A Feasibility Study of Automatic Multi-Organ Segmentation Using Probabilistic Atlas

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Abstract. Thoracic and abdominal multi-organ segmentation has been a challenging problem due to the inter-subject variance of human thoraxes and abdomens as well as the complex 3D intra-subject variance among organs. In this paper, we present a preliminary method for automatically segmenting multiple organs using non-enhanced CT data. The method is based on a simple framework using generic tools and requires no organ-specific prior knowledge. Specifically, we constructed a grayscale CT volume along with a probabilistic atlas consisting of six thoracic and abdominal organs: lungs (left and right), liver, kidneys (left and right) and spleen. A non-rigid mapping between the grayscale CT volume and a new test volume provided the deformation information for mapping the probabilistic atlas to the test CT volume. The evaluation with the 20 VISCERAL non-enhanced CT dataset showed that the proposed method yielded an average Dice coefficient of over 95% for the lungs, over 90% for the liver, as well as around 80% and 70% for the spleen and the kidneys respectively.

1 Introduction

Automatic thoracic and abdominal multi-organ segmentation on clinically acquired computed tomography (CT) has been a challenging problem due to the inter-subject variance of human thoraxes and abdomens as well as complex 3-D relationship among organs. On CT images, the inter-subject variability (e.g., age, gender, stature, normal anatomical variants, and disease status) can be observed in terms of the size, shape, and appearance of each organ. Soft anatomy deformation (e.g., pose, respiratory cycle, edema, digestive status) complicates the segmentation problem even more.

To solve this problem, Toro et al. [1] proposed a method using anatomical hierarchy guided by spatial correlations. Kahl et al. [2] presented a method using feature-based registration. He et al. [3] introduced a method using multi-boost learning and statistical shape model. All of these methods use organ-specific prior knowledge. Therefore, a complicated preprocessing is necessary to obtain

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organ-specific prior knowledge. Moreover, expanding the atlas becomes computationally expensive if more organs should be involved in the segmentation.

A probabilistic atlas-based approach [4] was proposed for the automatic segmentation of abdominal organs and revealed the benefit of probabilistic atlas. However, it only focused on the abdominal organs but didn't involve the organs in the thorax.

In this paper, we present a generic framework for automatic multi-organ segmentation using a probabilistic atlas with extension to the thorax. The atlas includes two lungs, liver, spleen, and two kidneys. The segmentation is then performed based on an atlas registration approach. No organ-specific prior knowledge is required in the proposed method.

2 Materials and methods

2.1 Overview of the proposed framework

Fig. 1 presents the flowchart of the proposed framework, which consists of two steps: the atlas construction and the multi-organ segmentation.

In the step of the atlas construction, all grayscale CT volumes of a training dataset are mapped onto one individual volume using affine transform at first. Subsequently, the alignments are improved by using non-rigid B-spline transform. After the alignments, an average CT volume is calculated. In order to generate a probabilistic atlas in the space of the reference volume, the ground truth segmentations of the training set are warped onto the reference space by using the results of the B-spline transform computed from their CT volumes. The presence of each voxel is then counted for each organ. The probability of a voxel belonging to a certain organ is then calculated by dividing the counts by the volume amount. The probabilities of all target organs build a vector-valued probabilistic atlas finally.

In the step of the segmentation, the coarse alignment of the new CT volume and the average volume is calculated by using affine transformation at first. The alignment is further improved with B-spline transformation. The probabilistic atlas is subsequently projected into the space of the test volume. In the vector-valued probabilistic atlas, one voxel can be labeled as different organ, we decide the organ type by taking the organ with the highest probability. The boundaries are estimated by a simple probabilistic threshold with 0.30.

2.2 Registration methods

As described previously, registration is an important part of the proposed framework, it is used in both atlas construction and segmentation steps. We used a Gaussian image pyramid approach in all registration steps to achieve better results and more reasonable processing time. Four resolutions (8,4,2,1) are applied for the affine transformation while two resolutions (8,2) are applied for the B-spline part. Similarity is measured by the Mattes' mutual information

method [5], which is obtained by double summing over the discrete PDF (probability density function) values. The PDF is estimated using Parzen histograms. Furthermore, the B-spline transformation is constrained by using bending energy penalty term [6]. The cost function of the non-rigid B-spline registration in the proposed framework is summarized as

$$\arg\min_{\mathbf{T}}(S(\mathbf{T}) + \alpha R(\mathbf{T})) \tag{1}$$

where $\mathbf{T}$ is the transformation between the reference and the test image.

$S(\mathbf{T})$ is the negative of mutual information between the reference image and the transformed test image based on Parzen histograms [5]

$$S(\mathbf{T}) = -\sum_{l}\sum_{k} p(l,k \mid \mathbf{T}) \log \frac{p(l,k \mid \mathbf{T})}{p_{\text{Test}}(l \mid \mathbf{T}) p_{\text{Ref}}(k)} \tag{2}$$

where p is the joint probability distribution of the pair of registered images. p_{Ref} and p_{Test} are the marginal probability distribution of the reference image and the test image respectively. k and l indicate the histogram bins of the reference image and the test image.

$R(\mathbf{T})$ in Eq. 1 regularizes the transformation [6], is defined as

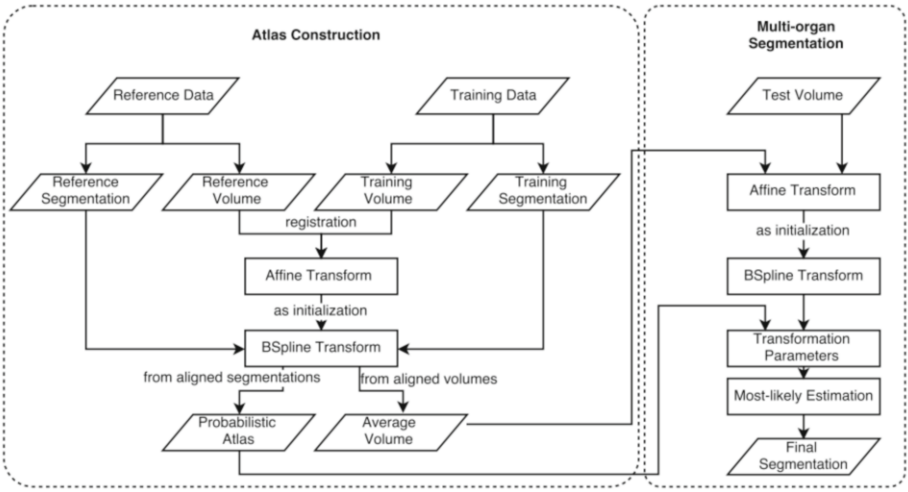


Fig. 1. Flowchart of the proposed method.

$$R(\mathbf{T}) = \frac{1}{V} \sum_x \sum_y \sum_z \left[\left(\frac{\partial^2 \mathbf{T}}{\partial x^2} \right)^2 + \left(\frac{\partial^2 \mathbf{T}}{\partial y^2} \right)^2 + \left(\frac{\partial^2 \mathbf{T}}{\partial z^2} \right)^2 + 2 \left(\frac{\partial^2 \mathbf{T}}{\partial xy} \right)^2 + 2 \left(\frac{\partial^2 \mathbf{T}}{\partial xz} \right)^2 + 2 \left(\frac{\partial^2 \mathbf{T}}{\partial yz} \right)^2 \right]$$

where V denotes the number of voxels.

The α in Eq. 1 determines the weight of the regularization with respect to the similarity measure.

To solve the optimization problem, CMA-ES [7] and ASGD (adaptive stochastic gradient descent) [8] are employed for affine transformation and B-spline transformation respectively. The registration is implemented using the open source image registration toolbox Elastix [9].

3 Results

The proposed method is evaluated with the 20 unenhanced whole body CT data from VISCERAL [10]. 0.30 was taken as the threshold for the boundary estimation. The evaluation tool of VISCERAL was used to compare the segmentation result and the ground truth.

The dataset included 12 male image volumes and 8 female image volumes, so the test was divided into 2 gender groups at first. Leave-one-out cross validation was performed for each gender group. Fig. 2 presents one slice of an average volume and a probabilistic atlas. Fig. 3 plots the Dice coefficients of the segmentation results of the cross validation.

Furthermore, the proposed method was compared with the state-of-the-art methods. The lines 1-3 of Tab. 1 display the average Dice coefficients from other state-of-the-art methods [1, 2, 3]. The line 4 of Tab. 1 list the average Dice coefficients of our tests with a total of 23 cases including male, female and unisex cases. Note that the training and test data setup of these three methods are different from ours. The average Dice of our tests is above 95% for both lungs, around 90% for liver, and between 70% and 80% for other three organs.

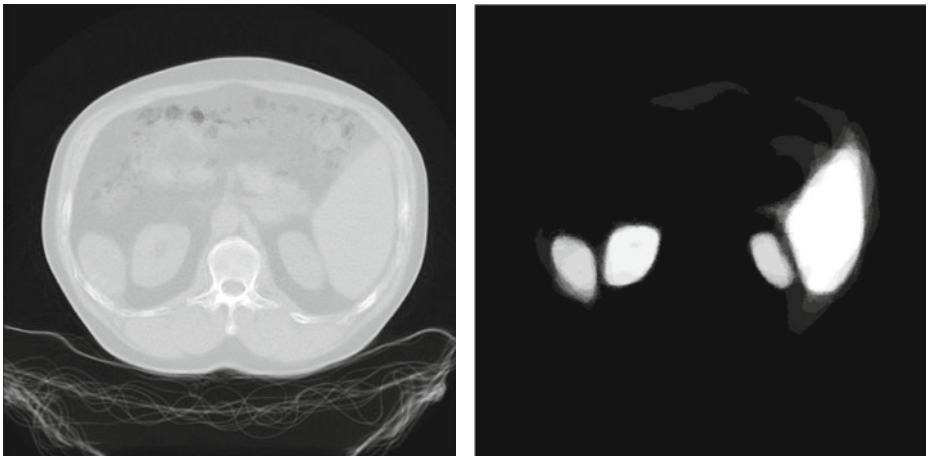
4 Discussion

We proposed a generic framework for an automatic segmentation of multiple organs in abdomen and thorax using probabilistic atlas and registration. We constructed probabilistic atlases and segmented the target organs successfully. The cross validation showed the feasibility and the strong robustness of the method. However, the male group had the higher accuracy for kidneys and spleen

Table 1. Comparison of the Dice coefficients with other methods. '*' means that the methods use other test data. '-' means that no segmentation was provided.

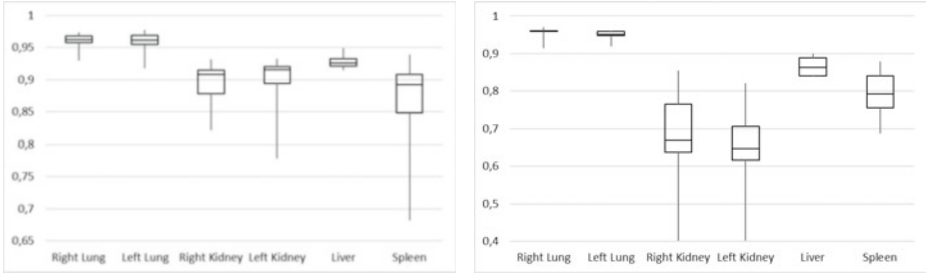
Line		Right Lung	Left Lung	Right Kidney	Left Kidney	Liver	Spleen
1	*Toro et al. [1]	97.5%	97.2%	79.0%	78.4%	86.6%	70.3%
2	*Kahl et al. [2]	97.5%	97.2%	91.5%	93.4%	92.1%	87.0%
3	*He et al. [3]	95.7%	95.2%	-	-	92.3%	87.4%
4	Proposed	96.0%	95.7%	79.4%	73.1%	90.0%	81.3%

than the female group. The reasons for this observations could be: 1. the male group had more samples; 2. the non-rigid tissue variation of the female group was higher. In addition, lungs and liver were more accurate in our registration due to the metric mutual information.



(a) Average volume (b) Probabilistic atlas

Fig. 2. Example of an average volume (left) and a probabilistic atlas (right).



(a) Dice coefficients for male group (b) Dice coefficients for female group

Fig. 3. Results of the cross validation. Left and right figures plot the Dice coefficients for each organ of the male group and the female group respectively.

Compared to the existing methods, our method provided competitive results. The comparison showed that the proposed method is promising and potential. These state-of-the-art methods used organ-specific prior knowledge such as anatomical spatial correlation, organ specific features, boundary profiles and shape variation information. Our method didn't employ any organ-specific prior knowledge. Our process is therefore compact and uncomplicated. Furthermore, it is easy to expand our atlas to incorporate more structures and organs.

To reduce the bias due to the reference selection, better solution for reference selection is required. In addition, using an automatic method [11] to detect the volume-of-interest can also improve the accuracy. Moreover, the decision of the organ type and the estimation of the boundary can be improved in the future work.

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Disclaimer. The concepts and information presented in this paper are based on research and are not commercially available.

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