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Modified Density-Based Data Clustering for Interactive Liver Segmentation

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***Abstract*—Identifying the liver region from abdominal Computed Tomography (CT) scans is still a challenging task due to the complexity of the liver's anatomy, similar intensity with adjacent organs and presence of pathologies. In this paper we propose a system which consists of three stages: preprocessing, segmentation and post processing. In the first stage, the input image is smoothed using anisotropic diffusion filter. In the second stage, we introduce a modified density-based clustering algorithm, DBSCAN, to segment the liver. Finally, morphological operations are performed to enhance the segmentation results. The proposed system is evaluated on 3Dircadb1 database which is publicly available. The experimental results show that the proposed system is effective for accurate detection of the liver surface in comparison with other related works in the literature.**

***Index Terms*—DBSCAN, liver segmentation, density-based clustering, CT scan**

I. INTRODUCTION

Liver segmentation from computerized tomography (CT) scans is a crucial and primary step for computer-aided liver disease diagnosis and surgical planning. In traditional clinical practice, however, liver tissue is usually delineated manually by radiological experts, which is time-consuming and suffers from human errors. Therefore, semi-automatic and automatic liver segmentation based on CT images for precise segmentation of liver tissue have attracted enormous research attention.

Liver segmentation is still a challenging task due to the following reasons. First, liver has large anatomical variation from different health individuals both in shape and size. Second, Liver tissue has to be separated from adjacent organs like heart and stomach which share similar gray values and fuzzy boundaries. Furthermore, due to the patient movements, spatial averaging, reconstruction artifacts and beam hardening, low contrast and blurry edges are caused in the CT images. Also, pathological abnormalities like tumors can be led to misclassification of the tumor as non-liver tissue because of the considerable intensity difference between the tumor and the liver.

In the last few decades, various approaches have been proposed to segment the liver from abdominal CT images. A comprehensive review of different algorithms including detailed analysis of their advantages and drawbacks [1] and a complete comparison of various approaches based on the public datasets of the Segmentation of the Liver Competition 2007 (SLIVER07) have been presented [2].

Existing liver segmentation approaches can be roughly classified as either image-based or model-based approaches. The first group is primarily based on image information such as thresholding [3] and region growing [4]. Their major drawback is the tendency to leak into adjacent organs which share similar gray values with the liver tissue. Therefore, for accurate and robust segmentation, local and global liver shape prior knowledge are employed in model-based methods, such as graph-cuts [5], [6], active shape models (ASMs) [7], [8] deformable models [9] and probabilistic atlases [10], [11]. Success of Model-based techniques depends on using proper training datasets. Limited number of training images can definitely not cover all the liver shape variations in different health individuals. Therefore, these methods often fail when the liver is in a complex shape.

In this paper, an interactive system, based on density-based clustering which works on the real dataset information, has been proposed to segment the liver tissue from CT images. To the best of our knowledge, the proposed system has not been suggested for liver segmentation so far. Density-based clustering algorithms have attracted attention because of their ability to recognize arbitrary clusters while keeping spatial adjacency of data points. Furthermore, these algorithms require fewer parameters at the start of the process than other comparable methods. In each cluster we have a typical density of points which is noticeably higher than outside of the cluster. The clustering algorithm DBSCAN (Density Based Spatial Clustering of Applications with Noise), which relies on a density-based notion of clusters, is modified for liver segmentation.

The remainder of the paper is organized as follows; Section 2 describes the proposed system. In Section 3 we present the obtained results in this approach and Section 4 concludes the work.

II. METHODOLOGY

The block diagram of the proposed system which consists of three stages: preprocessing, segmentation and postprocessing, is shown in Fig. 1.

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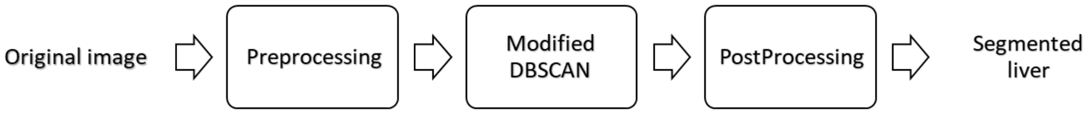

Figure 1. The block diagram of the proposed system

A. Preprocessing

Typically, presence of noise in medical images negatively affects the image contrast. Consequently, liver extraction without denoising may not have satisfactory results since the intensity distribution of the liver is irregular due to noise. An anisotropic diffusion filter [12] was employed to reduce the effect of noise while preserving the edges and fine details of the organs and tissues.

B. DBSCAN Algorithm

There are various data clustering algorithms including hierarchical, nearest neighbor, fuzzy, density-based, grid-based etc. In this work we apply a modified density-based clustering method to segment the liver tissue. Here we briefly present the DBSCAN algorithm. DBSCAN is a density-based clustering algorithm that is designed to recognize clusters of arbitrary shapes as well as identifying noise points in a spatial data set [13]. It was successfully used for synthetic dataset as well as earth science, and protein dataset [13], [14].

The algorithm has two main parameters: the radius of the cluster (Eps) and minimum required points inside the cluster (MinPts).

When the two parameters Eps and MinPts are determined, DBSCAN starts to cluster data points from an arbitrary point. The theoretical details of the DBSCAN algorithm is presented in [13].

Our novelty is using the Gaussian function for the distance measure between the points instead of the common Euclidean distance function. The Gaussian function is chosen because it better fits the liver histogram. The symmetric Gaussian function depends on two parameters standard deviation (σ) and mean (c) as given by

$$f(x;\sigma,c) = e^{-\frac{(x-c)^2}{2\sigma^2}} \tag{1}$$

The required parameters are also calculated according to the Gaussian curve fitted to the liver histogram.

The steps of DBSCAN clustering algorithm is summarized in Fig. 2 [17]-[20].

C. Postprocessing

Morphological operations are important in the digital image processing, since that can rigorously quantify many aspects of the geometrical structure of the way that agrees with the human intuition and perception [15], [16]. Therefore, morphological processing was performed to remove existing non-liver pixels or holes which may have occurred due to similar intensity. A closing process followed by a dilation process was performed to reach this aim.

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Function DBSCAN(Dataset D, Eps, MinPts)
1: Select an arbitrary object P in D;
2: Retrieve all objects density-reachable from P by arbitrary/random Eps and MinPts values;
3: if P is a core object then a cluster is formed;
4: if P is a border object then no objects are density reachable from P and DBSCAN visit the next object of the data set;
5: else assign P to noise object;
6: Continue the process (from step 1) until all of the objects have been processed.
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Figure 2. DBSCAN algorithm

III. RESULTS

We evaluate the performance of the proposed system on 3Dircadb1 database consists of CT scans with corresponding ground truth segmentation. Segmentation results and the evaluation criteria are reported in Table I. For evaluation purposes, we use following criteria:

$$\text{Volumetric Overlap Error} = 1 - \left(\frac{V_{seg} \cap V_m}{V_{seg} \cup V_m}\right) \times 100 \tag{2}$$

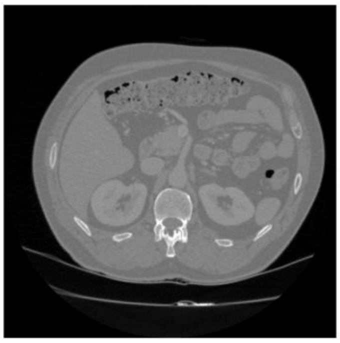
$$\text{Dice} = \frac{2TP}{2TP + FN + FP} \tag{3}$$

where:
TP: True Positive
TN: True Negative
FP: False Positive
FN: False Negative
V_{seg}: Segmented volume by the algorithm
V_m: Segmented volume by the experts

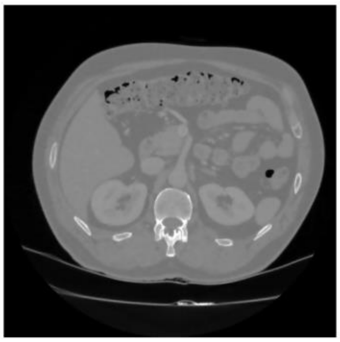
Table I shows the quantitative results of the liver segmentation and provide a fair comparison with three state-of-the-art interactive model-based methods based on the 3Dircadb1 database. These results show the acceptable efficiency of our proposed system and indicate that DBSCAN clustering method can achieve higher precision segmentation. Furthermore, user interaction is only required in specifying seed points inside the liver region which is considered as low user interaction in comparison with other related interactive systems [13]. To provide a visual sense, the segmetation results on a CT slice is shown in Fig. 3.

TABLE I. QUANTITATIVE COMPARATIVE RESULTS BETWEEN OUR PROPOSED METHOD AND THREE MODEL-BASED LIVER SEGMENTATION METHODS BASED ON THE 3DIRCADB1 DATABASE

Methods	**(VOE%)**	**Dice**
Erdt *et al*. [20]	10.34	N/A
Chung *et al*. [19]	12.99	N/A
Shi *et al*. [7]	8.74	N/A
The proposed method	8.51	95.48



(a)



(b)

(c)

(d)

(e)

Figure 3. Result of the proposed system on a CT slice. (a) original image (b) denoised image (c) segmented liver (d) postprocessed image (e) ground truth

IV. CONCLUSION

An interactive system for liver segmentation was proposed. The original CT images were smoothed using anisotropic diffusion filter. Then the modified DBSCAN algorithm was applied to segment the liver tissue. Finally, morphological operators have been set and employed to get better segmented results. The proposed system was examined on abdominal CT scans to segment the liver tissue. The performance of the proposed system was evaluated on 3Dircadb1 database and the segmented images were compared with the images segmented by experts. The experimental results are promising and showed that the proposed system can segment the liver effectively and accurately.

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