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Efficient liver segmentation in CT images based on graph cuts and bottleneck detection

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ABSTRACT

Liver segmentation from abdominal computed tomography (CT) volumes is extremely important for computer-aided liver disease diagnosis and surgical planning of liver transplantation. Due to ambiguous edges, tissue adhesion, and variation in liver intensity and shape across patients, accurate liver segmentation is a challenging task. In this paper, we present an efficient semi-automatic method using intensity, local context, and spatial correlation of adjacent slices for the segmentation of healthy liver regions in CT volumes. An intensity model is combined with a principal component analysis (PCA) based appearance model to exclude complex background and highlight liver region. They are then integrated with location information from neighboring slices into graph cuts to segment the liver in each slice automatically. Finally, a boundary refinement method based on bottleneck detection is used to increase the segmentation accuracy. Our method does not require heavy training process or statistical model construction, and is capable of dealing with complicated shape and intensity variations. We apply the proposed method on XHCSU14 and SLIVER07 databases, and evaluate it by MICCAI criteria and Dice similarity coefficient. Experimental results show our method outperforms several existing methods on liver segmentation.

1. Introduction

Accurate segmentation of liver tissue from abdominal medical images is an essential and vital step for computer-aided liver disease diagnosis and surgical planning. Currently, computed tomography (CT) is one of the most widely-used medical imaging techniques, thanks to its high signal-to-noise ratio and spatial resolution [1]. In clinical practice, segmentation is usually performed manually by expert radiologists through tracing the organ contours on each slice. Since the number of slices in a CT volume is very large, manual segmentation is time-consuming and tedious. Moreover, the results highly rely on experience and skill of radiologists. Therefore, a semi-automatic or automatic liver segmentation from CT images has attracted increasing research attention. However, it is a challenging task to develop an efficient, accurate and automatic liver segmentation scheme from CT volumes due to inhomogeneous intensities in liver, low contrast between liver and other organs, and the varying intensities and shapes of livers.

There are numerous methods proposed for liver segmentation from CT volumes. In general, they can be categorized into four types: image-based, statistical model-based, atlas-based, and hybrid methods. The image-based methods intend to segment objects based on intensity, texture, and other properties in an image, including thresholding [2], clustering [3], region growing [4], deformable models [5–7], and graph cuts [8–10]. Selver et al. [3] presented a liver segmentation approach from CT volumes based on morphology, K-means, and multi-layer perceptron network (MLP). Lu et al. [4] proposed an improved region growing algorithm for liver segmentation, where Quasi-Monte Carlo method was used to select seed points from the Region of Interest (ROI) and design region growing criteria. The deformable model based methods usually generate a local minimum of an energy function, which is sensitive to contour initialization and has large iterative computation burden [5,6]. Peng et al. [7] employed a constrained convex variation model in combination with intensity and regional appearance features for liver boundary delineation, in which an intensity based weight function was introduced to help identify ambiguous liver edges.

Some studies used statistical model and probabilistic atlas based techniques, which employ object population shape and

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appearance prior to segmenting livers from abdominal CT images, and achieved satisfactory results [11–13]. These techniques usually require a complicated and time-consuming model constructing and matching process and are sensitive to initialization and registration. One benefit of these methods is that, even when the information of some object regions is destroyed or lost, such regions can be recognized by drawing upon the prior information presented in the model. However, due to the variation in appearance and shape between different patient data sets, the advantage of an average model or standard template is weakened for practical application in spite of the heavy training efforts [14].

Recently, graph-cuts methods show great potential with the advantage of globally optimal solution computation. Afifi and Nakaguchi [8] proposed a liver segmentation approach using graph cuts, in which the correlation of neighboring slices is used to estimate the shape and intensity statistical information of liver. A strategic combination of the active appearance model, live wire, and graph cuts was proposed for abdominal organ segmentation, and was successfully applied in liver segmentation [9]. Lingutaru et al. [10] presented an automatic method for the simultaneous segmentation of multi-organs from multiphase CT data using graph cuts. Enhancement information from multiphase CT, shape information from Parzen windows, and location information from probabilistic atlas are integrated into graph cuts for segmentation. Peng et al. [15] proposed a semi-automatic method for liver segmentation based on multi-region appearance model and graph cuts, in which the liver was treated as multiple subregions and a geodesic distance based appearance selection scheme was introduced to utilize proper appearance constraint for each subregion. Song et al. [16] used an adaptive fast marching method (FMM) to delineate the liver contours, where the seed points and the parameters in FMM were achieved automatically according to the intensity characteristics of liver. The DICE coefficient achieved by this method on a local database is 96.7%. Beichel et al. [17] developed an interactive liver segmentation system, where the CT volume was segmented by graph cuts initially, followed by a 3D refinement method to correct the initial segmentation by the user. The average volumetric overlap error achieved by this method is 3.74%. Wu et al. [18] proposed an automatic liver segmentation method using supervoxel-based graph cuts. First, the supervoxels of the liver volume of interest (VOI) were generated using the simple linear iterative clustering. Then, the graph cuts algorithm was applied to the supervoxels of VOI to obtain the segmentation results.

Due to intensity similarity of adjacent organs and tissues, over-segmentation is very difficult to avoid. To solve this problem, some boundary refinement methods were proposed and applied for liver segmentation. For example, Selver et al. [3] utilized morphological operation and nonlinear filtering to remove the over-segmented regions and smooth the liver boundary. Similarly, morphology based methods were also applied as post-processing for over-segmentation correction and boundary smooth in [4] and [8]. All these morphology-based methods can only separate the over-segmented regions which are weakly connected with livers. Gloger et al. [19] used Fourier descriptor to remove some sharp edges and small over-segmented regions by discarding high frequencies on the boundary, which also reduces the accuracy of liver segmentation for real regions.

In this paper, we propose a semi-automated method for liver segmentation from abdominal CT volumes, which mainly consists of two steps: segmentation and refinement. In the segmentation step, a novel intensity model and a PCA-based regional appearance model are first built according to the characteristics of a given CT volume. Then the liver region is segmented by graph cuts integrated with the intensity and appearance models, and the location information from the previous segmented adjacent slice. In the refinement step, polygonal approximation is first applied to extract feature points from the initial segmented liver contour. Then a bottleneck based liver boundary refinement method is proposed to remove possible over-segmented regions, where the splitting point pairs for over-segmented region separation are identified by bottleneck detection and mean geometric distance judgment.

The main contributions of this paper are threefold. First, an intensity model is used to exclude complex background and highlight liver, which can deal with intensity variation across different patients. Second, pixel- and regional-based information together with location information from adjacent slice are integrated into graph cuts for liver segmentation. Third, a bottleneck based method is proposed to refine the contour of the initial segmented liver to avoid the possible over-segmentations. Compared to some existing methods, there are three advantages in our algorithm. First, the proposed method does not require removing adjacent tissues or organs in advance. Second, it can deal with complex liver shape and intensity variation. Finally, no prior model is needed, which can eliminate the burdens associated with model construction and matching.

2. Methodology

2.1. Overview of the approach

Fig. 1 presents an overview of the proposed method, where an iterative segmentation strategy is employed to extract liver slice by slice. To begin with, a small liver region is manually selected from the input CT volume to establish the intensity and appearance models to highlight the liver region. Then, the liver region in an initial slice is segmented by graph cuts combining the intensity and appearance models, and further refined by a bottleneck based method to remove the over-segmented regions. Finally, the remaining slices of the same volume are segmented iteratively from the initial slice to the last one and the first one, respectively. During the entire segmentation process, the liver location information derived from the previous segmented slice is integrated into graph-cuts cost computation for the current slice segmentation. This iterative process continues until all slices are segmented.

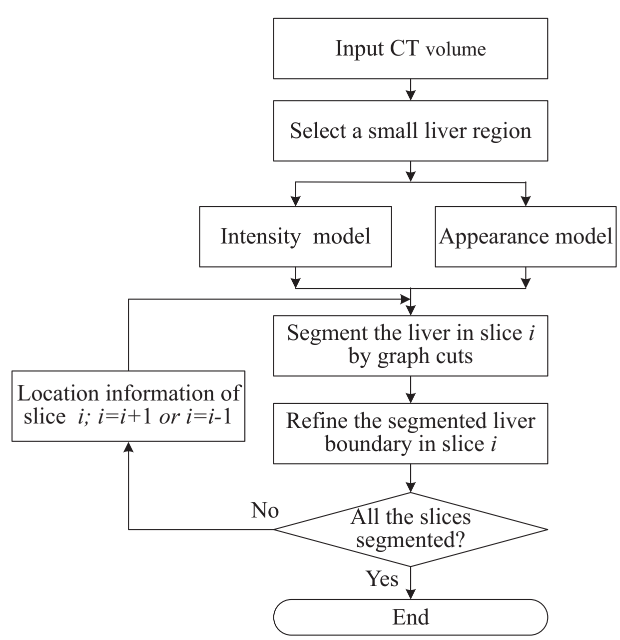

Figure 1. Flowchart of our proposed method.