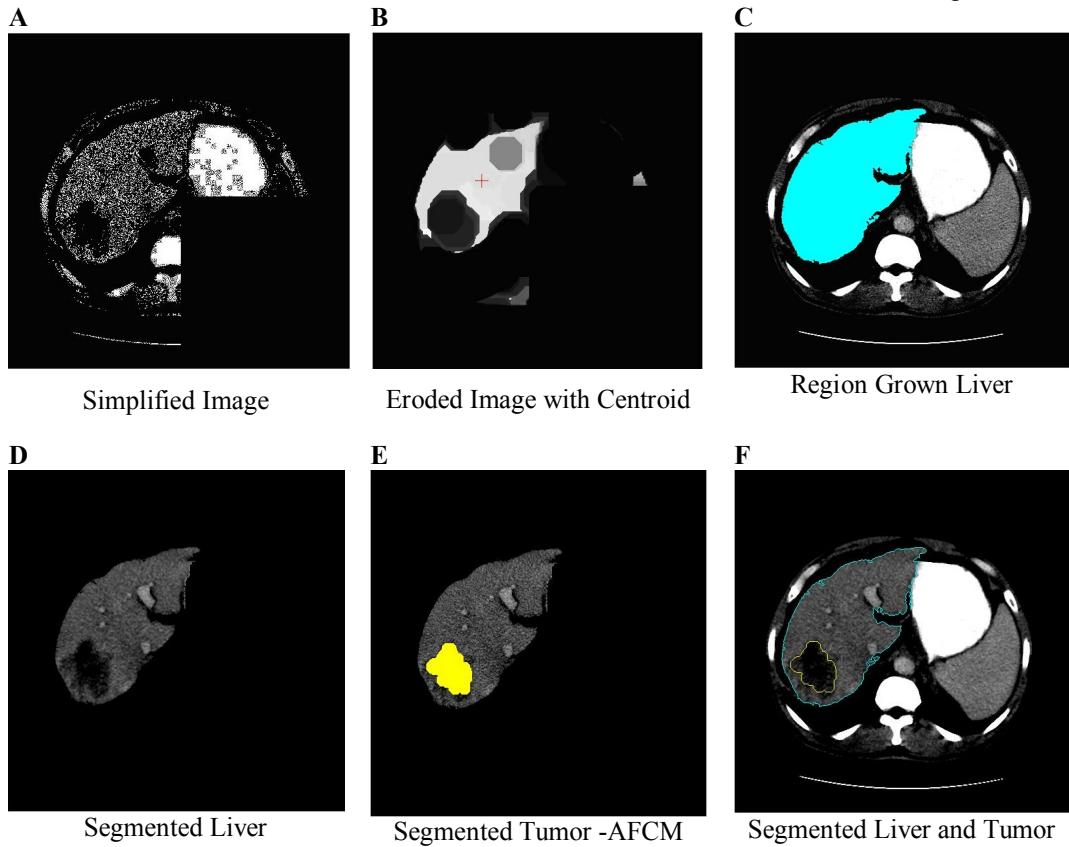


Figure 3. Experiment of Patient 1.

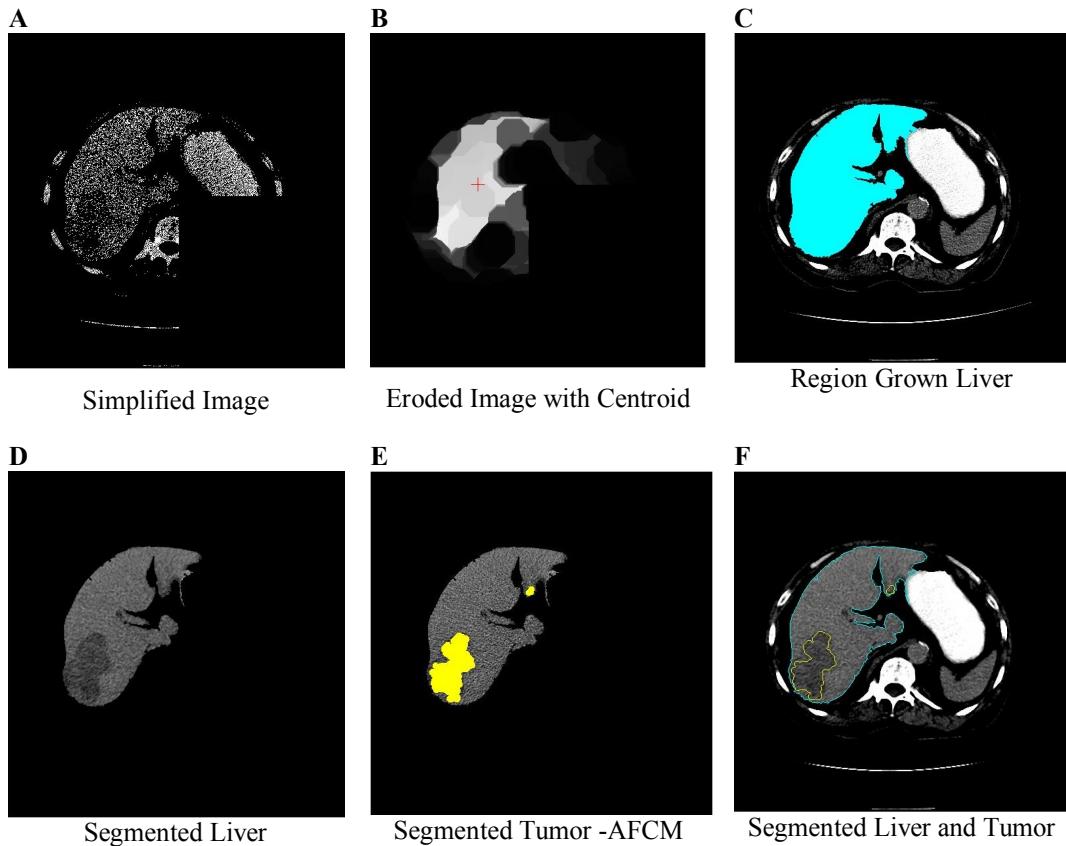


Figure 4. Experiment of Patient 2.

The co-ordinates of the centroid acts as the seed point for automatic region growing. The region grown liver is shown in "Fig. 3C" and "Fig. 4C". The segmented liver using the proposed method is shown in "Fig. 3D" and "Fig. 4D". The segmented tumor using AFCM is shown in "Fig. 3E" and "Fig. 4E". "Fig. 3F", "Fig. 4F", shows the segmented liver and tumor on the original CT image.

The results of the proposed algorithm were evaluated by comparing with the results of manual segmentation done by experts. Table I lists the segmentation results of liver from manual and automatic segmentation for 10 test datasets of continuous slices. Table II lists the segmentation results of tumor.

The validity of the segmented liver and tumor results are evaluated using quantitative comparison with manually segmented pixels. The above comparison is based on two criteria, "Coefficient of Similarity" and "Spatial Overlap" [20] as defined below:

Coefficient of Similarity:

$$\varepsilon = 1 - \frac{|L_{\text{manual}} - L_{\text{automatic}}|}{L_{\text{manual}}}$$

Spatial Overlap:

$$\eta = \frac{2 * [L_{\text{manual}} \cap L_{\text{automatic}}]}{L_{\text{manual}} + L_{\text{automatic}}}$$

where, L_{manual} and $L_{\text{automatic}}$ are the areas of the manually and automatically segmented liver and tumor respectively.

For the 10 tested cases listed in Table I and II, the mean and standard deviation of the coefficient of similarity between the manual and automatic extractions for liver is found to be 0.9582 and 0.0126 and for tumor it is 0.8983 and 0.0496 .

The mean and standard deviation of overlap for the 10 cases of liver are 0.9758 and 0.0050, and for tumor it is 0.9174 and 0.0293 respectively. Spatial overlap approach is more sensitive to small unmatched segmentation errors and is more accurate than that of using coefficient of similarity because it takes into account the spatial properties of segmented regions derived by the two methods. The spatial overlap measure is also more sensitive to differences between the two methods, since both denominator and numerator change with increasing or decreasing overlap. For the 10 cases, the best overlap metric is 0.9842 and the worst is 0.9677 for liver and the best overlap metric is 0.9453 and worst is 0.8484 for the segmented tumor. The distribution of the number of pixels segmented by manual and automatic methods for the 10 cases is shown in "Fig. 5" for liver and for tumor in "Fig. 6".

To elucidate the cause of differences between the manual and automated segmentation method, images showing the visual overlap of the two extractions superimposed upon the underlying original CT image are created. "Fig. 7" and "Fig. 8" show one such

composite image. Blue pixels represent the spatial intersection of the manual and automatic methods; green pixels represent the automatic pixels missed by the algorithm (false negative); red represents the pixels wrongly classified as liver as determined from the manual tracing (false positive). It is noticeable that most segmentation differences occur at the boundary of ROIs. On the basis of the spatial overlap, the automatic algorithm extraction is shown to be highly comparable to the manual extraction method.

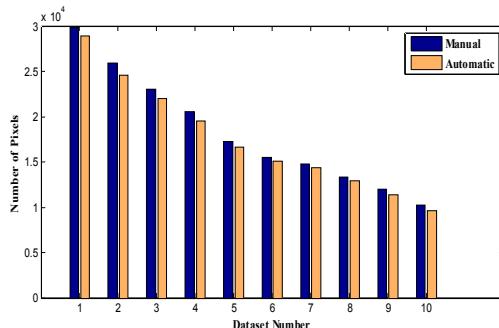


Figure 5. Distribution of the number of segmented liver pixels.

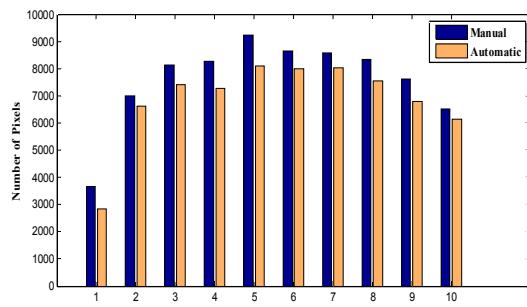


Figure 6. Distribution of the number of segmented tumor pixels.

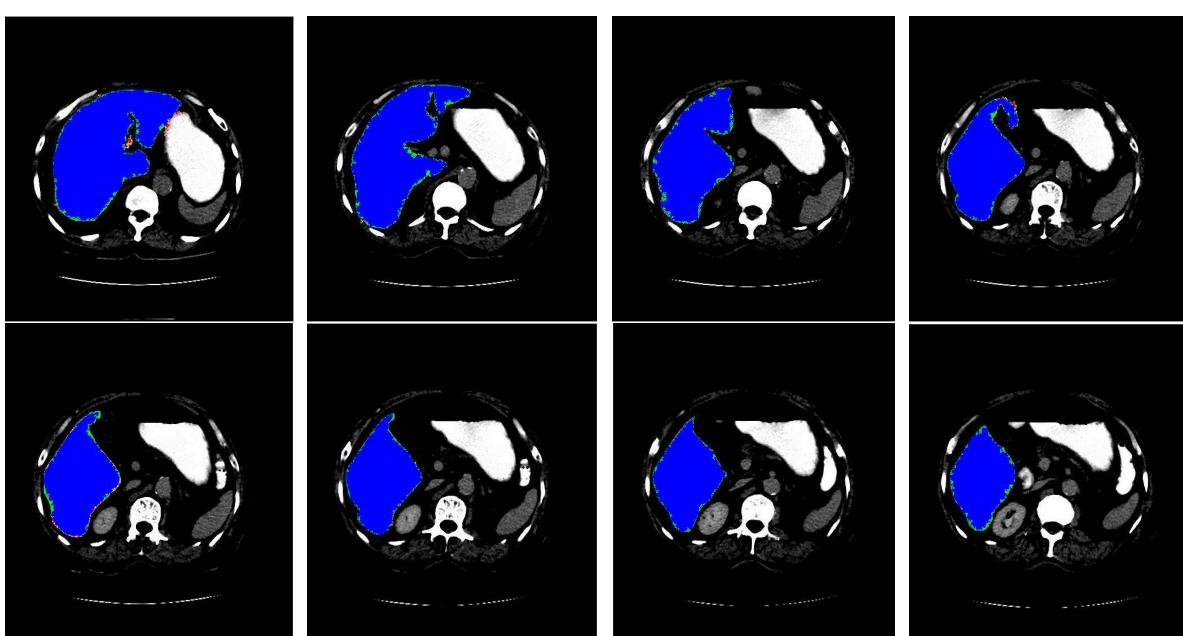


Figure 7. Difference analysis of manual and automatic segmented liver.

Table 1: Liver Segmentation Results

| Data | Manual | RG | ε | η | FN | FP |
|------|--------|-------|---------------|--------|------|-----|
| 1 | 29879 | 28961 | 0.9693 | 0.9776 | 1119 | 201 |
| 2 | 25879 | 24619 | 0.9513 | 0.9746 | 1272 | 12 |
| 3 | 23071 | 21970 | 0.9523 | 0.9755 | 1102 | 1 |
| 4 | 20607 | 19582 | 0.9503 | 0.9744 | 1026 | 1 |
| 5 | 17262 | 16669 | 0.9656 | 0.9786 | 659 | 66 |
| 6 | 15516 | 15127 | 0.9749 | 0.9720 | 623 | 234 |
| 7 | 14808 | 14384 | 0.9714 | 0.9842 | 442 | 18 |
| 8 | 13353 | 12888 | 0.9652 | 0.9821 | 468 | 3 |
| 9 | 12036 | 11367 | 0.9444 | 0.9713 | 670 | 1 |
| 10 | 10238 | 9601 | 0.9378 | 0.9677 | 639 | 2 |

Table 2: Tumor Segmentation Results

| Data | Manual | AFCM | ε | η | FN | FP |
|------|--------|------|---------------|--------|------|-----|
| 1 | 3668 | 2841 | 0.7745 | 0.8484 | 907 | 80 |
| 2 | 7007 | 6598 | 0.9416 | 0.8911 | 945 | 536 |
| 3 | 8124 | 7399 | 0.9108 | 0.9235 | 956 | 231 |
| 4 | 8263 | 7271 | 0.8799 | 0.9103 | 1193 | 201 |
| 5 | 9226 | 8090 | 0.8769 | 0.9146 | 1307 | 171 |
| 6 | 8630 | 7980 | 0.9247 | 0.9275 | 927 | 277 |
| 7 | 8581 | 8008 | 0.9332 | 0.9370 | 809 | 236 |
| 8 | 8333 | 7557 | 0.9069 | 0.9407 | 859 | 83 |
| 9 | 7627 | 6802 | 0.8918 | 0.9360 | 874 | 49 |
| 10 | 6512 | 6138 | 0.9426 | 0.9453 | 533 | 159 |

The experimental results were obtained from 10 datasets. However the work can be extended to more datasets irrespective of differences in gender composition or age differences and thus generalized.

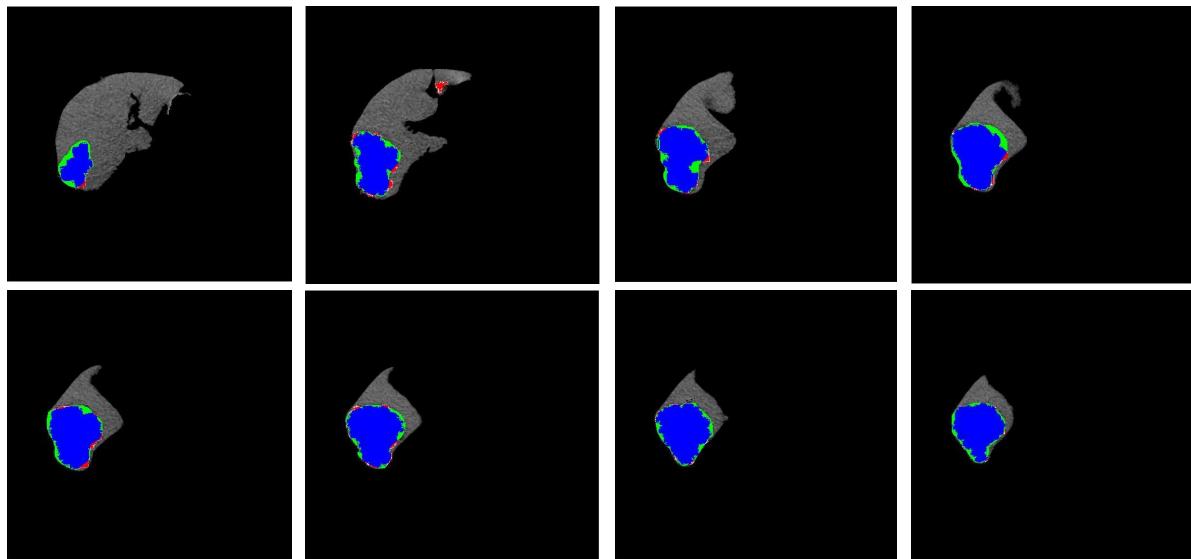


Figure 8. Difference analysis of manual and automatic segmented tumor.

V. CONCLUSION

An automatic segmentation algorithm for segmenting liver and tumor from abdominal CT images is proposed in this paper. The proposed algorithm uses thresholding based on analysis of intensity distribution and morphological erosion to simplify the image which helps to decrease the computation time and efforts by removing the regions of other structures and tissues. The liver is segmented using region growing method that starts from a seed point automatically detected and efficiently close around the vessels and tumors. The tumor segmentation from the segmented liver is done using the Alternative FCM clustering. The final results are compared to manually segmented results. The results show high spatial overlap between the ROIs generated from the two methods. The new algorithm developed effectively segments liver and tumor from CT images for computer aided diagnosis of liver.

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- Getting submissions, arranging review process, making decisions, and carrying out all correspondence with the authors. Authors should be informed the Instructions for Authors.
- Providing us the completed and approved final versions of the papers formatted in the Journal's style, together with all authors' contact information.
- Writing a one- or two-page introductory editorial to be published in the Special Issue.

Special Issue for a Conference/Workshop

A special issue for a Conference/Workshop is usually released in association with the committee members of the Conference/Workshop like general chairs and/or program chairs who are appointed as the Guest Editors of the Special Issue. Special Issue for a Conference/Workshop is typically made of 10 to 15 papers, with each paper 8 to 12 pages of length.

Guest Editors are involved in the following steps in guest-editing a Special Issue based on a Conference/Workshop:

- Selecting a Title for the Special Issue, e.g. "Special Issue: Selected Best Papers of XYZ Conference".
- Sending us a formal "Letter of Intent" for the Special Issue.
- Creating a "Call for Papers" for the Special Issue, posting it on the conference web site, and publicizing it to the conference attendees. Information about the Journal and Academy Publisher can be included in the Call for Papers.
- Establishing criteria for paper selection/rejections. The papers can be nominated based on multiple criteria, e.g. rank in review process plus the evaluation from the Session Chairs and the feedback from the Conference attendees.
- Selecting and inviting submissions, arranging review process, making decisions, and carrying out all correspondence with the authors. Authors should be informed the Author Instructions. Usually, the Proceedings manuscripts should be expanded and enhanced.
- Providing us the completed and approved final versions of the papers formatted in the Journal's style, together with all authors' contact information.
- Writing a one- or two-page introductory editorial to be published in the Special Issue.

More information is available on the web site at <http://www.academypublisher.com/jait/>.