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Abstract. Liver segmentation continues to remain a major challenge, largely due to its intense complexity with surrounding anatomical structures (stomach, kidney, and heart), high noise level and lack of contrast in pathological computed tomography (CT) data. We present an approach to reconstructing the liver surface in low contrast CT. 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, resulting from the 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 medical image computing and computer-assisted interventions grand challenge workshop. Various parameters in the algorithm, such as w , Δt , z , α , μ , α_1 , and α_2 , play imperative roles, thus their values are precisely selected. 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. © 2015 Society of Photo-Optical Instrumentation Engineers (SPIE) [DOI: 10.1117/1.JMI.2.2.024006]

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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 the 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 the weak edge between adjacent organs (e.g., heart, stomach, and kidney muscles), liver segmentation has become a challenging task and attracted enormous research attention. A rich tradition of work on image segmentation has focused on the establishment of appropriate object models; in fact, the literature on segmentation techniques is huge.^{1–8}

1.1 Challenges

Accurate segmentation of pathological liver is a difficult task due to its diversity in shape, the 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 computed tomography (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 the 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 semiautomated 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 semiautomated algorithms and explore the pros and cons of state of art algorithms.

Although level-set methods¹⁰ have gained tremendous popularity, they are not without drawbacks; some problems like computational complexity and reinitialization 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 band level-set methods¹¹ restrict the computation to a narrow band around the zero level set, but this does not reduce the computational cost to a reasonable limit. Goryawala et al.¹² propose a semiautomatic algorithm that is structured as a parallel-aware process so that a computationally taxing task

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can be distributed over various computing nodes. Wang et al.¹³ propose a novel fuzzy cellular neural-network based method addressing problems like uneven liver boundaries and the overlapping of organs. Liu et al.¹⁴ develop a concavity removal algorithm that deals with abnormal livers, particularly with those having lesions at the liver edges. Suzuki et al.¹⁵ present a method based on geodesic active contour coupled with a level-set algorithm to extract liver for measuring liver volumes in hepatic CT. Foruzan et al.¹⁶ propose a five-step procedure for liver segmentation. The liver contours are first extracted using a watershed algorithm and tumors are then segmented using a minimum cross-entropy multithresholding algorithm. The method by Choudhary et al.¹⁷ follows a procedure to segment the ribs first with simple thresholding and a cubic Hermite shape preserving interpolation on the slices. These obtained curves are further used as constraints for the liver segmentation.

1.3 Graph-Based Methods

Without a doubt, graph-based methods have advanced our understanding of image segmentation and have successfully been employed for sometime without heavy reliance on explicitly learned/encoded priors. Intelligent scissors is a boundary-based interactive method that computes the minimum-cost path between user-specified boundary points.¹⁸ However, this is unable to naturally integrate any regional bias, which is overcome by the graph cut method as follows. Graph cut¹⁹ is a combination optimization technique where the globally optimal pixel labeling can be efficiently computed by maxflow/min-cut algorithms. Graph partitioning problem has been another attempt²⁰ to segment the graph, however, its performance degrades when the 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 very difficult task for which to define a suitable function, especially for medical images. Grab cut²¹ extends graph cut by introducing an iterative segmentation scheme. There are also other graph-based image segmentation methods in the literature, such as random walk,²² however, the selection of initial seeds on labels of interest is difficult 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 (CA)-based method to segment liver from low contrast CT data.

1.3.1 Advantages of CA in image segmentation

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 -dimension concepts.

1.3.2 Challenges

Typically, a traditional CA method²³ 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 slightly different from the surrounding muscles. There have been numerous efforts^{24–29} to 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 CA and an active contour algorithm to segment the liver from CT data. Since we focus more on those data that have a low contrast and high level of noise, a preprocessing step before the actual segmentation is performed to enhance the image contrast using the constructive noise present in the data. Noise is usually thought to be a nuisance that disturbs the system or system performance. Stochastic resonance (SR), on the contrary, is a phenomenon in which noise can be used to enhance rather than hinder the system performance. Except for a few attempts (for example, Refs. 30–35), this is yet to get 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 Sec. 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 two-dimensional (2-D) 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 2.3 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 Sec. 3. Section 3.2 presents a thorough discussion on the portrayed algorithm and Sec. 4 concludes the paper.

2 Proposed Method

Our proposed methodology is divided into two modules: (1) image contrast enhancement by SR theory and (2) CA-based image segmentation on the contrast-enhanced image. The preservation of edges is essential; therefore, to avoid the loss of high-frequency components that occurs in most of the traditional methods such as smoothing, we have found a discrete cosine transform (DCT) is quite useful.³⁶ This is because DCT provides spectral separation, therefore, it is possible to enhance the features by treating different frequency components differently. DCT has also some more interesting features: it (1) transforms a signal from the spatial domain into a frequency domain, (2) provides a better approximation of a signal with a few

coefficients, and (3) decreases the computation time by discarding higher frequency DCT coefficients and preserving the information. Since important structural information is present in the low frequency DCT coefficients, the separation of high-frequency DCT coefficients from the low frequency ones certainly helps to enhance the contrast, thus preserving the edge information. There are some other advantages^{36,37} of DCT-based enhancement: (1) high processing speed, (2) low computational complexity, and (3) reduced storage requirements. There has been some research on the block DCT domain (for example, see Ref. 38), however, due to independent processing of blocks, the presence of blocking artifacts may become more visible in the processed data. Sometimes superfluous edges may appear at the image boundaries due to sharp discontinuities of the intensity distribution.

2.1 Image Enhancement Using SR

Typically, the presence of high level of noise in medical data negatively affects the contrast, therefore, subsequent operations (say, segmentation, registration, etc.) on these data may not provide satisfactory results.³⁹ SR is a counter-intuitive phenomenon where noise is used to suppress noise and enhance the system performance.⁴⁰ In this work, our aim is to enhance low contrast images without introducing any blocking artifacts by using the SR phenomenon. Basically, SR occurs if the signal-to-noise ratio (SNR) and input/output correlation have a well-marked maximum at a certain noise level.³⁰ Therefore, SNR is one of the most common quantifiers in SR. This can be represented as⁴¹

$$\text{SNR} = \left[\frac{4a}{\sqrt{2}(\sigma_0)^2} \right] \exp\left(-\frac{a}{2\sigma_0^2}\right), \quad (1)$$

where σ_0 is the standard deviation of the noise in the SR system. Unlike very low or high noise intensity levels, moderate ones allow the signal to cross the threshold, giving maximum SNR at some optimum noise level (Fig. 1). In the bistable SR model (Fig. 1), upon addition of zero mean Gaussian noise, the pixel is transferred from a weak signal state to a strong signal state, described by Brownian motion of a particle placed in a double well potential system. The double well represents the contrast of an image and the position of the particle as the intensity value. The state, at which performance metrics³⁰ are found to be optimum, is considered as the stable state that provides maximum SNR. On increasing the number of iterations beyond this, the state becomes oscillatory.

2.1.1 Mathematical formulation of SR in DCT domain

Considering the input image $u_0(x, y)$, having N rows and M columns, in an actual physical space, its corresponding DCT $u'_0(u, v)$ is obtained as

$$u'_0(u, v) = \sqrt{\frac{2}{M}} \sqrt{\frac{2}{N}} \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} \alpha_u \alpha_v u_0(x, y) \cos \frac{(2x+1)u\pi}{2M} \times \cos \frac{(2y+1)v\pi}{2N},$$

where u, v are the DCT frequency pair corresponding to spatial coordinate x, y , and

$$\alpha_u = \begin{cases} \sqrt{\frac{1}{2}} & \text{for } u = 0, \\ 1 & \text{otherwise,} \end{cases}$$

and

$$\alpha_v = \begin{cases} \sqrt{\frac{1}{2}} & \text{for } v = 0, \\ 1 & \text{otherwise.} \end{cases}$$

On applying SR to the DCT coefficients:

$$u'_0(x, y)_{\text{SR}} = \sqrt{\frac{2}{M}} \sqrt{\frac{2}{N}} \sum_{u=0}^{M-1} \sum_{v=0}^{N-1} \text{SR} \left[\alpha_u \alpha_v u'_0(x, y) \times \cos \frac{(2x+1)u\pi}{2M} \cos \frac{(2y+1)v\pi}{2N} \right].$$

A classic one-dimensional nonlinear dynamic system that exhibits SR is modeled with the help of the Langevin equation of motion⁴² in the form

$$m \frac{d^2x(t)}{dt^2} + \gamma \frac{dx(t)}{dt} = -\frac{dU(x)}{dx} + \sqrt{D}\xi(t). \quad (2)$$

This equation describes the motion of a particle of mass m moving in the presence of friction, γ . The restoring force is expressed as the gradient of some bistable potential function $U(x)$. In addition, there is an additive stochastic force $\xi(t)$ with intensity D .

If the system is heavily damped, the inertial $m[d^2x(t)/dt^2]$ term may be neglected. Rescaling the system in Eq. (2) with

Fig. 1 (a) Foreground (FG) and background (BG) seed placement. (b) Segmentation in the presence of a tumor. (c) Signal-to-noise ratio (SNR) versus noise density curve. (d) Stochastic resonance in the biphasic form: The area from $-x_m$ to x_m represents the transition under noise, crossing over the threshold.³⁰

the damping term γ gives stochastic overdamping which is frequently used to model nonequilibrium critical phenomena as given in Eq. (3).

$$\frac{dx(t)}{dt} = -\frac{dU(x)}{dx} + \sqrt{D}\xi(t). \quad (3)$$

The bistable quartic potential function $U(x)$ (Fig. 1) may be defined as

$$U(x) = -a\frac{x^2}{2} + b\frac{x^4}{4}. \quad (4)$$

Here, a and b are positive bistable double-well parameters. The double-well system is stable at $x_m = \pm\sqrt{a/b}$ separated by a barrier of height $\Delta U = a^2/4b$ when the $\xi(t)$ is zero.

The addition of a periodic input signal $[B \sin(\omega t)]$ to the bistable system makes it time-dependent, which is governed by Eq. (5).

$$\frac{dx(t)}{dt} = -\frac{dU(x)}{dx} + B \sin(\omega t) + \sqrt{D}\xi(t), \quad (5)$$

where B and ω are the amplitude and frequency of the periodic signal, respectively. It is assumed that the signal amplitude is small enough so that in the absence of noise, it is insufficient to force a particle to move from one well to the other.

Substituting $U(x)$ from Eqs. (4) into (5), we get

$$\frac{dx(t)}{dt} = [ax - bx^3] + B \sin(\omega t) + \sqrt{D}\xi(t). \quad (6)$$

In this manner, the SR is modeled. Conceptually, the noise term $\sqrt{D}\xi(t)$ and the input term $B \sin(\omega t)$ are replaced by DCT coefficients of $u_0(x, y)$, i.e., $u'_0(u, v)$. In Eq. (6), the SR is produced by the noise term $\sqrt{D}\xi(t)$, whereby the maximization of the SNR occurs at double well parameter a .

Application of SR on digital images necessitates the need for solving the stochastic differential equation given in Eq. (6) using the stochastic version of Euler–Maruyama’s method⁴³ that gives an iterative discrete equation as follows:

$$x(n+1) = x(n) + \Delta t\{[ax(n) - bx^3(n)] + \text{Input}\}, \quad (7)$$

where n is the iteration. It may be noted that $\text{Input} = B \sin(\omega t) + \sqrt{D}\xi(t)$ denotes the sequence of the input signal and noise, with the initial condition being $x(0) = 0$. The transformed coefficients contain the signal (image information) as well as noise. Here, Δt is the sampling time and is experimentally taken as 0.007 s.

The image can be inverted back into the spatial domain using

$$u'_0(x, y) = \sqrt{\frac{2}{M}} \sqrt{\frac{2}{N}} \sum_{u=0}^{M-1} \sum_{v=0}^{N-1} \alpha_u \alpha_v u'_{0SR}(u, v) \cos \frac{(2x+1)u\pi}{2M} \\ \times \cos \frac{(2y+1)v\pi}{2N}.$$

2.1.2 Parameters Selection for CE

SNR is maximized by differentiating SR with respect to a and equating it to zero. This leads to $a = 2\sigma_0^2$, where σ_0 is the noise level administered to the input image. At the same time, the maximum possible value of the restoring force can be obtained by

$$R = -\frac{dU}{dx} = ax - bx^3, \quad \frac{dR}{dx} = a - 3bx^2 = 0, \quad (8)$$

resulting in $x = \sqrt{a/3b}$. Assuming $R = B \sin(\omega t)$, the value of R becomes maximum $\sqrt{4a^3/27b}$ at this x . In other words, $B \sin \omega t < \sqrt{4a^3/27b}$; the inequality expression indicates that the value of b must be less than $\sqrt{4a^3/27}$.

CE Summary

The actual CE of the input CT image follows the steps as described below:

- 1) Compute DCT decomposition of the input CT image.
- 2) Apply SR to DCT coefficients.
 - (a) Initialize $x(0) = 0$, $a = w \times 2\sigma_0^2$, and $b = z \times \sqrt{(4a^3/27)}$; initially, w is an experimentally chosen constant which later becomes dependent on the input image standard deviation, while z is a number less than 1 to ensure subthreshold condition of the signal.
 - (b) Compute tuned DCT coefficients using iterative equation given in Eq. (7).
 - (c) Compute inverse DCT from these enhanced coefficients to give enhanced image after $(n+1)$ ’th iteration. The distribution separation measure (DSM)³⁰ of the output is computed after every iteration, i.e., $\chi = |\mu_T^E - \mu_B^E| - |\mu_T^O - \mu_B^O|$, where μ_T^E and μ_B^E are the mean of the selected target regions of the enhanced and original images, respectively; μ_T^O and μ_B^O are the mean of the selected BG region of the enhanced and original images, respectively. If χ no longer increases but, instead starts decreasing (as shown in Fig. 2), then this iteration is considered as optimal and the process stops. The contrast-enhanced image at this iteration is considered as the optimal output of the process.

Following the image enhancement, the resulted image is used as the input to the proposed segmentation method. The algorithm resembles a graph-based method, where the seeds for FG and BG are defined by the user in a polygon manner, as shown in Fig. 1; this provides an efficient mean of selecting the region of interest.

2.2 Dynamic CA

Brief BG of CA and the difficulties in its implementation on medical images need to be understood before describing the need of dynamic CA in liver segmentation.

2.2.1 Cellular automata

CA are a spatially extended decentralized system in which a set of cells is distributed in space and communicate only with their neighbors. Each cell is basically an automaton and the state of a cell at each instant of time depends on the state of its neighbors and its own previous state through a set of transition rules. Therefore, the full computational capabilities of the whole system are achieved by adequately choosing these rules and iterating the state transition process in time. CA considers each pixel as a cell; starting from a random number of labels, the value for each cell is updated using the information of its current state and its neighbors.

Fig. 2 (a) Distribution separation measure at every iteration in contrast enhancement (CE) process. In case of medical image computing and computer assisted interventions (MICCAI) database, values of (b) Hausdorff distance (HD). (c) Intraregion uniformity (I_h). (d) Mean error rate (MER). (e) False-positive ratio (FPR). (f) False-negative ratio (FNR). (g) Specificity. (h) Precision. (i) Accuracy. (j) Pratt's figure of merit (FOM). (k) Dice coefficient (DC). (l) Sensitivity.

There are certain problems associated with traditional CA when applied to real-time medical images; for example, some CA methods, in the presence of noise, produce directed percolation.⁴⁴ It is noteworthy to mention that noise is inherent in the process of medical data acquisition; therefore, naive application of CA usually leads to pseudo results (as shown in Sec. 3.1). Furthermore, most of the pathological liver CT images show poor contrast between liver and surrounding tissues thus giving minimal edge information. These two primary problems combined together exacerbate the convergence yielding erroneous results. We, therefore, propose to use dynamic cellular automaton (DCA)⁴⁴ that mitigates the convergence problem and improves the performance.

2.2.2 Dynamic CA

DCA is a hybrid approach of CA and active contour⁴⁵ for pixel labeling from an initialized curve C_{object} . The model consists of a grid of cells that influence a set of neighboring cells according to the transition or evolution rules. The state transition rules are applied iteratively to update the value of each pixel in the image during the process. In this application, some cells are initially assigned labels (user places seeds in the form of scribbles as shown in Fig. 1, one scribble for FG and the other for BG) and these cells attempt to propagate their labels to neighboring cells. At label boundaries, neighbors compete with each other based on the transition rules. The computation continues with label boundary propagation until the automaton converges to a stable configuration, where cell states cease to change. The maximum strength label is taken as the final label classification.

Mathematically, a (bidirectional, deterministic) DCA is a triplet $A = (S, N_e, \delta)$, where S is a nonempty state set, N_e is the neighborhood system $N_e = \|p - q\|_1 := \sum_{j=1}^2 |p_j - q_j| = 1$ $q \in \mathbb{R}^2$, where q is the adjacent pixel of p , and $\delta: S^{N_e} \rightarrow S$ is the local transition function (rule). This function defines the rule of calculating the cell's state at $t + 1$ time step, given the states of the neighborhood cells at the previous time step t . The cell state S_p is actually a quadruplet $(u_{0p}, \theta_p, E_p, \vec{C}_p)$ —current cell label u_{0p} , current cell strength θ_p (strength of a cell is a function of image features and is used to define the state transition function for updating the labels of cells at each time step), cell energy E_p , and cell feature vector $\vec{C}_p$, defined by the image; $\theta_p \in [0, 1]$. The meaning of the quadruplet remains the same with the change in subscript (say p to q), it is only a matter of a change in nodes. When the user starts the segmentation by specifying the segmentation seeds, the seeded labels are set accordingly, while their strength is set to the seed strength value; this sets the initial state of the process. At iteration $t + 1$, cell labels u_{0p}^{t+1} and strengths θ_p^{t+1} are updated, for example, if $g(\|\vec{C}_p - \vec{C}_q\|_2) \cdot \theta_q^t > \theta_p^t$, then $u_{0p}^{t+1} = u_{0q}^t$ and $\theta_p^{t+1} = g(\|\vec{C}_p - \vec{C}_q\|_2) \cdot \theta_q^t$; g is a monotonous decreasing function. If this transition rule is not satisfied, the cell state remains unaltered. This operation is performed for each pixel in the neighborhood until the automaton converges to a stable configuration.

2.2.3 DCA for image segmentation

The user needs to mark the FG and BG on the input image by two scribbles. The DCA is applied subsequently to both FG and BG that generate contours for both FG and BG at each iteration. The calculation continues until both contours meet a minimal energy criterion and the automaton converges to a stable configuration. At this iteration, cell states cease to further

changes. Thereafter, a min cut²⁰ is applied to separate the FG from the BG resulting in the desired boundary of liver.

Technically, the contrast-enhanced image is the input to this segmentation module, where the pixels $\{x_1, \dots, x_n\}$ are represented by a set of variables. The energy sum of (up to two) variables can be written as $E(x_1, \dots, x_n) = \sum_i E^i(x_i) + \sum_{i < j} E^{i,j}(x_i, x_j)$.

The goal is to find an equivalent monotonous decreasing function in terms of energy. Therefore, g is a function of $\vec{C}$ and can be represented as $g = E(\vec{C})$.

$$E(\vec{C}_p) = \sum_{p \in P} D_p(\vec{C}_p) + \sum_{p, q \in \mathcal{N}} V_{p,q}(\vec{C}_p, \vec{C}_q) - \frac{\vec{C}_p}{\max \|\vec{C}\|}, \quad (9)$$

where $\mathcal{N} \subset P \times P$ is a neighborhood (four in this case) system of pixels. The first term in the energy function is typically called the data term, D_p , consisting of the total penalty in assigning each pixel a label; it measures how appropriate a label is for the pixel p given the observed data. In image restoration, for example, $D_p(C_p)$ is typically $(C_p - i_p)^2$, where i_p is the observed intensity of the pixel p . The second term of the function is typically called the smoothness term, V , in Kolmogorov's terminology, also called the interaction potential $V(C_p - C_q) = |C_p - C_q|$.

The cells grow on the seeded region, but when the object cells are minutely different from the neighboring cells with respect to intensity (as is the case in a pathological liver CT image), the probability of the final contour to cross the actual boundary becomes higher. Therefore, in order to prevent the contour from crossing the actual boundary, we have put another scribble surrounding the object of interest and a similar operation is also performed on this seeded ($C_{\text{background}}$) region.

During DCA operation, at each iteration, new curves C_{object} and $C_{\text{background}}$ are determined by the transition rule defined in CA. When both snakes (one for FG and the other for BG) finally meet the minimal energy criterion, all CA operations stop, otherwise, the procedure continues. Due to the inefficiency of computing the global minimum for minimizing the energy, many authors have opted for a local minimum.⁴⁶ In general,

$$E(f) \leq E(f') \quad \text{for any } f' \text{ near to } f.$$

In the case of discrete labeling, the labelings near to f are those that lie within a single move of f . Many local optimization techniques use standard moves where one pixel can change its label at a time. We use a local method, iterated conditional modes, using standard moves introduced in Ref. 47. For each pixel, the label that gives the largest decrease of the energy function is chosen until convergence to a local minimum is reached.

2.2.4 Curve evolution

Let us generalize the sense of curve evolution by a curve Cr that basically represents both C_{object} and $C_{\text{background}}$ separately. Theoretically, parameterizing the curve arbitrarily $Cr(p) = \{x(p), y(p)\}$, where $p \in [0, 1]$ at each iteration, the curve energy can be calculated as

$$S[Cr] = \int_0^1 [|Cr_p|^2 + \alpha |Cr_{pp}|^2 + 2\beta g(Cr)] dx dy,$$

where $Cr_p = \{\partial_p x(p), \partial_p y(p)\}$. α and β are the smooth constant and propagation constant, respectively; they are always positive. The last term of the above equation represents the external energy, where $g(\cdot)$ is a positive edge indicator function that depends on the image $u_0(x, y)$; it has small values along the edges and higher values elsewhere. It may be defined as $g(x, y) = [1/(|\nabla u_0|^2 + 1)]$. Taking the variational derivative with respect to the curve, $\delta S[Cr]/\delta Cr$, we obtain the Euler-Lagrange equation:

$$-C_{pp} + \alpha C_{pppp} + \beta \nabla g = 0.$$

We start with the resulted curve (C_{object} and $C_{\text{background}}$, separately); using the Euler-Lagrange equations as a gradient descent process, the curve is lead to the proper position. Formally, we add a time variable t and write the gradient descent process as $\partial_t C = -\delta S[C]/\delta C$ or it can be represented as

$$\frac{dC}{dt} = C_{pp} - \alpha C_{pppp} - \beta \nabla g.$$

Therefore, starting with the initial shape, say, $Cr(\text{object})$ at time $t = 0$, one lets the dynamical system evolve until it stabilizes, i.e., $\partial Cr(t)/\partial t = 0$. The energy trend of the variational curve during the deformation is provided in Fig. 3.

In this manner, a liver CT slice gets segmented. Subsequently, segmentation on a few more (five to six, depending on the geometry complexity of the input liver) slices that are distantly placed from each other in a subject sequence is performed. Next, we generate segmentation on the rest of the intermediate slices of a subject by following a modified level-set procedure in order to build the liver surface.

2.3 Generation of Intermediate Contours

Suppose the initial image u_0 consists of only two concentric regions (u_0^i, u_0^o) of piecewise constant intensity (two regions virtually represented by two contours). The variable curve Cr resulted from the segmentation earlier is considered to be located at the boundary of u_0^i . It should move toward its interior normal and stop on the boundary of the outer contour of u_0^o by minimizing the following energy equation:⁴⁵

$$\begin{aligned} F(c_1, c_2, \phi) = & -\mu \int_{\Omega} \delta[\phi(x, y)] |\nabla \phi(x, y)| dx dy \\ & - \lambda_1 \int_{\Omega} |u_0(x, y) - c_1|^2 H[\phi(x, y)] \\ & dx dy - \lambda_2 \int_{\Omega} |u_0(x, y) - c_2|^2 \{1 - H[\phi(x, y)]\} dx dy, \end{aligned}$$

where constants c_1, c_2 are the averages of u_0 inside and outside Cr , respectively; the parameter μ is the weight of the regularizing term and $\mu \geq 0$. Since our active contour model is a particular case of the minimal partition problem, we look for the best approximation of u_0 , as a function taking only two values, namely, the average inside Cr and average outside Cr . Therefore, we take values of the fitting regularizing terms $\lambda_1 = \lambda_2 = 1$. For level-set formulation of the model, $Cr \subset \Omega$, Cr is replaced by ϕ and the Heaviside function (H) and Dirac measure δ_0 are used. The Euler-Lagrange equation for ϕ is deduced, keeping c_1 and c_2 fixed, and minimizing F with respect to ϕ . Parameterizing the ascent direction by a

time t , the equation in $\phi(t, x, y)$ [with $\phi(0, x, y) = \phi_0(x, y)$ defining the initial contour] is

$$\begin{aligned} \frac{\partial \phi}{\partial t} = & \partial_{\epsilon}(\phi) \left[-\mu \operatorname{div} \left(\frac{\nabla \phi}{|\nabla \phi|} \right) + \lambda_1 (u_0 - c_1)^2 + \lambda_2 (u_0 - c_2)^2 \right] \\ = & 0 \end{aligned}$$

$$\text{in } (0, \infty) \times \Omega \quad \frac{\partial_{\epsilon}(\phi)}{|\nabla \phi|} \frac{\partial \phi}{\partial n} = 0 \quad \text{on } \partial \Omega,$$

where $\partial \phi / \partial n$, $\vec{n}$ denote the normal derivative of ϕ at the boundary and the exterior normal to the boundary $\partial \Omega$, respectively. In this way, the intermediate/missing ones between two contours are extracted by noting and keeping track of ϕ at each iteration while Cr reaches the boundary of u_0^o .

Segmentation Method Summary

In this work, the average number of slices of a test subject's sequence is 80 along the long axis.

- 1) First, five to six distantly placed slices (one apex, one basal, and four to five midslices) of a subject sequence are empirically selected so that they could almost cover the entire subject sequence; if 6, $S_i, i = 1, \dots, 6$.
- 2) SR theory is applied to these selected slices to enhance their contrast.
- 3) Considering each contrast-enhanced slice individually, a scribble is drawn on both FG and BG of the slice and DCA is applied to label the image as binary.
- 4) Gradient operation on the label map determines the coordinates that carry a nonzero value as the desired contour coordinates.
- 5) Steps (2 to 4) are repeated on the rest of the selected slices.
- 6) We use level sets to generate segmentation on the intermediate slices between two selected slices (say, S_i and S_{i-1}). The recorded tracks are the intermediate contours/segmentation between the two segmented slices.
- 7) In this way, all the subject slices get segmented to construct the liver surface.

The flowchart illustrating the methodology is presented in Fig. 4.

3 Results and Discussion

Our proposed segmentation algorithm is tested on two databases from two different sources viz., a hospital [Hamad General Hospital (HGH)] and medical image computing and computer assisted interventions (MICCAI) Grand Challenge 2007.⁹ We prefer to use local hospital datasets to clinically test and validate the accuracy of the algorithm. In the case of the MICCAI 2007 workshop database, the pixel spacing varies between 0.55 and 0.8 mm, the interslice distance from 1 to 3 mm. The resolution is 512×512 voxels in-plane. A total of 40 datasets were used for the workshop. Most of them are pathologic and include tumors, metastasis, and cysts in different sizes. Datasets have been randomized into three groups: 20 for training, 10 for testing for the

Fig. 3 (a) Energy trend of gradient descent process in variational curve deformation. In case of HGH database, values of (b) HD. (c) I_h . (d) MER. (e) FPR. (f) FNR. (g) Specificity. (h) Precision. (i) Accuracy. (j) FOM. (k) DC. (l) Sensitivity.

qualifying, and 10 for the contest. All segmentations were created manually by radiological experts, working slice-by-slice in a transversal view. In the case of the HGH database that comprises 10 subjects, the interslice distance varies from 1 to 3 mm,

the resolution, the pixel spacing, bit depth, slice thickness are 512×512 , between 0.4 and 0.7 mm, 12 bits and 2 mm, respectively. The ground truth images have been provided along with the datasets by the respective organizations.

Fig. 4 Flow chart showing the proposed segmentation methodology, where Z is total number of slices selected initially.

3.1 Results

For curve evolution in DCA, a lower value of α is desirable, because this value decreases the strength of curve elasticity at a node. Similarly, when the elasticity is too low and there is missing or little information, it may not be possible to perfectly match the object shape. This problem can be managed by selecting a small value of α . Therefore, the value of α is empirically chosen as 0.05. On the other hand, if the value is increased an incorrect matching with the desired object boundary may be observed in Fig. 5. The value of the propagation constant or correction term β is chosen as 0.1.

The results after CE of input images are given in Fig. 6. In this enhancement process, the value of DSM χ is found to start decreasing after 200, indicating this as the optimal iteration count where one can expect an optimum enhancement. We have also quantitatively evaluated the enhancement algorithm (as shown in Table 1) by comparing it with SR in the Fourier domain³⁰ and a basic algorithm viz., adaptive histogram equalization technique⁴⁸ using four indices:⁴⁹ (1) DSM, (2) target to BG enhancement measure based on standard deviation $TBE_s = (\mu_T^E/\mu_B^E) - (\mu_T^O/\mu_B^O)/(\sigma_T^E/\sigma_B^O)$; where σ_T^E and σ_B^O are standard deviations of the selected target regions of the enhanced and original images, respectively, (3) and target to BG enhancement measure based on entropy $TBE_e = (\mu_T^E/\mu_B^E) - (\mu_T^O/\mu_B^O)/(e_T^E/e_T^O)$; where e_T^E and e_T^O are entropies of the target regions in the enhanced and original images, respectively, and (4) relative image enhancement factor $F = \sigma_B^2\mu_A/\sigma_A^2\mu_B$, where suffixes A and B stand for pre-enhancement and postenhancement, respectively. It may be noted that the values of DSM and F should be larger for better enhancement,

whereas the values of TBE_e and TBE_s should be sufficiently positive for achieving good enhancement. From Table 1, the proposed method is found to carry greater values of DSM and F , indicating its efficiency over others.

The contrast-enhanced images are further used as the input to the segmentation algorithm and the segmentation results are shown in Fig. 7, where a nearly complete match of segmented images with the ground truth equivalents could be realized indicating the competence of the proposed algorithm. To mark the difference between CA and DCA, we have compared it with conventional CA and some of the results are provided in Fig. 8. It may be observed that the resulting contours, in the case of CA, do not tightly seal the object of interest, unlike DCA. Interestingly, the DCA is also found to be effective and robust to segment the liver region despite the presence of big tumor tissues within the liver, as shown in Fig. 1.

Since the qualitative assessment depends partially on human judgement, quantitative assessment becomes a substantial complement in the performance analysis. Here, the employed metrics⁵⁰ considered for quantitative evaluation are supplied in Table 2; additionally, the evaluation measures include overlap error (overlap error), volume difference (Vol. Diff.), average distance (Avg. Dist.), root mean square distance (RMS Dist.), and maximum distance (Max. Dist.). As per the definitions of these measures, values of first five measures in Table 2 should be minimum, whereas that of the rest should be maximum for a good segmentation. The quantitative performances of the proposed method on two databases are shown in Figs. 2 and 3; a significant improvement by the proposed method over conventional CA is quite evident. Since energy at the actual object boundary is minimum, we compare the convergence of both CA and DCA

Fig. 5 (a) Improper segmentation result at a larger value of α . (b) Inappropriate CE result when $z > 1$. (c) Corresponding ground truth image of Fig. 3(d).

Fig. 6 (a and d) Input computed tomography (CT) images. CE of liver with iteration count (b and e) 100, (c and f) 200.

in terms of energy, as shown in Fig. 7. In the case of CA, the energy curve does not appear to meet the minimum level within the number of iterations the DCA requires to achieve the same. We have also compared the proposed method, with and without CE, to some standard reference methods on 10 randomly selected subjects (as shown in Table 3). We have found the performance of our method is better when CE is applied before segmentation. Furthermore, we have provided the performance of a few MICCAI 2007 Grand Challenge semi-automated methods for reference (in Table 4) and comparison purposes. The average time required by MATLAB R14 to perform the segmentation is 12 min for one subject by a 2GB RAM and core2duo processor.

3.2 Discussion

Morphological characterization of liver is important, since volume and shape characteristics are believed to be associated with various liver diseases. Therefore, segmentation is considered as

the first and foremost step for surgical planning. For investigating liver, CT is the most widely used imaging modality.²⁸ Segmentation of liver in CT data is becoming more challenging due to: (1) arrival of the new generation of CT scanners. The resolution of the new machines in the transverse direction is about three times better than that of the present CT scanners. Although one expects dense sets of data to provide more information for processing the images, the lack of successful algorithms implies that at least in the near future, a radiation oncologist would expect to spend significantly more time in segmenting the images and (2) low-level of contrast and blurry edges that characterize the CT images. The partial volume effect is evident due to the patient movement, spatial averaging, reconstruction artifacts, and beam hardening. Furthermore, neighbor organs like spleen, kidney, heart, and stomach might share similar gray levels. Meanwhile, the same organ may not show the same gray levels in the same subject. All of these facts, in addition to the complexity and wide variety of liver shapes, increase the difficulty of the segmentation task. We

Table 1 Performance evaluation of contrast enhancement algorithm with different methods.

Method	Data set 1				Data set 2			
	DSM	TBE _s	TBE _e	<i>F</i>	DSM	TBE _s	TBE _e	<i>F</i>
SR in DCT domain	53.3409	0.5712	0.4663	19.3243	61.2734	0.7023	0.6930	20.7551
SR in Fourier domain	44.0772	0.4172	0.4901	14.7611	50.9842	0.6652	0.6573	12.9681
Adaptive histogram equalization	43.5612	0.4143	0.4029	13.1374	47.8845	0.2372	0.3893	11.4792

Fig. 7 (a–d) Segmented liver images. (e–h) Corresponding ground truth images. (i–l) Segmented images superimposed on the ground truth images; segmented region and ground truth region are marked by red and white color, respectively. (m) Comparison of convergence between cellular automaton (CA) and dynamic cellular automaton (DCA). (n) Stack of liver slices of a subject. (o) Generation of intermediate slice contours. (p) Volumetric liver.

Fig. 8 Segmentation of liver CT images using (a–d) CA and (e–h) DCA. (i–l) Corresponding ground truth images.

Table 2 The employed metrics for quantitative evaluation.

Measure	Definition	Desired value for good segmentation
Hausdorff distance	Minimum distance between two sets of points	Low
False-positive ratio	Fragment of pixels incorrectly segmented	Low
False-negative ratio	Fragment of pixels incorrectly rejected	Low
Mean error rate	(False positive + false negative)/total samples $\times$ 100	Low
Intraregion (I_h) uniformity ⁵¹	Index of homogeneity inside a region	Low
Specificity	True negative/(true negative + false positive)	High
Precision	True positive/(true positive + false positive)	High
Accuracy	(True positive + true negative)/total samples	High
Sensitivity	True positive/(true positive/false negative)	High
Dice coefficient	Quantity of overlapping of two contours	High
Pratt's figure of merit ⁵²	Segmentation accuracy	High

Table 3 Comparative performance of liver segmentation accuracy.

Method	Overlap error	Vol. Diff. (%)	Avg. Dist. (mm)	Max. Dist. (mm)	Dice metric (%)
Grow Cut ²³	8.62	2.4 ± 1.4	1.41	21.50	88.8 ± 0.6
N Cut ²⁰	9.78	3.3 ± 1.1	1.49	22.96	86.2 ± 1.1
Grab Cut ⁵³	7.09	1.7 ± 1.4	1.30	20.28	90.0 ± 0.9
Goryawala et al. ¹²	6.97	1.2 ± 1.3	1.24	19.67	90.1 ± 1.1
Our method					
Without enhancement	6.79	1.2 ± 1.1	1.21	19.61	90.3 ± 1.2
With enhancement	5.28	0.7 ± 1.1	1.00	16.04	95.8 ± 1.2

Table 4 Comparative performance of liver segmentation accuracy.

Method	Overlap error	Vol. Diff. (%)	Avg. Dist. (mm)	Max. Dist. (mm)
Dawant et al. ⁵⁴	7.2	2.5 ± 2.3	1.1	17.1
Lee et al. ⁵⁵	6.9	1.3 ± 2.9	1.1	21.3
Beck et al. ⁵⁶	6.6	1.8 ± 2.5	1.0	18.5
Wimmer et al. ⁵⁷	8.1	6.1 ± 2.6	1.3	18.7
Slagmolen et al. ⁵⁸	10.4	3.7 ± 6.2	2.0	40.5

have attempted to address the issues of intensity complexity and high level of noise-low contrast by using energy-based DCA and SR theory, respectively.

In this paper, we propose a semiautomated method that uses DCA with level sets to segment the liver. One may draw its analogy with the active shape model (ASM),⁵⁹ however, the major difference can be drawn through the variational curve deformation. In our case, it iteratively deforms to fit to the object according to the image intensity and energy distribution, whereas in the case of ASM, this is governed by the shape resulting from training data. Unlike ASM, seeds placement is an important requirement in our method; improper scribble placement (say, FG

scribble extends to BG as well) leads to incorrect segmentation, as shown in Fig. 9.

The values of bistable system parameters play a crucial role in the process of CE using SR. The expression for SR on any data set contains additive terms of multiples of w and subtractive term of multiples of z . It is observed that the images that have low contrast and low dynamic range require larger values of w while those that have relatively more contrast and cover an appreciable gray level range require smaller values of w for proper enhancement. Values of Δt have been studied to be similar to that of w . The value of w for DCT-based SR is found to be of the order of 10^8 . It is also perceived that w is inversely proportional to overall variance signifying the contrast of the input image. Optimization process leads us to the optimum value of w ; the value of z should be less than 1 so that the condition $b < \sqrt{4a^3/27}$ holds, assuring that the system is bistable and the signal is subthreshold so that SR can be applicable. We prefer a very small value of this factor, i.e., 0.00029 to remain well within the allowable range of b . However, when the value of $z > 1$, the stability gets disturbed and an inappropriate result is obtained, as shown in Fig. 5.

Level sets are proven to be quite efficient to generate the segmentation of intermediate slices in the course of reconstructing the liver surface, as shown in Fig. 7. This step is deemed necessary since the number of images is in the order of 80 and it is quite tedious and time consuming to segment all the images individually and build the surface.

Fig. 9 (a and b) CE of liver at iteration count 300. (c) Scribble placement (one for FG and one for BG, but here FG scribble should not have crossed FG, i.e., liver region). (d) Result due to improper scribble placement.

The value of Dice measure is found to be 95.8 ± 1.2 , which is quite encouraging; the best semiautomated method⁶⁰ in the MICCAI 2007 grand challenge has received the final score, 82 ± 2 . The corresponding volume difference is 1.0 ± 1.7 which is higher than our method, suggesting better matching of the segmented liver with ground truth in our case.

If the quantitative figures of the proposed method with and without CE in Table 3 are analyzed, volume difference, for instance, it may be noticed that CE plays a significant role in improving the quality of segmentation. The user needs to carefully monitor χ and determine the optimal iteration value in the process of CE, otherwise unnecessary artifacts in the output may result. In this experiment, the average optimal iteration number is found to be 200; any change in the iteration count could alter the output and result in artifacts, as can be observed in Figs. 9(a) and 9(b). Time wise, there is still some space for improvement in the proposed algorithm. Presently, the method takes 12 min for one subject to complete the segmentation in contrast to the physicians' preference, i.e., 10 min.⁶¹

4 Conclusions and Future Work

In this paper, we have demonstrated a CA-based method to reconstruct the liver surface from low-contrast CT images. In this method, the input images are first contrast enhanced by the SR algorithm in the DCT domain and then the segmentation procedure is performed. The segmentation results substantiate the potential of the proposed model where 2-D segmentations on a few slices finally lead to liver surface reconstruction. The level-set method is proven to be efficient to generate the segmentation of the rest of slices in the subject sequence; the stack of all slice 2-D contours build the liver surface. The major strength of this work is the integration of snakes into the cellular automaton approach which provides a certain control over the boundary smoothness and potentially prevents smaller leakages. Furthermore, the method is found to have outperformed the reference methods as can be observed in its performance analysis. A fixed value for each control parameter— z , α , w , Δt , μ , α_1 , and α_2 —was employed leading to impressive surface reconstruction. Additional clinical data acquisition for extensive evaluation will be a major focus of our future research. Also, we plan to incorporate this method with various body organs in different modalities in future.

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