Efficient Pancreas Segmentation in Computed Tomography Based on Region-Growing

Tran Duc Tam[(⊠)] and Nguyen Thanh Binh

Faculty of Computer Science and Engineering,
Ho Chi Minh City University of Technology, Ho Chi Minh City, Vietnam
tamtd@hcmup.edu.vn, ntbinh@cse.hcmut.edu.vn

Abstract. Pancreas segmentation in computed tomography data is one of difficult problems in medical area. Segmentation of pancreas tissue in computed tomography is difficult even for human, since the pancreas head is always directly connected to the small bowel and can in most cases cannot be visually distinguished. In this paper, an efficient method to extract the pancreas from such computed tomography images is proposed. Histogram equalization is used to enhance the contrast of computed tomography images. After that, region-growing technique is applied to label pancreas region and return the result of segmentation. The proposed method will be experimented and evaluated by using Jaccard index between an extracted pancreas and a true one. For evaluating the proposed method, we have compared the results of our proposed method with the other recent methods available in literature.

Keywords: Computed tomography · Pancreas · Segmentation · Medical image

1   Introduction

Nowadays, the computed tomography (CT) is most widely used to determine and diagnose medical problems. With this technique, we can detect abnormal organs to treat as soon as possible. For example, pancreatic cancer is the most difficult type of cancers to treat, which has a high mortality. It is the first leading cause of cancer-related mortality in many countries [1]. In order to detect pancreatic cancer, the entire abdominal area will be scanned. However, segmentation of pancreas tissue in CT is difficult even for a human, since the pancreas head is always directly connected to the small bowel and can in most cases cannot be visually distinguished. Additionally, pancreas is an organ that includes pancreatic juice as liquid. Therefore, the CT scan of pancreas has a low contrast.

In recent years, some algorithms have been built to pancreas segmentation [2]. The algorithm of Shimizu [3, 9] based on anatomical and radiological observations. He proposed an automatic pancreas segmentation algorithm from contrast-enhanced multiphase CT and verify its effectiveness in segmentation. The algorithm is characterized by three unique ideas as: the two-stage segmentation strategy with a spatial standardization of pancreas, a patient-specific probabilistic atlas-guided segmentation, and fine segmentation incorporated with a classifier ensemble learned by a Boosting algorithm tomography.

In the other works, Marius [4] gets information about liver and spleen and uses them as starting points for detection of splenic and mesenteric veins where pancreas lies near. He detected clinically meaningful support structures and building a classifier that models local spatial relationships between the pancreas and the support structures. Furthermore, performance texture descriptors based on wavelets and cosine transform are proposed to model local appearance. Marius uses texture descriptors to build the final pancreas tissue feature vector $\vec{Z}(\vec{t}) = \{\vec{F}(\vec{t}), \vec{\Phi}(\vec{t}), \vec{W}_\eta^-(\vec{t}), \vec{W}_\eta^+(\vec{t}), \vec{H}(\vec{t})\}$ as details in [4]. All the methods discussed above have local advantages or disadvantages depending on the features they have used.

In this paper, we have proposed an efficient approach for pancreas segmentation, using region-growing technique with intensity value. In order to enhance the contrast of medical images, we also use histogram equalization method for increasing equality. We also base on the ideas of general method for segmentation which is mentioned in the above part to improve the proposed method. By using intensity value as a feature to distinguish pancreas with other surrounding organs, we can detect and segment the pancreas image in the area which localized in [4]. Therefore, the proposed method can get a good result. For performance measure, we computed the Jaccard index (J.I) between an extracted region and a true one, which was manually defined by an expert and compared with the method of Shimizu [3] and Marius [4].

The rest of the paper is organized as follows: in section 2, we described the background of histogram processing and region-based segmentation; in section 3, we shown details of the proposed method; the result and conclusion of the paper are orderly presented in section 4 and section 5.

2   Background

2.1   Histogram Processing

Histograms are the basis for numerous spatial domain processing techniques. Statistics obtained directly from an image histogram can be used for an image enhancement. The histogram of a digital image [5, 10] with intensity levels in the range $[0, L-1]$ is a discrete function

$$h(r_k) = n_k \tag{1}$$

where r_k is the kth intensity value, n_k is the number of pixels in the range with intensity r_k and L is the number of possible intensity levels in the image.

Let r denote a discrete random variable representing intensity values in the range $[0, L-1]$ and let $p(r_k)$ denote the normalized histogram component corresponding to value r_k, and it is viewed as an estimate of the probability that intensity r_k occurs in the image from which the histogram was obtained.

The probability $p(r_k)$ of intensity level r_k occurring in a given image is estimated as

$$p(r_k) = \frac{n_k}{MN} \qquad k = 0, 1, 2, \dots, L-1 \tag{2}$$

where MN is the total number of pixels.

A transformation function of particular importance in image processing has the form

$$s = T(r) = (L-1) \int_0^r p_r(w)dw \qquad (3)$$

where w is a dummy variable of integration. The right side of this equation is recognized as the Cumulative Distribution Function (CDF) of random variable r. The discrete form of the above transformation is:

$$s_k = T(r_k) = (L-1) \sum_{j=0}^k p_r(r_j) \qquad k = 0, 1, 2, \dots, L-1 \qquad (4)$$

Thus, a processed image is obtained by mapping each pixel in the input image with intensity r_k into a corresponding pixel with level s_k in the output image. The transformation $T(r_k)$ is called a histogram equalization transformation. Figure 1 shows the CT image of enhanced image using histogram equalization.
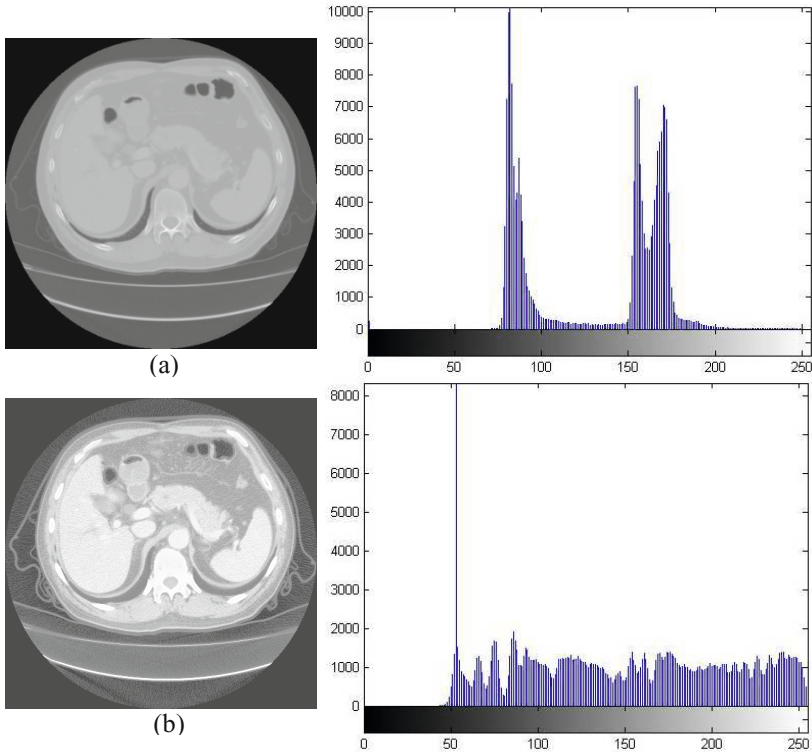
Fig. 1. The CT image of abnormal area and its histogram: (a) Original image, (b) Enhanced image using Histogram Equalization

2.2   Region-Based Segmentation

Region-based segmentation methods attempt to partition or group regions according to common image properties [5]. These image properties consist of:

(i) Intensity values from a given image or a processed image;

(ii) Textures or patterns that are unique to each type of region;

(iii) Spectral profiles that provide multidimentional image data;

In this paper, intensity value is used as a characteristic in region-growing algorithm. Using a seeding and region-growing technique, a segmented pixel set is created by initially selecting one or more pixels from the image (called the seed pixels). The seeds are often specified interactively by the user and start from these growing regions by appending to each seed those neighboring pixels that have predefined properties similar to the seed. The region-growing algorithm will then add to the segmented pixel set all the pixels that are r-connected to the initial seed pixels and fall within the threshold limits. To be r-connected to one another, two pixels must share at least r corner points. The algorithm recursively adds to the segmented pixel set all the pixels that are connected to the current members of the pixel set. Region growth should stop when no more pixels satisfy the criteria for inclusion in that region.

   Let: $f(x, y)$ denote an input image array; $S(x, y)$ denote a seed array containing 1s at the locations of seed points and 0s else where; and Q denote a predicate to be applied at each location (x, y). Arrays f and S are assumed to be of the same size. A basic region-growing algorithm based on 8-connectivity may be stated as follows [5].

(i) Find all connected components in $S(x, y)$ and erode each connected component to one pixel; label all such pixels found as 1. All other pixels in S are labeled 0.

(ii) Form an image f_Q such that, at a pair of coordinates (x, y), let $f_Q(x, y) = 1$ if the input image satisfies the given predicate, Q, at those coordinates; otherwise, let $f_Q(x, y) = 0$.

(iii) Let g be an image formed by appending to each seed point in S all the 1-valued points in f_Q that are 8-connected to that seed point.

(iv) Label each connected component in g with a different region label. This is the segmented image obtained be region growing.

After that, we have to specify a predicate and append to each seed all the pixels which are k-connected to that seed as well as similar to it. Using intensity differences as a measure of similarity, our predicate applied at each location (x,y) is

$$Q = \begin{cases} TRUE & \text{if the absolute difference of the intensities between the seed} \\ & \text{and the pixel at (x,y) is} \leq T \\ \\ FALSE & \text{otherwise} \end{cases}$$

where T is a specified threshold.

3   The Proposed Method

In this section, we propose an efficient approach for pancreas segmentation that is based on region-growing technique combine to histogram equalization.
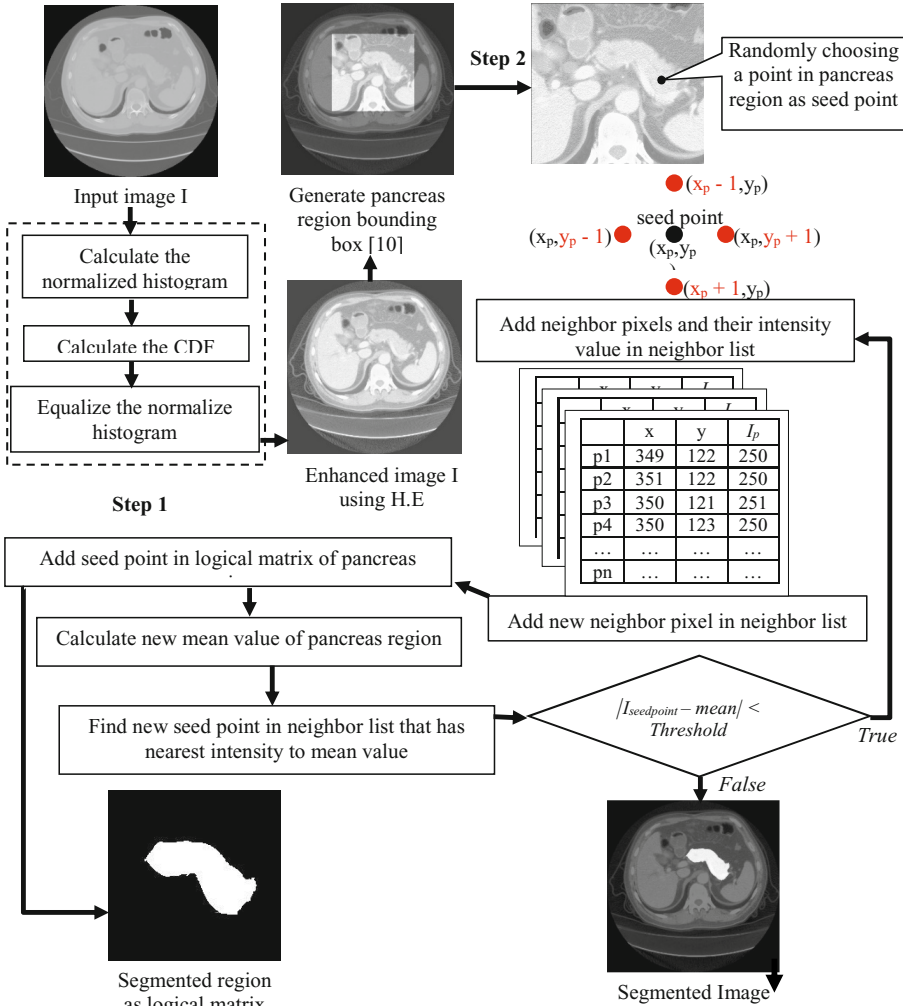

Fig. 2. Block diagram of the proposed method for pancreas segmentation

Because pancreas has unusual shape and dual location in the abdomen [1], the head of the pancreas always contact the superior mesenteric vein while body and tail follow the pathway of the splenic vein, thus the segmentation is so complex and

time-consuming. Therefore, in order to reduce a number of processed data, we utilize the described anatomical information. Liver and spleen are automatically segmented by [6]. The axis-aligned bounding boxes $\vec{l}$ and $\vec{s}$ of the liver and spleen masks are computed and a pancreas region bounding box $\vec{p}$ is generated. All subsequent calculations are limited to the region described by $\vec{p}$.

$$\vec{p} = \left(\frac{\vec{l}_{xmax} - \vec{l}_{xmin}}{2}, \min(\vec{l}_{ymin}, \vec{s}_{ymin}), \frac{\vec{s}_{xmax} - \vec{s}_{xmin}}{2}, \max(\vec{l}_{ymax}, \vec{s}_{ymax}) \right) \qquad (5)$$

Figure 2 presents a flowchart of proposed algorithm. The input, which has low-contrast, will be enhanced by histogram equalization method as a pre-processing data. The second step performs a segmentation method based on region growing technique using difference of intensity between pancrease and other organs in abdomen.

Firstly, we enhance the input image by Histogram processing. In this stage, this stage can be described as follows:

1. Calculate the histogram of the input image according to Eqn. (1)

2. Calculate the CDF of the input image according to Eqn. (4)

3. Equalize the histogram of the input image.

$$I_p = T(I_p) \qquad (6)$$

where I_p is intensity value of pixel in the input image

Secondly, we choose a one point on the pancreas region to be a seed point(x, y). Pancreas region is segmented by region growing technique. This stage can be described as follows:

1. For each pixel (x, y) has four neighbors whose coordinates are given by

$$(x + 1, y), (x - 1, y), (x, y + 1), (x, y - 1)$$

Check if neighbor pixel is still inside the image and not already part of the neighbor list then add new neighbor pixel to neighbor list and mark them as checked pixels.

2. Add current seed point in segmented region.

3. Find pixel with intensity nearest to mean value of segmented region and use it as a new seed point in next iteration. The minimum distance is the difference between the chosen pixel and mean value of intensity:

$$min_{distance} = \min_{i=1..n} |I_i - m_{mean}| \qquad (7)$$

where I_i is an intensity of pixel p_i in neighbor list, m_{mean} is mean of the segmented region which is calculated by:

$$m_{mean} = (m_{mean} * |R| + I_p)/(|R| + 1) \qquad (8)$$

where $|R|$ is size of segmented region.

4. Calculate the new mean of the segmented region and remove the chosen pixel from the neighbor list.

5. Repeat the above processes until distance between region and possible new pixels become higher than a certain threshold.

Proposed algorithm will return the segmented region as a logical matrix that contains pancreas region which has the same characteristics to seed point.

4   Experiments and Evaluation

In this section, we implemented the proposed approach in section 3 and achieved good results in our segmentation experiments as demonstrated. We applied the proposed method for single-phase CT data that obtained from many cases, the number of slices per case ranged from 92 to 112. Inter-slice spacing was 2mm abdominal control standard protocol whereas spacing within an axial slice varied between 0.6 mm and 0.7 mm.

To evaluate the segmentation performance quantitatively, we computed the Jaccard index (J.I) between an extracted region and a true one [7], which was manually defined by a medical expert.

$$JI(A, B) = \frac{|A \cap B|}{|A \cup B|} \times 100 \tag{9}$$

where A is extracted region, B is true region. If A and B are both empty, we define $JI(A, B) = 100$. The index ranges from 0 to 100%, with higher values representing better performance. Resolution of tested images are 512 x 512 and threshold is used in experiments ranges from 0.06 to 0.1. We have experimented on many image. Here, we report the results in some cases as Figure 3.

Figure 3 shows results separately for the original images and compares the result of the proposed method with others (using value of Jaccard index). Generally, the below results have high accuracy giving the low contrast of pancreas regions.

As mentioned in section 3, we find pixel with intensity nearest to the mean of segmented region and use it as a new seed point in next iteration to add to segmented region. Although this predicate is based on intensity differences and uses a single threshold, we could specify more complex schemes in which a different threshold is applied to each pixel, and properties other than differences are used. In this paper, the preceding predicate is sufficient to solve the problem. Therefore, our proposed method is better than other methods.
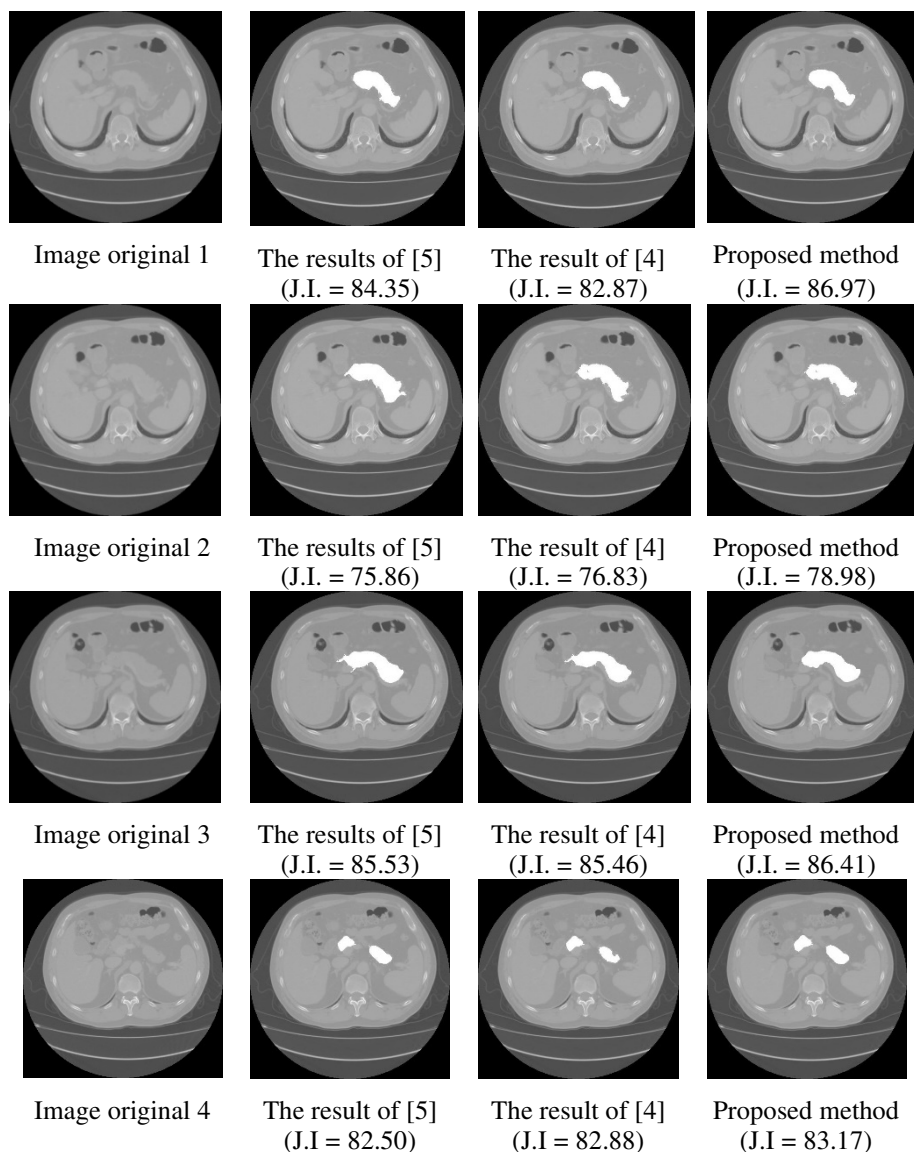
| Image original 1 | The results of [5] (J.I. = 84.35) | The result of [4] (J.I. = 82.87) | Proposed method (J.I. = 86.97) |

| Image original 2 | The results of [5] (J.I. = 75.86) | The result of [4] (J.I. = 76.83) | Proposed method (J.I. = 78.98) |

| Image original 3 | The results of [5] (J.I. = 85.53) | The result of [4] (J.I. = 85.46) | Proposed method (J.I. = 86.41) |

| Image original 4 | The result of [5] (J.I = 82.50) | The result of [4] (J.I = 82.88) | Proposed method (J.I = 83.17) |

Fig. 3. Exemplary segmentation results on unseen data

5   Conclusion and Future Work

This paper presented an efficient pancreas segmentation algorithm from CT images. Histogram equalization is used to enhance the contrast of computed tomography images. After that, region-growing technique is applied to label pancreas region and return the result of segmentation. Based on the prior work, the proposed method

allows to enhance the contrast and improve the accuracy of segmentation. The effectiveness of the proposed method was validated with CT images from many tested cases. The Jaccard index between an extracted region and true one ranges from 73.37 to 86.97. From the results of the above section, we conclude that the proposed method is efficient and better than the other recent methods available in literature. To further improve accuracy and flexibility of the method, we will use more characteristics to describe pancreas objects more clearly. Additionally, we will apply classification method to boost the performance for segmentation algorithm.

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