Pathological liver segmentation using stochastic resonance and cellular automata ☆

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ABSTRACT

Liver segmentation continues to remain a major challenge, largely due to its intensity complexity with surrounding anatomical structures (stomach, kidney, and heart), high noise level and lack of contrast in pathological computed tomography data. In this paper, we present an approach to reconstructing the liver surface in low contrast computed tomography. The main contributions are: (1) a stochastic resonance based methodology in discrete cosine transform domain is developed to enhance the contrast of pathological liver images, (2) a new formulation is proposed to prevent the object boundary, resulted by cellular automata method, from leaking into the surrounding areas of similar intensity, and (3) a level-set method is suggested to generate intermediate segmentation contours from two segmented slices distantly located in a subject sequence. We have tested the algorithm on real datasets obtained from two sources, Hamad General Hospital and MICCAI Grand Challenge workshop. Both qualitative and quantitative evaluation performed on liver data show promising segmentation accuracy when compared with ground truth data reflecting the potential of the proposed method.

1. Introduction

In the area of computer-aided diagnosis, appropriate segmentation of liver tissue from medical images is a prerequisite for hepatic diseases diagnosis and surgery planning. This is because most of the diseases associated with liver are believed to be strongly correlated with its shape and image segmentation provides adequate information about the shape and size of an object. However, due to the highly varying shape of liver and weak edge between adjacent organs (e.g., heart, stomach, and kidney muscles), liver segmentation has become a challenging task and attracted enormous research attention [1–8].

1.1. Clinical challenges

Accurate segmentation of pathological liver is a difficult task due to its diversity in shape, presence of high noise level, and low contrast. Since the tumor pattern in liver varies greatly in different cases, accurate segmentation of liver region by computer requires the use of a more sophisticated algorithm than that for a normal liver. Furthermore, other factors such as blurring artifacts or low signal-to-noise ratio also increase the difficulties in segmentation.

1.2. Related work

Generally, pathological CT images are preferred to be segmented manually by trained clinicians, because most of the existing automated methods do not match with the expectations of clinicians. However, manual methods are often a time-consuming and tedious procedure to achieve good segmentation due to presence of edge blurring and occlusions in input data. Furthermore, the trained eye of a medical expert could only be able to segment regions of interest with prior knowledge of anatomy (shape), which could also be a difficult task for the livers having serious pathologies. On the other hand, a semi-automated method with reasonable interactions, is believed to be more suitable because of being able to guide the resulting contour as per the desire of the clinician [9]. We restrict ourselves within the periphery of semi-automated algorithms and explore the pros and cons of state of art algorithms.

Although level-set methods [10] have gained tremendous popularity, they are not without drawbacks; some problems like computational complexity, re-initialization of the zero level set still exist. In the early level-set methods, the computation is carried out on the entire domain making the computation slow. Narrow

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band level-set methods [11] restrict the computation to a narrow band around the zero level set, but it does not reduce the computational cost to a reasonable limit. Goryawala et al. [59] propose a semi-automatic algorithm that is structured as a parallel-aware process so that a computationally taxing task can be distributed over various computing nodes. Wang et al. [12] propose a novel fuzzy cellular neural network based method addressing problems like uneven liver boundaries and organs overlapping. Liu et al. [13] develop a concavity removal algorithm that deals with abnormal livers, particularly with those having lesions at the liver edges. Suzuki et al. [14] present a method based on GAC coupled with level-set algorithm to extract liver for measuring liver volumes in hepatic CT. Foruzan et al. [15] propose a 5-step procedure for liver segmentation. The liver contours are first extracted using watershed algorithm, tumors are then segmented using a minimum cross-entropy multi-thresholding algorithm. The method by Choudhary et al. [16] follows a procedure to segment the ribs first with simple thresholding and Cubic-Hermite shape preserving interpolation on the slices. These obtained curves are further used as constrains for the liver segmentation.

1.3. Graph-based methods

Without doubt, graph-based methods have advanced our understanding of image segmentation and have successfully been employed since sometime without heavy reliance on explicitly learned/encoded priors. Intelligent scissors is a boundary-based interactive method, that computes minimum-cost path between user-specified boundary points [17]. However, this is unable to integrate any regional bias naturally, which is overcome by the Graph Cut method as follows. Graph Cut [20] is a combinatorial optimization technique where the globally optimal pixel labeling can be efficiently computed by maxflow/min-cut algorithms. Graph partitioning problem has been another attempt [47] to segment the graph, however, its performance degrades when noise level in medical data is high. Furthermore, the performance typically relies on the weighting function that measures the similarity between two pixels. This has been a really tough task to define a suitable function, especially, for medical images. Grab Cut [21] extends Graph Cut by introducing iterative segmentation scheme. There are also other graph based image segmentation methods in the literature, such as Random Walk [23], however, the selection of initial seeds on labels of interest is a tough task in slow intensity varying medical images. Despite having a huge literature on graph based algorithms, more attempts are still being made to develop a robust, suitable and user friendly method. In this context, we apply a cellular automata based method to segment liver from low contrast CT data.

1.3.1. Advantages of cellular automata in image segmentation

Cellular automata (CA) theory is based on a discrete dynamic system, defined on a lattice, where the system states are iteratively propagated via local transition rules. Since CA is an iterative method, each cell independently follows a set of rules, this naturally lends itself to an efficient parallel implementation. Further, the iterative nature of this method enables the user to interact with the method and visualize the results during the segmentation process. Increasing the number of labels does not increase the computational time or complexity, in other words, it supports m-labels and n-dimensions concept.

1.3.2. Technical challenges

Typically, a traditional CA method [54] uses local pixel information to guide the evolution, making it prone to errors where sharp boundaries do not exist. Therefore traditional CA, when implemented on real pathological liver datasets, leads to pseudo object boundaries. This is because, liver region pixel intensity is sightly different from the surrounding muscles. There have been numerous efforts [24–29] till date to test and improve the efficiency of CA. However, most of the methods that include CA have been hand created ad hoc and, even though some do consider multidimensional images, they are still far from the dimensions of hyperspectral images and are usually projected onto a lower dimension during the segmentation process. Furthermore, high-level noise and low contrast characteristics in medical images continue to present major challenges in their segmentation despite increased imaging modalities.

In this paper, a hybrid approach is proposed that combines cellular automata and active contour algorithm to segment the liver from CT data. Since we focus more on those data that have low contrast and high level of noise, a pre-processing step before the actual segmentation is performed to enhance the image contrast using the noise present in the data constructively. Noise is usually thought to be a nuisance that disturbs the system or system performance. Stochastic resonance (SR), on contrary, is a phenomenon in which noise can be used to enhance rather than hinder the system performance. Besides a few attempts ([30–36] for example), this is yet to get the full-fledged attention from the image processing community.

We present a new method that integrates the label priors learned from the user interactions into the energy associated with the labels in order to grow the foreground (FG) and background (BG) cells over similar intensity regions of interest, eventually segmenting the liver. The basic idea is to segment liver from a few selected slices of a subject sequence, for which, a CA-based technique is combined with the active contour method. The next goal is to build the surface of the liver; to achieve this, we utilize level sets to automatically segment the rest of the slices from the segmented slices. The remainder of this paper is structured as follows: in Section 2, the proposed method is described in detail. This section includes the procedure to (1) enhance the contrast of pathological liver images, and (2) segment 2D CT images detailing their mathematical formulations. Since the objective is to reconstruct the liver surface from a few selected slices of a subject, this segmentation method is actually applied to these selected slices. Section 2.4 discusses the technique to automatically segment the rest of the slices in order to reconstruct the liver surface. The experimental data description and performance analysis of the method are given in Section 3. Section 3.2 presents a thorough discussion on the portrayed algorithm and Section 4 concludes the paper.

2. Proposed method

Our proposed methodology is divided into two modules: (1) image contrast enhancement (CE) by stochastic resonance theory, and (2) CA-based image segmentation on the contrast enhanced image. There have been some methods that use SR in different domains such as Fourier [30] and discrete cosine transform [42]. However in this work, a technique, based on SR in discrete Heartly transform (DHT) domain [32], is suggested for the enhancement of low contrast images since outliers are resulted by using the discussed domains, say DCT, as shown in Fig. 3(a). We use discrete Gabor transform (DGT) that uses DHT features to enhance the contrast. The DHT advantages, typically for medical datasets, are manifold: it (1) does not produce any artificial discontinuities, (2) allows the use of more elegant fast transform algorithms when the input data are real, (3) it has also superior energy compaction efficiency.

2.1. Image enhancement using stochastic resonance

Typically, presence of high level of noise in medical data negatively affects the contrast, therefore, subsequent operations (say,