A Supervoxel Classification Based Method for Multi-organ Segmentation from Abdominal CT Images

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***Abstract*—Multi-organ segmentation is a critical step in Computer-Aided Diagnosis (CAD) system. We proposed a novel method for automatic abdominal multi-organ segmentation by introducing spatial information in the process of supervoxel classification. Supervoxels with boundaries adjacent to anatomical edges are separated from the image by using the Simple Linear Iterative Clustering (SLIC) from the images. Then a random forest classifier is built to predict the labels of the supervoxels according to their spatial and intensity features. Thirty abdominal CT images are used in the experiment of segmentation task for spleen, right kidney, left kidney, and liver region. The experiment result shows that the proposed method achieves a higher accuracy of segmentation compares to our previous model-based method.**

***Index Terms*—multi-organ segmentation, computer-aided diagnosis, supervoxel, random forest**

I. Introduction

Medical images are important information source for clinical diagnosis of physicians. However, the examination of the medical images is a time-consuming task for physicians, which may furtherly lead to misdiagnosis and missed diagnosis. With the development of computer technique and machine learning, Computer-Aided Diagnosis (CAD) has developed into a practicable technique to extract useful information of patients as well as providing more objective opinion for diagnosis of physicians, in addition to their own experiment. Organ segmentation is one of the key tasks in CAD among many fundamental medical image processing tasks. The volume data obtained from the segmentation can be used in 3-D organ reconstruction, pathological analysis, disease tracking and so on clinical practice. In recent years, a new requirement of multi-organ segmentation is rising along with the evolution from organ-based to organism-based approaches in modern medical diagnosis, and the analysis of multiple organ can also be helpful for comprehensive diagnosis or pre-operative planning and guidance in CAD system [1].

Multi-organ segmentation methods are generally developed from single organ segmentation in which field statistical atlas and shape model are widely used. Shimizu *et al.* [2] proposed an atlas guided segmentation method on twelve organs with level-set refinement. Twelve organs are simultaneously extracted from non-contrast 3D abdominal CT images, by using abdominal cavity standardization process and segmentation of roughly atlas guided segmentation with Expectation Maximization (EM) algorithm based parameter estimation and the following multiple level set fine segmentation. In [3], Chu *et al*. used spatially-divided probabilistic atlas to reduce the inter-subject variance in organ shape and position with global and local weight assigned and conducted the segmentation incorporating a Maximum A Posterior (MAP) estimation and a graph cut method. Okada *et al*. [4] constructed a hierarchical multi-organ statistical atlas with constrains for multi-organ inter-relationships embedded by introducing prediction-based conditional shape–location priors from Organ Correlation Graph (OCG). The predictor organs are pre-segmented and used to guide the segmentation of the remaining organs hierarchically by the conditional shape–location priors. This method increases the accuracy as well as extend the applicability to various imaging conditions without supervised intensity information. These atlas and shape model based methods show better robustness in favor of the prior knowledge obtained from the training set. However, more accurate registration is required to match the pre-trained atlas to the test image, and shape correspondence within the training set is necessary for shape models.

Instead of training models, deep convolutional neural network learning technique are also introduced to this

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field, benefited from their outperformed semantic segmentation ability based on the mechanism of feature extraction using multiple convolution layers. Zhou *et al*. [5] used a Fully Connection Network (FCN) to realize a sematic segmentation of nineteen anatomical structures. Roth *et al*. [6] used a cascaded 3-D FCN to improve the inaccuracies of smaller organs and vessel in a coarse-to-fine approach. For the problem of small, partially annotated dataset in deep learning training process, weak supervised training are combined in recent methods. Zhou *et al*. [7] proposed a Prior-aware Neural Network (PaNN) using anatomical priors on organ sizes and domain-specific knowledge in the training process. In [8], Wang *et al*. focused on the training sample selection problem instead of network architecture. A Relaxed Upper Confident Bound (RUCB) strategy for sample selection was proposed to mitigate the influence of annotation errors during the training process and increase the segmentation performance. To relieve the inaccuracy on small organ and vessel, which is caused by imbalance of background and foreground differentiation, and lower layers, the coarse-to-fine strategy was employed in [9] and [10]. The accuracy of the multi-organ segmentation tasks is tremendously improved by the deep neural networks, benefit by the automatically selected features. However, the training of deep networks requires large calculation resources and manually labeled training data, which is difficult to obtain. The overfitting and gradient vanishing are still or even more serious problems for deep neural networks applied to medical image segmentation tasks, especially for 3-D tasks.

To reduce the complexity of methods that directly operated on massive voxels in 3-D images, supervoxel pre-segmentation is introduced to the image segmentation field. Supervoxel is a set of voxels with similar intensities locations and textures, which is separated from a 3-D image volume [11]. In [12], Takaoka *et al*. proposed a supervoxel based graph cut method for multi-organ segmentation. Tong *et al*. proposed a patch-based segmentation framework for the abdominal multi-organ segmentation. Dictionaries and classifiers are used to generate a subject-specific probabilistic atlas and the graph-cuts method is combined. Local information is obtained from local voxel-wise atlas selection to inter-subject variability problem [13]. In [14], Soltaninejad *et al*. proposed a brain tumor segmentation method from MRI brain image using random forest classifier for supervoxel textures. The individually over-segmented supervoxel are the tiniest elements in these methods for a further process, which merges the similar voxels and lower the requirement of calculation for 3-D image processing.

In this article, we present a supervoxel and random forest based method for automatic multi-organ segmentation from abdominal CT images. After an adjustment of quality, each image is separated into a group of supervoxels and a classifier for them is trained by extracted spatial and intensity features to label the image volume and conduct the segmentation. In Section II, the proposed method is described, including preprocessing, supervoxel clustering, feature extraction, and random forest model. Section III presents our experiment on random forest classification and image segmentation result. In Section IV, the method and experiment result are discussed with a conclusion of the research followed.

II. Method

In this section, an automatic multi-organ segmentation method is introduced, as shown in Fig. 1. Firstly, a preprocessing on original image data is performed to acquire equidistant volumes and unified intensity of each voxels. Then, the 3-D images are participated into supervoxels, each of which can be categorized as label representing background, or other organs. Then, some features of distinctiveness are extracted from the participated supervoxels and fed to a random forest trainer to obtain a classifier for supervoxels label. Finally, given a test image, each of the participated supervoxels can be labelled by the classifier as background or other organs and the final segmentation result can be obtained by merging the supervoxels of the same label.

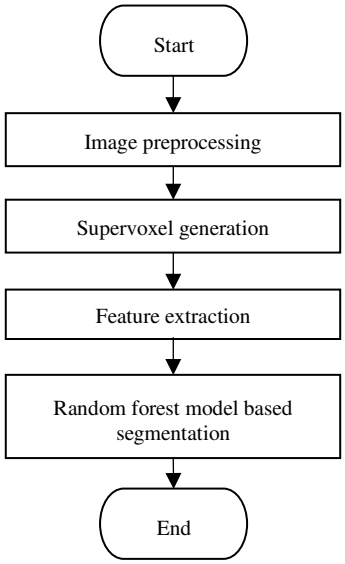

Figure 1. Flowchart of the proposed method.

A. Preprocessing

The preprocess step of images including two aspects: volumetric operation and intensity operation. The voxel spacing in the transverse planes images from the original dataset varies among each case, which makes the 3-D ratio of the CT scan different from these in the real world. To remove this difference and recover the real spatial pattern of the patients, the images are uniformly resampled to 2 mm in each direction. Also, to emphasize the object organ and enhance the contrast of the images, a histogram equalization is performed to the images by referring the histogram of a chosen case from the training set before a windowing operation on the intensities from a Hounsfield scale (HU) from -256 to 256.

B. Supervoxel Clustering

After the preprocessing, the images are separated into smaller units of supervoxels. As the CT images data are

organized in tensors of rank 3, it is natural and convenient to develop algorithms based on the smaller cubic patches. However, the shapes of anatomical structures are irregular, and the cubic division of the image may lead to isolation of the identical tissues and organs. In thus process, many useful connectivity information and communal features of the same region are ignored. Instead of using cubic patches, supervoxel that formed by adjacent voxels of similar intensity can be a better minimal unit for medical image analysis.

In our research, the Simple Linear Iterative Clustering (SLIC) [15] is used to generate the supervoxel division. The voxels of an image are clustered into k groups of supervoxels by using k-means method, in which the voxel intensities and spatial positions are used to measure the distance between voxels. The distance of intensity d_c and position d_p between the i-th and j-th voxel can be defined as:

$$d_c = \sqrt{(c_i - c_j)^2}$$

$$d_p = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2 + (z_i - z_j)^2} \quad (1)$$

where c_i and c_j are the grayscale intensity of the i-th and j-th voxel; (x_i, y_i, z_i) and (x_j, y_j, z_j) the position of the i-th and j-th voxel respectively. A comprehensive measurement of the intensity distance d_c and position distance d_p, represented as D is used in practice:

$$D = \sqrt{(d_c)^2 + \left(\frac{d_p}{S}\right)^2 m^2} \quad (2)$$

where S represents the sampling interval. The m in (2) is a constant helps balance the importance of intensity and spatial distance, which also influences the irregularity of the obtained supervoxels. When m is smaller, the edges of the obtained supervoxel are more coincided to the real boundaries of existing tissues or organs, while m is larger the edges are tended to approach regular grids and the shape of the supervoxel would be more regular.

The number of supervoxel k is decided by the floored quotient of voxel number in the image, N_v, and the interval S:

$$k = \left\lfloor \frac{N_v}{S^3} \right\rfloor \quad (3)$$

The clustering of supervoxel is an iterative process. At first, k centers of supervoxel are initialized at the voxel of minimal gradient within each equally divided grid of the input image. Then for each center of the initial grids, its distance to each voxel within a range (set as a $2S \times 2S \times 2S$ region) are calculated and the voxels are assigned to the nearest cluster. In each iteration, the centers are recalculated, and the voxels are reassigned until the residual error converges.

C. Feature Extraction

After the supervoxels are obtained, suitable features are required to distinguish supervoxels as the organs or background. In our method, the spatial position and statistical intensity features are considered beneficial for the supervoxel classification.

As the abdominal organ of interest shares similar anatomical relations in the abdominal cavity, the same organ in different cases of patients processes an approximate position. We introduce the position of the central voxel from each supervoxel as the spatial feature, which are previously normalized according to the image size. Also, the intensity features are varied for supervoxels that belongs to different tissues, organs or so on matters. While the difference of intensity among different images are reduced in the preprocessing, a gradient map of the image can furtherly help decrease the influence from the data diversity caused by many imaging environments. The maximum, minimum, and mean of the intensity value and gradient value are calculated as intensity features. The three position features, three intensity features and three intensity gradient features form the feature vector for each supervoxel.

D. Random Forest

After the supervoxels are obtained, suitable features are required to distinguish supervoxels as the organs or background. In our method, the spatial

Random forest [16] is a classification model using bagged decision trees in which the attributes at each node are chosen randomly as well. The whole training set are firstly sampled into N_t sampling sets, each of which are composed of n_s random samples. Then N_t decision trees are trained separately from the sampling sets. In the training process of the decision trees, the optimal attributes in each node are selected from a random sampled subset of the attribute set. For the multiclass classification task, the result can be obtained by a voting from the results of each decision tree. The randomness from the bagging and attributes help increase the generalization ability.

In our method, each set of training data for a random forest classifier contains supervoxels obtained from all the image data. The attribute space is a nine-dimension vector containing nine features extracted by using the method described in Section II.*C*. The labels of each supervoxel, which indicate the category that the current supervoxel belongs to, are decided by the maximum of the voxel labels within the supervoxel. The label space contains five labels: background, spleen, right kidney, left kidney, and liver. In the segmentation procedure, an abdominal image is firstly separated into supervoxels by using the SLIC algorithm, and the supervoxels are classified and labeled as corresponding background or organs with the trained random forest classifier. The labels of the supervoxels from the random forest are distributed to their voxels and a labeled multi-organ segmentation result is obtained.

III. Experiment

A. Data Preparation

In our experiment, a dataset from the "Multi-atlas labeling beyond the cranial vault-workshop and challenge"

[17] was used to evaluation the proposed method. In the dataset, 30 cases of abdominal CT images were acquired from the Vanderbilt University Medical Center (VUMC). Thirteen abdominal organs were manually labeled and the labels of voxels which were not organs of segmentation targets were excluded in the experiment, i.e. organs labeled except for spleen, right kidney, left kidney or liver, are relabeled as background.

B. Supervoxel Classification

The supervoxels partitioned from each image were classified by the random forest multiclass classifier into five labels: 'background', 'spleen', 'right kidney', 'left kidney', and 'liver' from the training set. To measure the performance of the classifier, several evaluators were used on the classification results. As the research focus on organ segmentation and there is an extreme imbalance of supervoxel number of organs or background, we only analysis the relative measurement on four organs, except for background. For each organ, four basic measurements counting numbers of correctly or wrongly classification samples (supervoxels) are used: TP (True Positive), FN (False Negative), FP (False Positive), and TN (True Negative). The definition is as below:

TP: number of supervoxels belong to the organ and were correctly classified as the organ; FN: number of supervoxels belong to the organ but were wrongly classified as the other organ or background; FP: number of supervoxels do not belong to the organ but were wrongly classified as the organ; TN: number of supervoxels do not belongs to the organ and were correctly classified as the other organ or background.

The accuracy and specificity are used to evaluate the classification of supervoxels. The evaluators referred before are calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Specifity = \frac{TN}{TN+FP} \tag{4}$$

The mean accuracy and specificity are shown in Table I.

TABLE I. MEAN ACCURACY AND SPECIFICITY

Organ	Metric	
	Accuracy	Specificity
Spleen	0.6711	0.9990
Right Kidney	0.3822	0.9997
Left Kidney	0.3168	0.9997
Liver	0.7891	0.9997

C. Organ Segmentation

To evaluation the result of segmentation task, the Sorensen–Dice coefficient (DSC) is used to gauge the similarity of the segmentation by out method and the ground truth from the training set:

$$DSC = \frac{2|P \cap G|}{|P|+|G|} \tag{5}$$

where P and G are the voxel numbers of segmentation result and ground truth, respectively. DSC ranges from $[0,1]$ and a higher DSC represents a better segmentation result. In the experiment, we compared the segmentation result with our previous research [18] using random forest regressor and statistical shape model. The mean DSC of spleen, right kidney, left kidney, and liver segmentation results are shown in Table II. Compared with the previous method, the segmentation accuracy is increased by using the proposed method.

TABLE II. MEAN DSC OF EACH ORGAN

Organ	DSC	
	Previous method [18]	Proposed method
Spleen	0.351	0.635
Right Kidney	0.310	0.443
Left Kidney	0.343	0.370
Liver	0.571	0.808

IV. DISCUSSION AND CONCLUSION

The supervoxel clustering is a crucial step in the method. A fundamental requirement for an appropriate supervoxel is that its boundaries must fully cover the edges of organs. As the supervoxels are the tiniest inseparable element in our method, voxels within the supervoxel must process a communal label. That is to say, each voxel on the edges of the ground truth must be included in the set of all the supervoxel boundaries. Hence, a larger number of over segmentations supervoxel is required.

The preprocessing for supervoxel separation focuses on preserving edge information and individual intensity information of each small supervoxel, as well as dividing region of diverse intensities so that the supervoxel clustering can capture tiny edges and distinguish regions of different organs. Hence, usual image smoothing operations to remove noise are not performed in this process, but introduced in the feature extraction stage.

Feature extraction is another key step in supervoxel classification. Proper feature can be used to distinguish supervoxels belong to different organs. In abdominal CT images, the anatomical knowledge is learned by the correspondent relevance between fixed adjacent tissue and organs which are represented by the normalized spatial coordinate feature. However, as the widespread existence of physical differences and body postures, the current spatial feature can only provide information within limited precision. More complicated structural relativities combining adjacent supervoxels can be more effective.

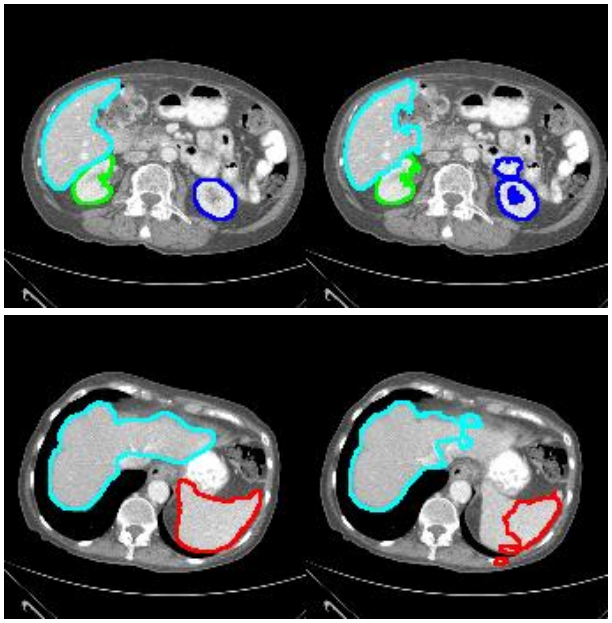

Figure 2. Comparison of ground truth (left) and segmentation result (right), spleen, right kidney, left kidney, and liver are declined in red, green, blue, and cyan, respectively.

Two groups of segmentation result (on the right) and ground truth from manually delineation (on the left) are compared in Fig. 2. In the top group, a redundant tissue belongs to the background is misclassified as left kidney, which is adjacent in position and similar in intensity. In the bottom group, some of the regions belong to liver and spleen are misclassified as background, even the texture of the missed regions is similar. This is probably influenced by the inaccurate spatial features arise from the unaligned images, where improvement is required in the future.

Except for alignment in the preprocess of images, feature extraction is another importance process in this frame. The feature used in the proposed method relies on statistical intensity and their gradient value with limited size. To extract more representative features and distinguish supervoxels better, some more complicated features extraction method that combines local intensity and gradient from different directions can be applied to the supervoxel. As the 3-D super voxel are irregular shapes that contains voxels of uncertain quantity, a proper improvement is required to fit the traditional feature extraction method that are regularly applied to square or cubic cells of images.

When not focusing on the feature of individual supervoxels, the global anatomical priors can also be introduced to the classification and segmentation scheme. In the proposed method, only the spatial position of each single supervoxel are considered as feature. However, for each of the supervoxels that belong to a specific organ, it is adjacent to at least one supervoxel of the organ. The spatial relevance of these adjacent supervoxels can be taken into consideration, which helps maintain the integrity of the organ.

The anatomical priors can also be used to refine the segmentation result after the supervoxel classification by referring statistical atlas which comprising shape or appearance of organs. Given a coarse segmentation result from the classification, like shown in the Fig. 2, a matching is required to fusion the anatomical shape models or atlases. In this procedure, the inter-individual variability is still a challenge and statistical atlas with adequate specification ability is required.

In this article, a random forest classifier based method is proposed for multi-organ segmentation from abdominal CT images. The images are clustered into small units of supervoxels with similar intensities and positions. A group of spatial and intensity features are extracted to distinguish supervoxels by using a random forest classifier. The experiment result shows an improvement in segmentation accuracy especially for spleen and liver compared to our previous shape model based method. To reduce missed segmentation, more distinguishable features are required to represent the differences of object organs and background in the future work.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Jiaqi Wu conducted the research and wrote the manuscript with support from Guangxu Li and Huimin Lu. Tohru Kamiya supervised the project and provided suggestion and recommendations along the way. All authors had approved the final version.

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