Segmentation of liver and spleen based on computational anatomy models

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ABSTRACT

Accurate segmentation of abdominal organs is a key step in developing a computer-aided diagnosis (CAD) system. Probabilistic atlas based on human anatomical structure, used as a priori information in a Bayes framework, has been widely used for organ segmentation. How to register the probabilistic atlas to the patient volume is the main challenge. Additionally, there is the disadvantage that the conventional probabilistic atlas may cause a bias toward the specific patient study because of the single reference. Taking these into consideration, a template matching framework based on an iterative probabilistic atlas for liver and spleen segmentation is presented in this paper. First, a bounding box based on human anatomical localization, which refers to the statistical geometric location of the organ, is detected for the candidate organ. Then, the probabilistic atlas is used as a template to find the organ in this bounding box by using template matching technology. We applied our method to 60 datasets including normal and pathological cases. For the liver, the Dice/Tanimoto volume overlaps were 0.930/0.870, the root-mean-squared error (RMSE) was 2.906 mm. For the spleen, quantification led to 0.922 Dice/0.857 Tanimoto overlaps, 1.992 mm RMSE. The algorithm is robust in segmenting normal and abnormal spleens and livers, such as the presence of tumors and large morphological changes. Comparing our method with conventional and recently developed atlas-based methods, our results show an improvement in the segmentation accuracy for multi-organs ($p < 0.00001$).

1. Introduction

Organ segmentation refers to the process of separating the organ of interest from its surroundings for clinical medical images. Manual segmentation of organ structures by an expert is a laborious and time-consuming task. Therefore, automatic or semi-automatic organ segmentation methods have been developed to provide a reproducible, accurate and robust alternative. In order to segment the organs from their medical images, a variety of sophisticated methods of segmenting organs have been proposed [1–4]. This methodological explosion reflects the difficulty of organ segmentation for clinical applications. These methods can be summarized as classification-based [5–7], region-based [8,9],

contour-based [10,11], graph cut-based [12,13] and random walks-based [14,15] segmentations. However, these segmentation methods depend solely on gradient or intensity analysis, and omit the use of anatomical information. Hence, their performance is insufficient when the image contains noise or the contrast between object and background is low.

Recently, significant effort has been focused on the development of anatomical model-based methods, such as probabilistic atlas [16–24] and statistical shape model [25,26] for organ segmentation. In anatomical model based methods, the anatomical model can be used as a priori location and shape information of organs. These methods are robust against noise, but they are sensitive to initialization of their parameters, such as pose and initial contour. Our research focused on the probabilistic atlas-based segmentation method. Most of the work has involved the construction of atlases for organ segmentation [27–31]. Probabilistic atlas-based organ segmentation, however, poses a number of challenges. Accurate mapping of the probabilistic atlas onto the

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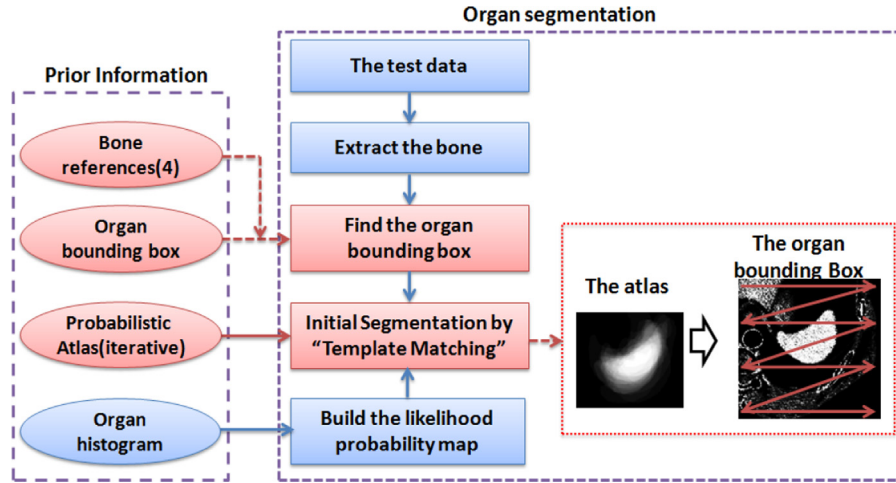chen@is.ritsumei.ac.jp (Y.-w. Chen).

Fig. 1. The framework of our proposed segmentation method.

input CT volumes is difficult because of the variability in organ shape. To resolve this problem, we investigated utilizing an automatic registration method for this application. Park et al. [16] first proposed using probabilistic atlases to model the multiple organs, by manually extracting landmark points on each organ for registering probabilistic atlases based on thin plate spline (TPS). Using a similar principle, the priori information from probabilistic atlases was used to initialize the segmentation of abdominal organs in [17,18]. Both methods used measures of relationship and hierarchy between organs and manual landmarks. Meanwhile, in [19], Zhou et al. constructed the liver atlas for improved liver segmentation that controlled the points of diaphragm surface according to TPS. Linguraru et al. [20] suggested to segment the liver and the spleen from the CT images using the position of the xiphoid to register the probabilistic atlas based on affine transformation. Yamaguchi et al. [21] applied the region-growing method and the probabilistic atlas to segment the liver from the CT images by registering the usage of the anatomical landmarks of the liver based on TPS. Notably, the construction of these abdominal atlases required manual landmarks through user interaction. On a different note, Okada et al. [22,23] developed a hierarchical statistical atlas of the liver normalized to the abdominal cavity as part of a process of automatically segmenting the liver. Recently, Li et al. [24] also proposed an automated liver segmentation method using the rib cage to map the probabilistic atlas onto the input volume. They only considered one type of rib cage as the reference for registration.

However, there are two limitations to these segmentation methods: (1) Errors in landmark extraction may cause incorrect estimation of the transformation. (2) Eventhough the transformation of landmarks can be accurately estimated, it is difficult to achieve the accurate transformation of the organ because of the large variation of anatomical structure.

Taking these two points into consideration, we propose a template matching framework based on a probabilistic atlas for organ segmentation. In our proposed method, we first need to construct a bounding box around the organ based on human anatomical structure, which complies to the relatively rigid characteristics of organ position; and then the probabilistic atlas is used as a template to find the organ in this bounding box by the use of template matching.

Additionally, as described in [16], the main disadvantage of the conventional probabilistic atlas is that it may cause a bias for the specific patient studies due to the single reference. Numerous investigations showed that an iterative atlas construction can reduce the dependence on the reference patient [24]. Hence, in

this paper, we construct an iterative probabilistic atlas for our proposed method to address this bias issue.

The rest of this paper is organized as follows: In Section 2, we describe our proposed method, which explains how to construct the organ bounding box, how to realize the Gaussian intensity model, how to build the iterative probabilistic atlas model, and how to segment the organ. Extensive evaluation of our method is presented in Section 3. Section 4 is devoted to the discussion of performance and Section 5 concludes the paper.

2. Materials and methods

2.1. The segmentation framework

The proposed method segments an abdominal organ based on a set of priori information. Priori information includes the approximate location of an organ, histogram of the organ's intensities, and a probabilistic atlas of the organ. The organ bounding box is employed to estimate the approximate location of an organ for the observed data. The histogram of the organ's intensity is used to build the Gaussian intensity model (likelihood map). The likelihood map together with the probabilistic atlas is employed in the template matching technique. Template matching aims to estimate an initial segmentation of the organ. In the estimation of the organ bounding box, construction of the probabilistic atlas and template matching, the affine registration method is employed. Furthermore, the Geodesic Active Contour (GAC) algorithm [10] is used to refine the initial segmentation results so that they can guarantee the smoothness of the final result. The framework of our proposed method is shown in Fig. 1.

The basic idea of our proposed method is based on Bayes framework. To estimate the organ label L we can follow the principle of the maximum a posteriori probability (MAP) estimation. The posteriori probability can be estimated as:

$$P_{i,j,k}(L|A) \propto P_{i,j,k}(A|L)P_{i,j,k}(L) \begin{cases} Liver & L=1 \\ Spleen & L=2 \end{cases} \tag{1}$$

where $A(i,j,k)$ and $L(i,j,k)$ are the intensity values and organ labels of voxel (i,j,k) in the CT volume, where (i,j,k) is the coordinate for each voxel. $P(A|L)$ is the likelihood map for an organ, $P(L)$ is the iterative probabilistic atlas which is used as a prior probability map. In the following sections, we describe how to segment the multiple organs in the abdominal region.