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Liver parenchyma segmentation by FCM-based confidence connected region growing method

Sun Yongxiong[1,a], Huang Liping[1,b], Liu Lipeng[1] ,Guan Tiejun[2],Huang Qiuyang[1]

[1].College of Computer Science and Technology, Jilin University, Changchun 130012,China

.[2] Tumor Hospital of Jilin Province, Changchun 130012,China

[a]sunyx@jlu.edu.cn, [b]huangliping5727@163.com

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Abstract:A FCM-based segmentation algorithm is proposed in this paper to improve the accuracy and efficiency of liver parenchyma segmentation. The proposed segmentation method consists of four steps as follows:First,we characterized the gray distribution of the unfiltered image. Second, combined with the Otsu algorithm and associated with a cropped liver image, we defined a gray interval as the liver's intersity range. Third, The fuzzy c-means clustering algorithm was applied to define the confidence interval of traditional confidence connectivity method. Finally, we employed the improved confidence connected algorithm to extract the liver parenchyma from a large cross-section liver image. Experimental results show that the proposed segmentation method is feasible even for diseased liver images.

Introduction

With the development of computer technology, computer-aided diagnosis has become a key diagnostic techiniques of various diseased. When it comes to liver diagnosis, the liver parenchyma segmentation is the basis of liver 3D visualization and it has become a research focus. Difficulties of liver segmentation exist in various aspects:The geometric characteristics of liver,such as positon,shape and size, vary from person to person, causing that it is difficult to extract. The intensity of hart and abdominal wall is extremely close to liver's intensity. In several image, it includes multiple connected regions, even it exists civitation in diseased liver. Therefore, there is still not an effective segmentation method that is suitable for all liver images. From the perspective of liver segmentation process, the liver parenchyma segmentation can be divided into single liver image segmentation and sequence image segmentation[1]. Single liver image segmentation only consider the information of the current image, which is the foundation of the sequence liver image segmentation. The main liver parenchyma segmentation method includes:the threshold segmentation method, the active contour based senmentation method[2],level-set based method[3],region growth based method and the interactive segmentation method based on graph cut.

Because of the simplity and efficiency of the region-based segmentation, it's still a segmentation methode to research and improve[4,5]. In this paper, we combine FCM with confidence connectivity segmentation, and apply the proposed methods to extract the liver parenchyma from a slice in which liver is of a large cross-section. The proposed segmentation algorithm eliminate the filtering process from traditional liver segmentation methods. Fist, combined with the domain knowledge, we apply Otsu algorithm to estimate the intensity distribution of liver. Then we calculate the mean gray of

liver area with FCM clustering algorithm. Finally, we apply the proposed segmentation method to imply the liver parenchyma segmentation. Experiment results show that the proposed algorithm achieves an effective segmentation even of diseased liver image. Its effectiveness and efficiency can provide services for liver clinical diagnosis.

Related works

(1)Distribution characteristics of liver region

In reference[6,7],Foruzan AH et al proposed a liver sequence image segmentation method combined with domain knowledge and anatomy knowledge. It starts with a slice in which the liver is both a single part and of a large cross-section. In this paper, we focus on the segmentation method of large cross-section liver images. The anatomical information shows that, the liver tissue mostly locates in the left part of the image, and it is surrounded by ribs. Therefore, we crop the part out of the ribs. It ensures a larger proportion of the valid information. The histogram of the cropped image is show as figure 1(remove gray leve 0 and 255):

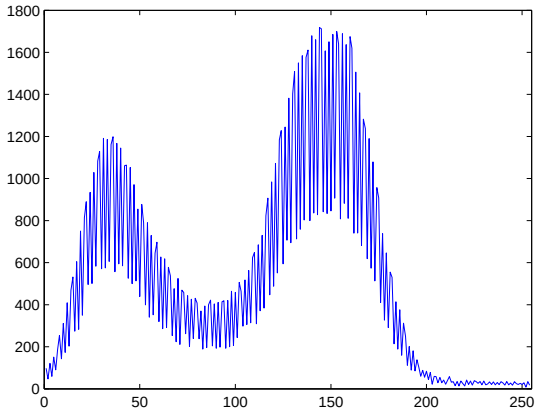

Figure 1 Histogram of cropped image

As shown in figure 1, the second peak is the liver section. As the existance of blood vessels, dark lesion and noise, therefore, in the unfiltered image, the distribution characteristics as shown in figure 1 can be described by the following formula: $|n(i)-n(j)| \gg |i-j|, |i-j| \le \sigma$. Where i,j is gray level, and $n(i), n(\mathrm{j})$ represent the pixel number of gray level i,j. σ is the standard diviation of the second peak.

(2)The estimation of liver's intensity range

In reference[6], it proposed a liver segmentation based on gray analysis. In this paper, we apply Otsu algorithm to estimate the lower limit of the liver intensity range. Assume that T was the segmentation threshold of object and background. The object pixel number ratio is w_0,and the average gray is u_0, and the background's is w_1 and u_1. Traverse T from the minimu gray-level to the maximum gray-level. The optimal threshold is T* that maximize the between-class variance $\sigma^2 = w_0 \times w_1 \times (\mu_0 - \mu_1)^2$. Then the liver gray-level range is set as[low,up],where low=T*, $up = \{i \mid i > T, \forall j(j > i \,\&\, n(j) < n(T))\}$.

The improved confidence connectivity segmentation method

(1)FCM clustering

We denote a pixel numberl sequence $n(i), low \le i \le up$ and a possibility density function $pdf(i) = n(i) / \sum_{j=low}^{up} n(j)$, which are corresponding to gray-level interval[low,up].Then we estimate a binary sequence $Seq =< i, pdf(i) >, low \le i \le up$ .The possibility density sequence $pdf(i)(low \le i \le up)$ is clustered with FCM clustering algorithm to achive k clusters $C_j (j = 1, 2, \cdots, k)$.Combined with the binary sequence, we estimate the following cluster as shown in formula 1:

$$G_j = \left\{ i \mid \forall i, pdf(i) \in C_j \right\}, (j = 1, 2, \cdots, k) \quad (1)$$

(2)The improved confidence connected region growing algorithm

Confidence connection is iteration region growing method based on the simple intensity statistics of current growing region.It start from the seed points. Then calculate the mean intensity and standard variance u，σ and determine whether the intensity of the neighbor pixel in the range $I(X) \in [u - \lambda\sigma, u + \lambda\sigma]$,where λ is the constant factor that control the brightness range. The pixels in this range are included into the current region, then recalculate the value of u，σ ,and the confidence interval is redefined. The expansion process above is repeated until no new pixel is expanded or it reaches to the iteration times[8].

In this paper, we improve the traditional confidence connected region growing algorithm by redefining the confidence interval as formula 2:

$$I(X) \in [u - \lambda_1\sigma, u + \lambda_2\sigma] \quad (2)$$

Where $u = \overline{G}_t$,t is equal to the j value that maximize the size of G_j. λ_1, λ_2 is the constant factor . When the value of λ_1, λ_2 is not equal, the confidence interval is not symmetric for the center u.

Experiment Results

In order to evaluate the proposed liver parenchima segmentation by FCM-based confidence connected region growing method in this paper, a large number of liver parenchima segmentation experiments were carried out. In the experiment, the image size is 512×512 ,and the parameter is set as following: $\lambda_1 = 1.2, \lambda_2 = 1, k = 6$. Two group experiment results are shown as figure 2 and figure 3:

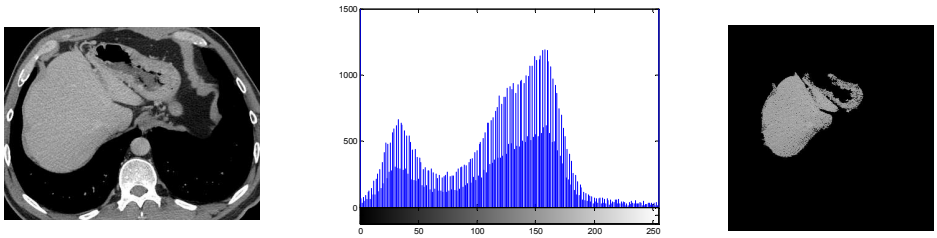

Figure 2 left: Cropped image. middle histogram of the cropped image. right: segmentation result

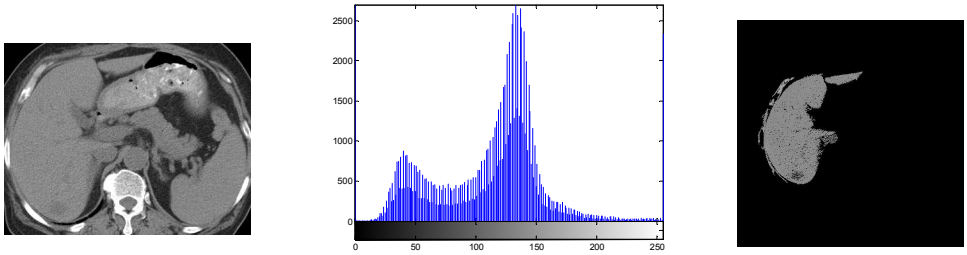

Figure 3 left: Cropped image. middle histogram of the cropped image. right: segmentation result

From the experiment results in figure 2, we can conclude that the proposed segmentation method is suitable for the diseased liver. And from the experiment result in figure 3, it shows that the proposed segmentation method is feasible when the liver cross-section consists of multiple connected regions. And the segmentation results is not sensitive to the seed points.

Conclusions

In this paper, we combine the FCM clustering algorithm with the confidence connected region growing algorithm, and apply the proposed segmentation method in liver parenchyma segmentation in unfiltered liver image which simplifies the liver parenchyma segmentation process. Experiment results show that the proposed segmentation method is not sensitive to the seed points and the segmentation results is effective for diseased liver and liver of multiple connected regions.

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Email: sunyx@jlu.edu.cn,huangliping5727@163.com

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