Segmentation of Medical Imagery with Wavelet Based Active Contour Model

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Abstract  
A novel method for Medical image segmentation is proposed in this paper. Segmentation is one of the important key tools in medical image analysis. The main application of segmentation is in delineating an organ reliably, quickly, and effectively. In this paper, we have proposed efficient region based segmentation with wavelet transform based Active Contour (WAC) model. The proposed algorithm is segmentation of the brain and bone tissue sarcoma (BTS) present in 2D medical images. The 2D medical images large amounts of inhomogeneities are present in the foreground and background. WAC model can easily distinguish the image regions in the interior, exterior, background, edges of tissues by enhancing the wavelet coefficients. The proposed WAC model utilizes the energy minimization function for solving energy functional inside and outside the contours to ensure stability. After that, it eliminates the costly re-initialization and complexity from Level Set Equation. The proposed model is stable, accurate, and immune from boundary anti-leakage and easy to implement. We get promising results obtained on real world medical images over the conventional methods.

Keywords: Medical Images, Brain and Bone Tissue Sarcoma, Wavelet transform, Active contour Model.

Introduction  
MRI for the analysis of body fat and its distribution over the past two decades, many authors has investigated on it. However, manually it performed in MR images can be an arduous task. In order to alleviate this burden, numerous segmentation algorithms have developed for the quantification of fat in MR images such as automated and Semi-automated segmentation algorithms. An increasing portion of medical imaging problems concerns segmentation, thin objects, vessel filtering and classification. Example applications include vascular tree analysis in the heart, brain, the liver, detection of aneurysms, stenoses, and arteriovenous malformations in the coronal tree and brain analysis in relation to the prevention of myocardial infarction. Thin, vessel-like objects are very difficult to process in general over most images features, precisely because they are thin. When using many common image analyses, they are prone to disappear. Segmentation looked into from many angles. In computer vision, the segmentation task often seen as a low-level operation, which consists of separating an arbitrary image scene into reasonably alike components such as regions that are consistent in terms of color, texture and so on. In contrast, in image analysis, segmentation is a high-level task and knowledge about the object. This methodological difference is due to the application field of medical image processing. In computer vision and image processing, the main objective of segmentation (and grouping) is to recognize objects in an arbitrary scene, such as walls, sky, persons, doors and sky, etc. It might be for instance to find the contours of lungs in the X-ray photograph [1].

In general, we classify segmentation techniques into two main categories, which are (a) segmentation methods that are allowed users to specify explicitly the desired feature and (b) algorithms where the specification is implicit. The segmentation as a real-time interaction process between the user and the algorithm. The user is provided with the output,
allowed to perform feedback directly in order to modify the segmentation until we get satisfactory results. In the extreme case, this framework might degenerate into manual segmentation with the user forcing desirable results. Some examples of this approach are the livewire segmentation algorithms [2-5]. These algorithms produce a boundary representation of an object, by viewing the image as a weighted graph and specified boundary points of the user to finding the shortest path between them. A more recent example of this approach based on the concept of random walks described in [6]. The majority of segmentation methods belong to the second category, where the desired result specified implicitly. Segmentation algorithms belonging to this category include thresholding, contour-based and region-based segmentation. The paper organized as follows, the proposed wavelet based active contour model in Section II, Experimental results and discussion in section III, conclusion in section IV.

Proposed Method

Medical Image Decomposition using Wavelet Transform:
The wavelet transform [7] is a good tool for study of non-stationary signals [8]. The 2D Medical images are the typical examples of a non-stationary signal. Some researchers have applied the wavelet transform on the MRI brain and Bone tissue images for de-noising and have reported good results [9, 10]. The 2D separable wavelets can capture the singularities in three directions only (vertical, horizontal and diagonal) while a non-separable wavelet [11-13] can provide more directional information. The quincunx wavelet [11] is the simplest non-separable decomposition. We have reported our initial studies on the above images using the Quincunx transform [14, 15]. In the first method, the 2D medical images were de-noised in the Quincunx domain, while in subsequent work [15], brain cancerous cells and bone tissue sarcoma are distinguished by characterizing their texture in the combined domain of the watershed transform and the Quincunx transform. In the work [15], the watershed transform was applied on the low-resolution image and the overall result is marginally affected by it. In this paper, we extend our work by providing a more robust and sophisticated solution for the segmentation of the 2D brain and bone tissue images.

Our image model
An observed tissue image, I(x, y), contains the original noise free image I'(x, y) and noise n(x, y).

\[ I(x, y) = I'(x, y) + n(x, y) \]  

(1)

The noise free image I'(x, y) contains the edge information and interiors of the tissue cells. Then the image model in (1) becomes

\[ I(x, y) = (T + E + B) + n(x, y) \]  

(2)

Here ‘T’ represents the interiors of the brain and bone tissue sarcoma and ‘E’ represents the edge information’s of all the cells present in the tissue image. B represents the background. The presented method in this paper separates out each component of the image model. The gray scale image I(x, y) is assumed to be normalized between 0 and 1.

Image decomposition using Wavelet Transform

The image is decomposed using a non-separable wavelet scheme. Based on the lifting scheme [16], the quincunx interpolating filter bank having 2 primal and 2 dual vanishing moments, designed by Kovacevic and Sweldens [17] has been used. Here we use the undecimated version of the transform, since the same size of image obtained at each scale and it is easy to analyze the inter-scale relationship. For the undecimated version, we remove the decimation operator from the quincunx lifting scheme and the N-times quincunx upscaled versions of predict and update filters are used, where N represents the decomposition level. In this way, for higher decomposition levels, the corresponding filter support widens. However, we did not find significant improvements on using this scheme and confined our self to a two-step method.

LMMSE based Image de-noising

To separate out the noise, we performed de-noising of the brain and bone tissue image. The Linear minimum mean squared error estimation (LMMSE) based noise filtering method [18] is applied on the wavelet coefficients. When a non-separable undecimated Quincunx wavelet transform is applied on the observed image I, all singularities due to image components and noise are captured.

\[ W_T[I(x, y)] = WT[I'(x, y)] + WT[n(x, y)] \]  

(3)

The noise free wavelet coefficients are assumed to be conditionally independent zero mean Gaussian random variables, given their variances \( \sigma_n^2 \) [18]. The noise assumed to be an additive white Gauss-ian noise with variance \( \sigma_n^2 \). Thus, the noise free wavelet coefficients calculated using the formula.

\[ \hat{W}_T = \frac{\hat{\sigma}^2(j)}{\hat{\sigma}^2(j) + \sigma_n^2} W_T \]  

(4)

Where \( \hat{\sigma}^2 \) represents the maximum likelihood Estimator (MSE) of local variance \( \sigma^2 \) and computed from the wavelet coefficients as follows [18].

\[ \hat{\sigma}^2(k) = \sum_{\beta \in \Omega_k} (W_T^{(\beta)})^2 - \sigma_n^2 \]  

(5)

Where \( W_T^{(\beta)} \) represents the wavelet coefficients at scale ‘i’ location \( \beta \), \( \alpha_i \) represents the set of coefficients in the square neighborhood window centered at location k and \# denotes the number of elements in the set. The standard deviation of noise \( \sigma_n \) can be estimated using the empirical equation of Donoho and Johnstone [19], which is represented as below,

\[ \sigma_n = \text{median}[W_T] \cdot 0.6745, j = 1 \]  

(6)

where \( |.| \) denotes the absolute value. The median value of absolute wavelet coefficients at finest scale (\( j = 1 \)) is utilized, since the finest scale tends to contain more of noise [19].

Implementation to Region based Chan-Vese ACM model:
Active Contour Model (ACM) is proposed by Chan and Vese (C-V) [20] with the special case of Mumford-Shah model
[21]. Given an image \( I(x, y) \) in the wavelet domain \( \Omega \). The energy minimizing function \( E_{cv} \) proposed by C-V model as follows.

\[
E^v(c_1, c_2, C) = \lambda_1 \int_{\Omega_{inside}} [I(x, y) - c_1]^2 \, dx \, dy + \lambda_2 \int_{\Omega_{outside}} [I(x, y) - c_2]^2 \, dx \, dy, \quad x, y \in \Omega
\]  

(7)

Here \( I(x, y) \), \( C_1 \) and \( C_2 \) are the Transformed image, average intensity of the inside and outside the contour respectively. In the level set model, we assume

\[
C = \{ x \in \Omega : \phi = 0 \}
\]

(8)

\[
C_1 = \{ x \in \Omega : \phi > 0 \},
\]

(9)

\[
C_2 = \{ x \in \Omega : \phi < 0 \}
\]

(10)

The Contour \( C \) can represent in terms of \( \phi \). By keeping the level set function \( \phi \) as fixed and we can solve the values \( C_1 \) and \( C_2 \) minimizing the equation (7).

\[
c_{1(inside)} = \frac{\int_{\Omega_{inside}} I(x, y) H(\phi) \, dx \, dy}{\int_{\Omega} H(\phi) \, dx \, dy}
\]

(11)

\[
c_{2(outside)} = \frac{\int_{\Omega_{outside}} I(x, y), (1-H(\phi)) \, dx \, dy}{\int_{\Omega} (1-H(\phi)) \, dx \, dy}
\]

Here \( H(\phi) = \) Heaviside function, which is defined as

\[
H(\phi) = \begin{cases} 
1, & \text{if } \phi \geq 0 \\
0, & \text{if } \phi < 0
\end{cases}
\]

(12)

\[\delta(\phi) = \frac{d}{d\phi} H(\phi)\]  

(13)

**Figure 1:** level set function \( \phi \) with different propagation

The curve has the non-empty interior in \( \Omega \), Heaviside functions \( H(\phi) \) and \( 1-H(\phi) \). We get the corresponding level set formulation by incorporating the area energy and length terms in eq. (7) as follows.

\[
\frac{\partial \phi}{\partial t} = \delta(\phi) \left[ \mu \nabla \cdot \left( \nabla \phi \over \left| \nabla \phi \right| \right) \right] - \lambda_1 \left( 1 - c_{1(inside)} \right)^2 - \lambda_2 \left( 1 - c_{2(outside)} \right)^2
\]

(14)

Here \( \lambda_1 > 0, \lambda_2 > 0, \mu \geq 0, \nu \geq 0 \) are fixed parameters and \( \mu \) is to control the smoothing the zero level set \( \nabla = \) gradient operator of an image \( I(x, y) \) and \( \delta(\phi) = \) Dirac function as follows.

**Algorithm 1:**

__________________________

**Wavelet Transform based ACM model:**

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Step 1. Decompose the normalized gray value tissue image \( I(x, y) \) using the undecimated quincunx wavelet.

Step 2. De-noising on the wavelet coefficients using LMMSE as described in Section II(c).

Step 3. Apply the Wavelet Transformed Image \( I(x, y) \) to the Active Contour Model using eq. (7).

Step 4. Equation (7) is minimized for solving the eq. (9)\&(10).

Step 5. We get the corresponding level set equation for Regions Presents inside and outside the contours eq. (12).

Step 6. Obtain the final segmented output from step 5.

**Results and Discussions**

The experimental results demonstration of proposed model with two different image segments for segmented brain tissue cells and bone tissue sarcoma of abnormal patient. The proposed experimental results of WBAC model compared with the Conventional 2D OTSU thresholding model for segmentation of tissue images. Figure 3 and 4 shows the fist column (a) represents the original brain tissue cells and Bone tissue sarcoma images; Second column (b) represents the segmented output of Conventional Model and third Columns (c) is the Final contour evolution of Proposed WBAC model and (d) is the corresponding final segmented regions of fig (c) with 50 iterations.

The original images with the size of \( 512 \times 512 \). The proposed method utilizes the both edge indicator function and contour fitting energy. In the below figures fig. 3 and fig. 4 shows the second columns (b) using the conventional thresholding model, this model is failed to segment the tissues presence in the original image. The proposed model gets satisfactory results for segmenting the tissues presence in the brain and bone images, it utilizes the both edge indicator function and contour fitting energy.

**Figure 2:** Flow chart of Proposed WBACM Method
Figure 3: Experimental results on (a) Bone tissue Sarcoma and (b) is the basic thresholding segmented output with N=3 by 2D Otsu method (c) Final Contour Evolution using proposed WBAC Model (d) represents the corresponding Bone tissue segmented Output image.
These experimental results done in Matlab 7.8 (2009a) with 1GB of RAM and 3Ghz processor. The comparative analysis of TABLE 1 shows that the filled area covered by both the methods and Calculate the mean and Standard Deviation (SD) of the proposed and conventional methods respectively. The Conventional model fails to cover the maximum pixels area over the proposed model. The proposed model covered the maximum pixels area of the tissues images see fig 3(d) and fig 4(d). Similarly, we calculate the mean and SD of both the methods but mean and SD values are decreased over the proposed model see table 1.

**Table 1**: Comparative analysis for Actual Area, filled area, MEAN, SD and pixels area error measure.

<table>
<thead>
<tr>
<th></th>
<th>Actual Area</th>
<th>Filled Area</th>
<th>Area Error</th>
<th>Mean</th>
<th>SD</th>
<th>Filled Area</th>
<th>Area Error</th>
<th>Mean</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Image1 (Bone tissue Sarcoma)</td>
<td>360880</td>
<td>132947</td>
<td>227933</td>
<td>2.37</td>
<td>46</td>
<td>201624</td>
<td>159256</td>
<td>1.80</td>
<td>0.56</td>
</tr>
<tr>
<td>Image2 (Brain tissue Cells)</td>
<td>115248</td>
<td>50156</td>
<td>65092</td>
<td>2.30</td>
<td>74</td>
<td>47144</td>
<td>2.10</td>
<td>0.60</td>
<td>0.56</td>
</tr>
</tbody>
</table>

**Conclusion**

The proposed strategy of 2D bone and brain tissue analysis for de-noising to segmentation of the tissue cells from the true images. The proposed new approach for decomposition of better image characterization of interior regions and the edges of medical tissue images by non separable wavelet based Active contour Model. This model overcomes the inhomogeneities of the images by utilizes the single threshold, independent of the gray values, edge indicator function and contour fitting energy. This is very helpful for segmenting the tissues accurately. The demonstrated results are superiority in terms of feasibility, effectiveness and accurate of the proposed model.

**References**


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