CT Image Segmentation with Supervised Clustering Using Hierarchical Support Vector Machines

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Abstract

Medical image analysis has been widely used for the segmentation, detection, and classification of lesions in radiological images. Such analysis help physicians in computer assisted diagnosis from radiological images. A machine learning based image analysis system may help physicians in rapidly screening lesions in large images volume. Moreover, such learning based system may help an inexperienced physician in concluding the diagnosis and may assist an experience physician in ambiguous diagnosis. In this study, a supervised clustering method is proposed to provide a visual representation of segmented organs and tissues in the CT images. The main elements of the clustering framework include: (1) The input abdominal CT image is automatically segmented in regions by seeded region growing (SRG) method; (2) Use hierarchical support vector machines (SVM) to divide abdominal CT image into seven parts: gallbladder, liver, kidneys, spleen, stomach, bones and other parts; and (3) Delineate the regions into different colors results by the support vector machine (SVM) classifier. The results demonstrate that the presented method can automatically segment and recognize the organs in the abdominal CT image effectively.

Keywords: medical image analysis, abdominal CT image, image segmentation, seeded region growing, texture segmentation, machine learning, support vector machine.

1. Introduction

Image segmentation is one of the most important and challenging areas in computer vision aided medical imaging processing. Image segmentation has been applied to different image modalities, including the magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET) or ultrasonography, etc. Usually, without a computer assisted diagnosis system, physicians carefully examine the radiological images to make diagnosis by analyzing locations or texture features of the lesions. However, if there are lots of images needed to be analyzed, it is very time consuming if analyzed manually. An assistance with the computer to screen and diagnose the lesions would help physicians in such situations. Moreover, a well learned computer may also help an inexperienced physician as well as an experienced physician in ambiguous diagnosis.

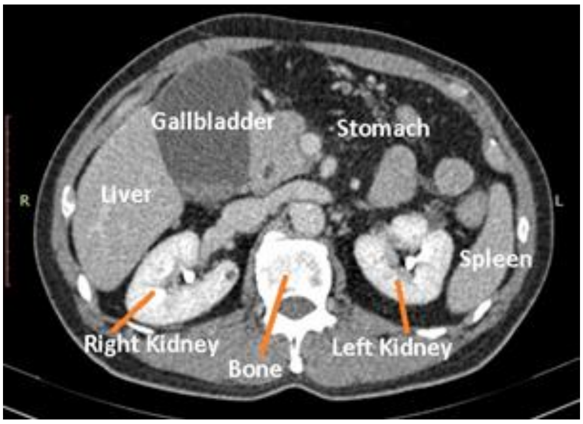

Figure 1: The example of the complex and large variations of abdominal CT image.

Fig.1 illustrates an example of an abdominal image, which is divided into several parts, e.g. gallbladder, liver, kidneys, spleen, stomach and bones. Automatic segmentation of medical images is a difficult task as these images are complex and diverse in nature.

The image segmentation methods can be classified into several types such as region-based, model-based and hybrid-based. There are many methods proposed in liver and kidneys segmentation. Region based methods [1]-[4] include thresholding, region growing or edge detection. Rikxoort et al. [2] proposed a voxel procedure where the probability that each voxel is part of the liver is estimated using a k-nearest-neighbor classifier and a multi-atlas registration procedure to automatically delineate the liver. Another method based on statistical shape model (SSM) [5]-[7] was proposed by Zhang et al. [7], a coarse liver shapes model is calculated with a test CT images using a normal Hough transformation

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based subspace initialization of the SSM (??) method, and then liver contours are detected using optimal surface segmentation. Lin et al. [8] proposed to combine the region-based and model-based methods to develop an automatic kidney segmentation system. Most of the previous work proposed method to segment only few organs in the images. This study presents a method on automatically delineate multi-organs for the abdominal CT images. In this study, a supervised clustering method is proposed to provide visual representation of organs and tissues in the CT images. By using the hierarchical support vector machines (SVM) classifier, it divides the abdominal CT image into seven parts: gallbladder, liver, kidneys, spleen, stomach, bones and other parts. Experimental results demonstrate the effectiveness of the proposed method. The rest of the paper are organized as follows: section II and III present the proposed algorithm in detail. The experimental results and discussion are shown in Section IV. Finally, Section V concludes this paper.

2. Proposed Method

In the following, we describe our segmentation method by three parts. Section A describes the automatic seed selection algorithm to obtain candidate seeds. Section B adopts the seeded region growing to segment the image. At the end of section C, we apply a region-merging algorithm to deal with over-segmentation problems.

A. Automatic Seed Selection Algorithm

For automatic seed selection, the following three criteria must be satisfied. First, the seed pixel must have high intensity and texture similarity to its neighbors, and it makes sure that the seed pixel is not on the boundary of two regions. Second, for an expected region, in order to produce this region, at least one seed must be given. Therefore, the seeds generated can be one pixel or one region with several pixels. Third, seeds for different regions must be disconnected.

The three conditions for the seed pixel candidate are defined as follow

Condition 1. To know the high intensity similarity, we examine the Euclidean distances of the seed pixel candidate to its eight neighbors as

$$\left|((\bar{Y})_i - (\bar{Y})_j)^2\right| < T_1$$

where i and j are the opposite side of pixels, as shown in Fig. 2, related to the candidate seeds. i is a pixel which is going to be classified, j is adjacent region of i, $\overline{Y_i}$ is intensity of i and $\overline{Y_k}$ is the mean values of Y components in region of k. If all the Euclidean distances of these eight neighbors are less than the threshold T_1, it can be one of pixel candidate.

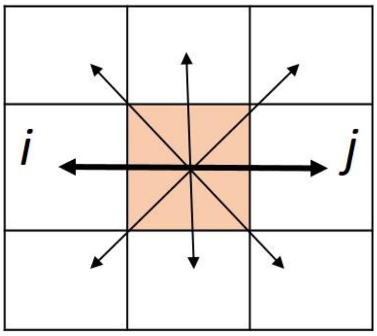


Figure 2: i and j are the opposite sides of pixels related to the candidate seed.

In order to fix the texture problem, we consider not only the similarity of intensity feature but also similarity of texture feature using the entropy and the discrete cosine transform (DCT) in a neighborhood.

Condition 2. We estimate the entropy of the seed pixel candidate to its eight neighbors as

$$-\sum_{i=0}^{n-1} P_i \log_2 \frac{1}{P_i} < T_2$$

where T_2 is a positive real number, n is the number of gray levels and P_i is the probability associated with gray level i.

Condition 3. We estimate the DCT of the seed pixel candidate to its eight neighbors as

$$\left||\mathrm{D}(0,1)|_{max} - |D(0,1)|_{min}\right| < T_3$$
$$\left||\mathrm{D}(1,0)|_{max} - |D(1,0)|_{min}\right| < T_3$$
$$\left||\mathrm{D}(1,1)|_{max} - |D(1,1)|_{min}\right| < T_3$$

where T_3 is a positive real number, and the D(0,1), D(1,0), D(1,1) are the transform of DCT by

$$\begin{aligned}&\mathrm{D(i,j)}\\&= \frac{1}{\sqrt{2n}} C(i)C(j) \sum_{x=0}^{n-1}\sum_{y=0}^{n-1} f(x,y)\\&\times \cos\left[\frac{(2x+1)i\pi}{2n}\right] \cos\left[\frac{(2y+1)j\pi}{2n}\right]\end{aligned}$$

where n is the block size . When $i = 0$, $C(i) = 1/\sqrt{window\ size}$, otherwise $C(i) = \sqrt{2}/\sqrt{window\ size}$; when $j = 0$, $C(j) = 1/\sqrt{window\ size}$, otherwise $C(j) = \sqrt{2}/\sqrt{window\ size}$.

If the seed pixel candidate satisfies the above three conditions, that pixel is regarded as a seed pixel. The detected seeds are shown in Fig. 3(b).

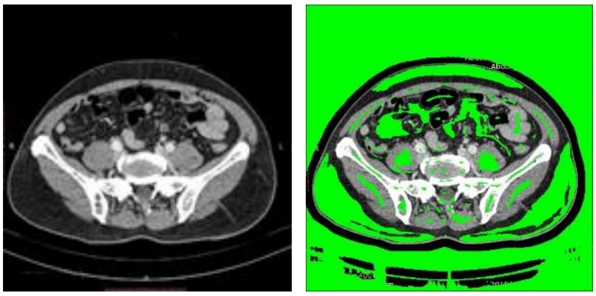

(a) (b)

Figure 3: Seed selection. (a) Original image (b) the detected seeds are shown in green color.

B. Seeded Region Growing Algorithm

This paper proposed a SRG algorithm for the initial segmentation of the medical images, and the details are described below:

1) Apply automatic seed selection algorithm.
2) Estimate the average of intensity feature and assign a label to each seed region.

After step 2, we calculate the Euclidean distance of the pair of all seed regions. We select the smallest value as the variable value $diff_{min}$. This parameter can later be used.

3) Find the set of pixels that are unclassified, then estimate the pixel if it can be connected to its neighboring seed region.
4) If there are still any pixels that are unclassified, repeat step 3.

Note in the step 3, we are using the relative Euclidean distance C_{ik} as the seeded region growing. The relative Euclidean distance between the pixel i and its adjacent region k is calculate by

$$C_{ik} = \frac{\sqrt{(\bar{Y_i} - \bar{Y_k})^2}}{\sqrt{(\bar{Y_i})^2}}$$

where i is a pixel which is going to be classified, k is the adjacent region of i, $\bar{Y_i}$ is the feature of i and $\bar{Y_k}$ is the mean values of Y components in region of k. The C_{ik} means the differences between intensity values, if C_{ik} is smaller, it means they are more similar.

We estimate the similarity between all adjacent regions and unclassified pixels. If we encounter a situation that the unclassified pixel connects to several seed regions, we estimate the distance between them and find the minimum one. After that, adding the unclassified pixel to the seed region which has the minimum distance.

In Shih and Cheng's [9] paper, we know that sorting step will take lots of time. In order to speed up the growing part, we define another threshold T_4 by

$$T_4 = \frac{diff_{min}}{I} \times \alpha$$

where I is a positive constant; and whenever there is no any other C_{ik} is smaller than T_4, then we will increase our α by time as

$$\alpha = \alpha + t$$

where we will we select 1 as our initial value α, and t is presetting as 0.009. Therefore, the threshold T_4 will be larger and larger.

For example, as shown in Fig 4, there are three initial seed regions, pink, green and blue; the red pixels are the 4-neighbor pixels of the seed regions. As the same time, if the distance of any 4-neighbor pixels p is smaller thanT_4, we allow p added to the most similar adjacent region. Next, after the pixel p is classified, the 4-neighbor pixels of p are added to list T.

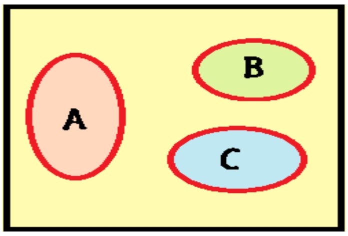


Figure 4: There are three initial seed regions, pink, green and blue.

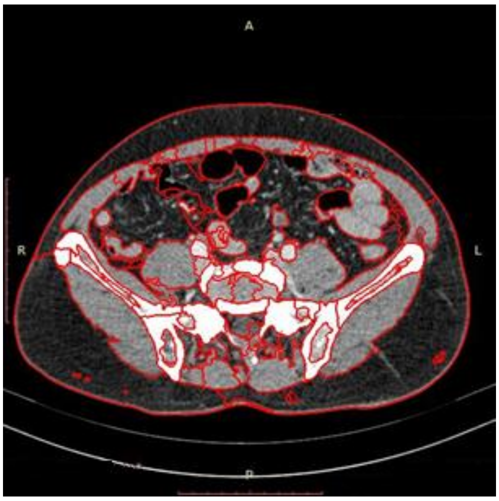


Figure 5: The result of the proposed seeded region growing method.

The pixel p will be suspended, if its distance is larger than T_4. As regions grow bigger and bigger, the distance will also be lager. While all the unclassified pixels are suspended, we increase value α in order to raise up the value of T_4. After that, we have to check all the unclassified pixels again; if any pixel p satisfies the condition, then add p to the seed region, otherwise, p is suspended. Repeat this step again and again until all of the unclassified pixels are classified. The image is almost segmented at the moment. The result of seeded region growing can be seen as Fig 5.

C. Region-Merging Algorithm

It is possible that several seeds split a region into several small ones. To overcome the over segmentation problem, we apply a region-merging algorithm. We defined two conditions for merging as follows

Condition 1. Intensity difference

$$c(R_i, R_j) = \frac{\sqrt{(\bar{Y_i} - \bar{Y_j})^2}}{\min(\sqrt{\bar{Y_i}^2}, \sqrt{\bar{Y_j}^2})}$$

Condition 2. Texture difference

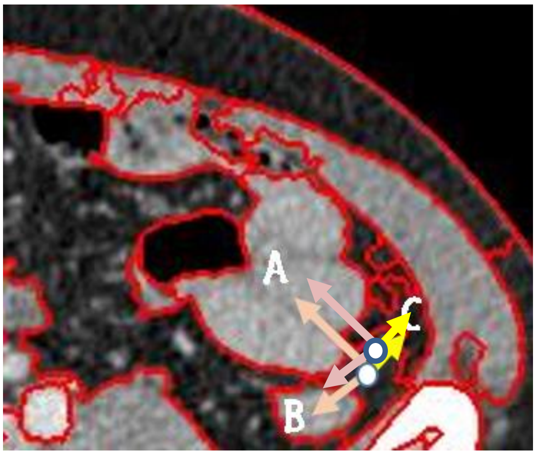
$$d(R_i, R_j) = \frac{\sqrt{(\overline{D_i(0,1)} - \overline{(D_j(0,1)})^2 + (\overline{D_i(1,0)} - \overline{(D_j(1,0)})^2 + (\overline{D_i(1,1)} - \overline{(D_j(1,1)})^2}}{\min(\sqrt{\overline{D_i(0,1)}^2 + \overline{D_i(1,0)}^2 + \overline{D_i(1,1)}^2}, \sqrt{\overline{D_j(0,1)}^2 + \overline{D_j(1,0)}^2 + \overline{D_j(1,1)}^2})}$$

If both $c(R_i, R_j)$ and $d(R_i, R_j)$ between two neighboring regions, R_i, R_j, are less than the threshold value T_5 and T_6, we merge two regions together. As shown in Fig 6(a), the region of a point on it will be merged to region C but not A or even B, because it is similar to region C.

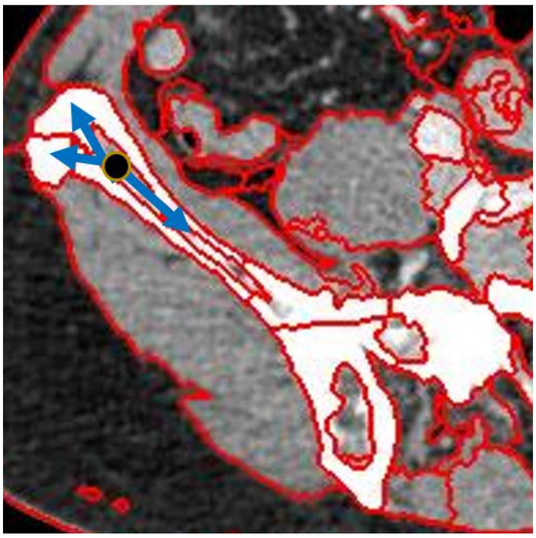
Except merging by the similarity, several seeds in medical images are generated to split a bone region into several small ones, as shown in Fig. 6(b). Due to the difference in the intensity and texture, we have to merge them together. Three criteria are used (small region i and its adjacent region k)

1) After merging by its similarity, we have label some small region i.
2) The region i must have low similarity to its neighbors k.
3) The region k must have high intensity (>200). If there are many adjacent region k near region i, then merge i to the maximum intensity region, and re-compute the mean of the new region.

After region-merging algorithm, the result can be seen in Fig. 7.



(a)



(b)

Figure 6: Part of seeded region growing images. (a) merge by its intensity and texture similarity; (b) merge regions of bone.

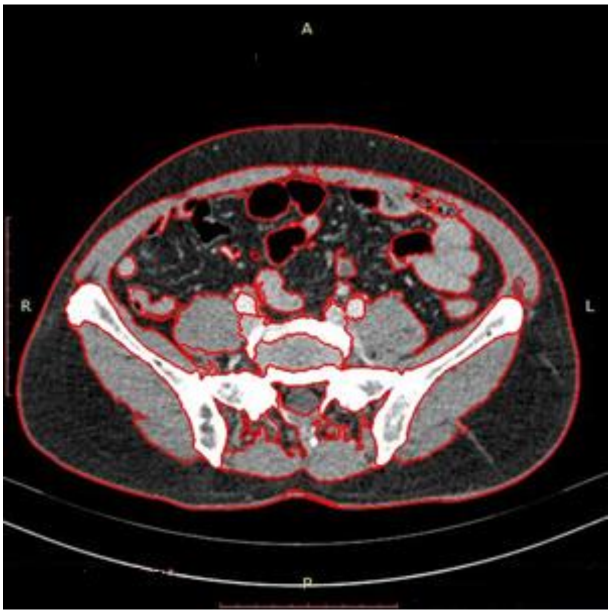


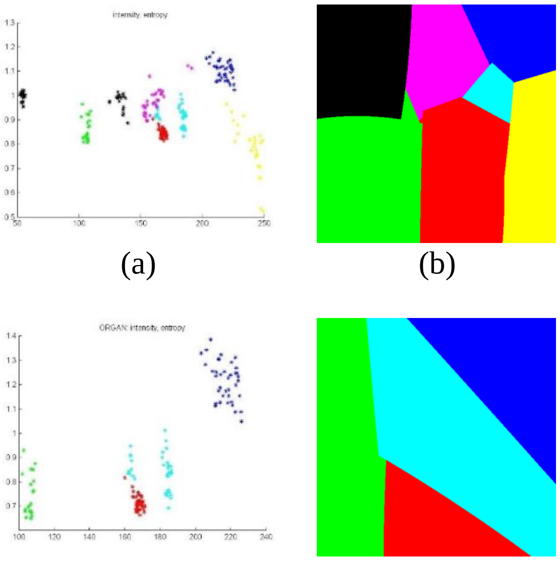
Figure 7: The result after region-merging algorithm.

3. Hierarchical Machine Learning Approach

A number of classification tools are available such as decision tree, neural networks or KNN algorithms. We choose support vector machine (SVM) which achieves smart separation between classes by adding dimensions to the vector space and limiting over learning problems.

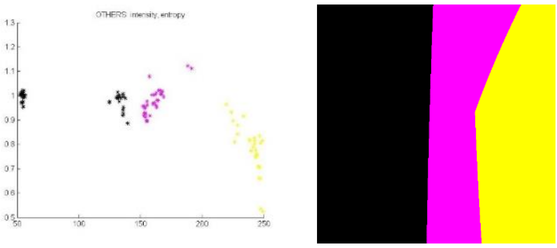
Once the images have been segmented, a set of color and texture features from each one of the significant regions are extracted. Four types of features are obtained from the regions in each image as mean of intensity, entropy, standard deviation and the coefficients of DCT.

The training data of organ image has been divided into six parts: gallbladder, liver, kidneys, spleen, stomach, bones and other parts. For this work, we adapted three SVM for organ classification. As we can see in Fig. 8(a), it is the distribution of six classified training data. As shown in Fig. 8(b), all regions have taken up their places. However, it would give wrong judgment by only using one SVM to sperate these six parts. For exmaple, gallbladder and liver take up too large places, it would cause some other regions mistaken for these two parts. In order to solve these problems, we first separate these six parts of region into two parts, organ and non-organ, by using only intensity and entropy features in one SVM framework. Next, we use another SVM to distinguish gallbladder, liver, kidneys and spleen by using four features, as shown in Figs. 8(c) and (d). At final, we use the other SVM to distinguish stomach, bones and others using only intensity and entropy features, as shown in Figs. 8(e) and (f).



(a) (b)

(c) (d)



(e) (f)

Figure 8: In these distributions, x-axis represents the intensity and y-axis represents the entropy of each region of training data. Color green represents gallbladder, color red represents liver, color blue represents kidneys, color cyan represents spleen, color purple represents stomach, color yellow represents bones and color black represents other parts. Figs. (a)(b) show the first SVM for separating organs and non-organs, Figs.(c)(d) show the second SVM for separating the organ part, and Figs. (e)(f) show the third SVM for separating the non-organ part.

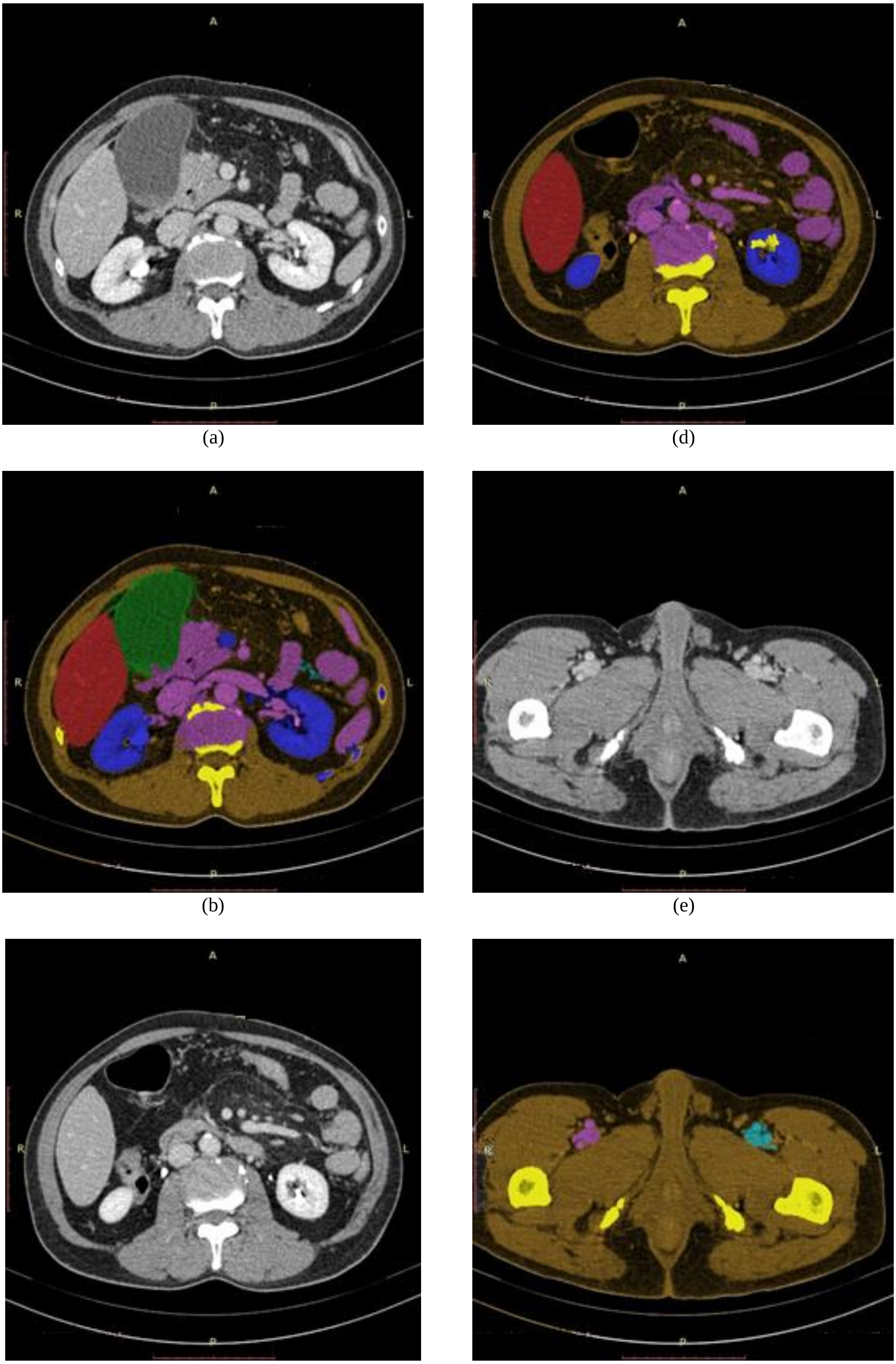
4. DATA AND EXPERIMENT RESULTS

A. Data

All abdominal CT scans acquired from 10 adults were used for evaluation, and all of images were provided by Show Chwan Memorial Hospital. Images are automatically cropped at 1.5 mm.

B. Experimental Results

We select the value 10 as threshold T_1, 0.5 as threshold T_2, 0.5 as threshold T_3, 5 as threshold T_5 and 0.7 as threshold T_6 based on our experiment. 10 adults CT scans were used for evaluation. Each case contains average 350 slices due to the different cross section thickness (1.5 mm). The proposed system was applied to delineate the gallbladder, liver, kidneys, spleen, stomach, bones and other parts. Our experiment results are shown in Fig. 9, and they show that the proposed method achieves the satisfactory segmentation results.

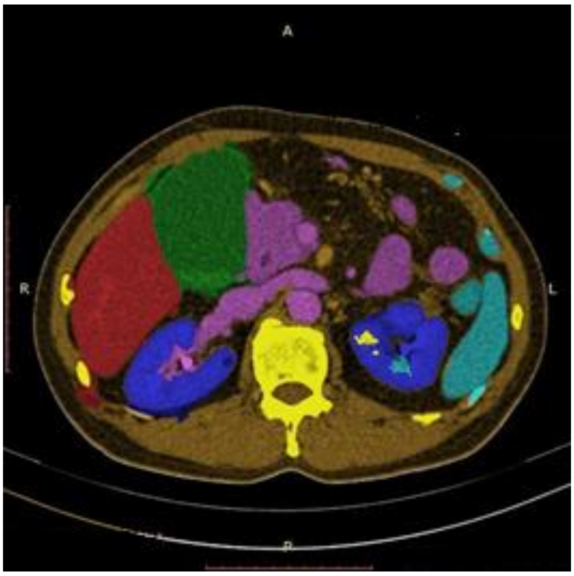


(a) (d)

(b) (e)

(c) (f)

(g)



(h)

Figure 9: The clustering result of the proposed method, in which, the color green represents gallbladder, color red represents liver, color blue represents kidneys, color cyan represents spleen, color purple represents stomach, color yellow represents bones and color black represents other parts. (a)(c)(e)(g) abdominal CT images, (b)(d)(f)(h) delineate regions into different colors result by Hierarchical SVM.

5. Conclusion

This paper presents a supervised clustering method for the medical images. By using the seed region growing for the initial segmentation, and the hierarchical SVM for the trainable clustering, our proposed method segments automatically the organs in an abdominal CT image, which effectively delineate regions we defined. In order to help physicians analyze continuous CT images efficiently, the processing image of the proposed method only takes less than 5 seconds for a medical image.

Medical image segmentation is still an important and challenging problem. The automatic or even semi-automatic segmentation arise helpful in clinical applications for physicians. In the future, we will focus on how to construct the three-dimensional (3D) CT models from our series of CT slices based on the current segmentation results. Therefore, the physicians can diagnose problems by removing organs and tissues, and such procedures are possibly considered as a part of clinical analysis and medical intervention.

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