Bone Contour Tracing in Digital X-ray Images Based on Adaptive Thresholding

Oishila Bandyopadhyay¹, Arindam Biswas²,
Bhabatosh Chanda³, and Bhargab B. Bhattacharya³

¹ Department of CSE, Camellia Institute of Technology, Kolkata

² Department of IT, Bengal Engineering and Science University, Howrah

³ Center for Soft Computing Research, Indian Statistical Institute, Kolkata

Abstract. An orthopedic X-ray captures bone images along with surrounding flesh and muscle components. Segmentation of the bone component with a sharp contour is a challenging task as the bone and flesh regions often have pixels with overlapping intensity range. In this paper, we propose a new technique of contour extraction by integrating an entropy-based segmentation approach with adaptive thresholding. The method eliminates the shortcomings of earlier derivative or deformable model based approaches, and can be fully automated. Experiments with several digital X-ray images reveal encouraging results especially for long-bone X-ray images.

Keywords: Medical Imaging, Bone X-ray, Entropy, Standard Deviation, Adaptive Thresholding, Tracing.

1 Introduction

Contour detection in X-ray or ultrasound bone images is an important task in emerging health-care automation systems [1][2][3]. Machine identification of fractures first requires extraction of the exact contour of the concerned bone structure. However, segmentation of the bone part and its contour extraction is a hard problem in digital X-ray image analysis as the pixel values of the bone shadow appear inseparably with those of the flesh and muscle components. The conventional image analysis methods based on derivative techniques or deformable models [2] either fail to detect the bone contour correctly or fail to admit full automation. The presence of noise and low contrast between bone and flesh regions makes the problem even worse. In this paper, we have proposed a new technique by integrating an entropy-based segmentation method [10] with adaptive thresholding-based contour tracing. The novelty of the technique lies in the fact that it rectifies the false discontinuities of bone contour while retaining the real (uneven) discontinuities caused by fractures. Experiments on several long-bone digital X-ray images demonstrate the suitability of the proposed method for contour generation and fracture related abnormality analysis.

2 Contour Detection

Common edge detectors like Prewitt, Sobel and Canny edge detector measure the gray level transition of locally connected pixels [4]. Goshtasby and Turner used Laplacian of Gaussian function [5] in their work on segmentation of cardiac MR image [6]. Canny edge detector uses two levels of thresholding. Scepanovic et al. used this function in their work on fast algorithm for probabilistic bone edge detection [7].

Deformable models such as active contour [8], active shape [9], and level set method [4] have also been used for medical image segmentation [4]. These methods are contour-based instead of region-based. An inherent weakness of these approaches is that they typically require good initialization of the model contour. If the model is poorly initialized, these approaches can be easily affected by noise and extraneous edges in the image, resulting in incorrect segmentation of the regions.

Atlas based or model based approaches overcome the weakness of deformable models by roughly applying atlas to the image before applying the deformable model. For these approaches, a training set or a reference map is required.

3 Proposed Algorithm

In an *X*-ray image, the bone parts appear along with the surrounding tissues or muscles (i.e., flesh). In many regions of an *X*-ray image, the intensity range of pixels belonging to the bone region and that of its surrounding flesh region may overlap, which makes the segmentation inaccurate. The proposed algorithm segments the bone region of an *X*-ray image from its surrounding flesh using an entropy-standard deviation based segmentation method and then applies an adaptive thresholding based technique to generate the bone contour. This modification overcomes the shortcomings of an earlier method [10].

3.1 Bone Region Segmentation from an *X*-ray Image

The major challenge in segmentation of bone region in any *X*-ray image lies in identification and extraction of flesh to bone transition region. Overlapping intensity range of flesh and bone region restricts the use of pixel-based thresholding or edge-based approaches as they often fail to produce accurate results. In the proposed algorithm, we generate local entropy image from the input *X*-ray image [10]. Local entropy image clearly identifies the flesh-bone transition points in a *X*-ray image with bright bone region and relatively darker flesh region. Few *X*-ray images appear with bright flesh region resulting in overlapping flesh and bone intensity range. In such cases, the entropy image often fails to identify the flesh to bone transition correctly. To overcome this problem, we compute local standard deviation for each pixel and multiplied it with local entropy to facilitate bone image segmentation.

Entropy Computation and Construction of Entropy Image. The entropy value represents the measure of randomness associated with pixel values

belonging to a region. Following Shannon's definition of entropy and Pun's representation of image entropy, for an image with G gray level and probability of k^{th} gray level P_k , the image entropy can be represented as

$$E = \sum_{k=0}^{G-1} P_k \log_2 \left(\frac{1}{P_k} \right) = - \sum_{k=0}^{G-1} P_k \log_2 (P_k) \quad (1)$$

where $P_k = \frac{n_k}{M \times N}$ and n_k is the number of pixels with gray level k and $M \times N$ is the size of the image [11]. Local entropy represents the discrepancy between two probability distributions on the same event space [12]. It is related to the variance of gray levels in the neighborhood of a pixel. Local entropy divides the image into separate regions and then analyzes each region as a separate information source. If a small neighborhood window Ω_k of size $M_k \times N_k$ is defined within the image, then entropy of Ω_k can be represented as:

$$E(\Omega_k) = \sum_{j=0}^{G-1} P_j \log_2 \left(\frac{1}{P_j} \right) \quad (2)$$

where $P_j = \frac{n_j}{M_k \times N_k}$ denotes the probability of gray level j in the neighborhood Ω_k , n_j is the number of pixels with gray level j in Ω_k and $E(\Omega_k)$, the local entropy of Ω_k . Yan et al. had applied local entropy based thresholding for transition region extraction [12]. It was shown that the local entropy is larger for heterogeneous regions and smaller for homogeneous neighborhoods. So a transition region will have larger local entropy values than those in the non-transition regions of the image. Kang et al.[12] used local entropy values to identify transition regions on region extraction from coronary angiogram .

Statistical analysis of neighborhood pixel intensity distribution can be performed by calculating the local standard deviation of total number of pixel values in 9×9 neighborhood of each pixel. Standard deviation of a function is calculated from variance of the function. The variance of a data set represents the dispersion of data values about its mean. If a data set X is $[a_1 a_2 a_3 \dots a_n]$ and its mean value is b , then variance

$$V(X) = [(a_1 - b)^2 + (a_2 - b)^2 + (a_3 - b)^2 + \dots + (a_n - b)^2] / (n - 1) \quad (3)$$

Standard deviation of the data set is represented by square root of variance, i.e., $S = \sqrt{V(X)}$. A low standard deviation indicates that data points tend to be very close to mean value whereas a high standard deviation indicates that data points are spread out over a large range of value.

In the X -ray images where a bright flesh region appears with overlapping flesh-to-bone transition, the entropy image fails to identify the transition region distinctly (Fig. 1(b)). It has been empirically observed that this problem can be resolved by taking the product of the matrices of local entropy and local standard deviation (Fig. 1(c)). In the proposed algorithm, we calculate the local entropy values (LE) and local standard deviation values (LS) over a (9×9) neighborhood for each pixel of the X -ray image. Then we construct an intermediate gray image

Fig. 1. (a) Wrist X-ray (b) Entropy Image (c) $\text{Entropy} \times \text{Standard deviation}$ image (d) Intensity Graph (s1 and s2) (e) Entropy graph (s1 and s2) (f) $\text{Entropy} \times \text{Standard deviation}$ graph (s1 and s2)

with each pixel value $I_i = (LE \times LS)$. In this process, the gray levels of the pixels at the transition region are enhanced compared to those of the neighbors.

In the X-ray image of wrist Fig. 1(a), it is found that the transition s1 of intensity from background to flesh varies between 40 to 160 and the intensity transition from bone to flesh s2 varies from 140 to 200. So there is a overlapping zone from 140 to 160 where the entropy change in two transition regions cannot reveal a distinct boundary for bone to flesh transition. In such a situation the product of local entropy and local standard deviation of input image generates distinct in-phase peaks for both s1 and s2 as shown in Fig. 1(d) and the resulting product image highlights the bone boundary distinctly [see Fig. 1(f)].

Contour Generation Using Adaptive Thresholding: The proposed algorithm takes the segmented bone image (entropy-standard-deviation image) as input to adaptive thresholding method [13] to generate the contour of bone part.

Threshold Computation: In the proposed algorithm, we traverse the segmented bone image J using a small window. For each pixel α of J , we construct the window consisting of its 8 neighboring pixels. The window is divided into four cells, top-left (C_1), top-right (C_2), bottom-left (C_3) and bottom-right (C_4). All these four cells incident on α . To determine whether a cell C_i has a portion of bone boundary in it, we use the adaptive thresholding approach [13]. In this approach, if $\max_i$ and $\min_i$ denote the respective maximum and minimum gray

level values in C_i , then the global maximum, at max_g , is defined as the maximum of all max_i for $i = 1, 2, 3, 4$, corresponding to the four cells incident on α . Similarly, the global minimum min_g is defined as the minimum of all min_i s for $i = 1, 2, 3, 4$. Based on max_g and min_g , we define the local threshold value as $\tau_{loc} = \frac{1}{2}(max_g - min_g)$. Then, the adaptive value of the threshold τ_{adpt} is computed in accordance with the following equation

$$\tau_{adpt} = \gamma\tau_{loc} + (1 - \gamma)(\tau_{loc} + \tau_{prev}) \quad (4)$$

where, $\gamma \in [0, 1]$ is the smoothing factor for the exponential moving average, and τ_{prev} is the adaptive threshold calculated for the previous point lying on the boundary of the cellular region. Realization of above equation is computationally simplified if we consider $\gamma = \frac{1}{2}$. For $\gamma = \frac{1}{2}$, equal weightage is given to the threshold of the previous inter-cell point and the local contrast, and hence the computation of τ_{adpt} can be effected by a right shift operation only. Once the adaptive threshold τ_{adpt} for a given common point is computed, then a cell C_i is said to contain a portion of bone boundary, provided $max_i - min_i \geq \tau_{adpt}$.

Initial Threshold Value: Initial value τ_0 is selected from the histogram of the intermediate entropy-standard-deviation image. As the bone boundary consists of a few pixels of intermediate image, we consider intensity value corresponding to 99.95 percentile in the intermediate image histogram as τ_0 .

Contour Generation: The segmented bone image is traversed from five different directions like : (a) Top left to right bottom (Traverse-0) (Fig. 2(a)), (b) Top right to left bottom (Traverse-1) (Fig. 2(b)), (c) Top to bottom vertically (Traverse-2) (Fig. 2(c)), (d) Bottom right to top left (Traverse-3) (Fig. 2(d)), (e) Bottom left to top right (Traverse-4) (Fig. 2(e)). Based on the computed adaptive threshold value, the algorithm decides the direction of next movement and computes co-ordinates of the next pixel on bone boundary.

Computation of Direction: The algorithm decides on the selection of the next boundary pixel by checking the intensity values of its neighboring eight pixels. The direction of checking neighboring pixels may be clockwise (CW) or counter-clockwise (CCW). This direction depends on the traversal mode like Traverse-0: CCW, Traverse-1: CW, Traverse-2: Top CW, Traverse-3: Bottom CW and Traverse-4: Bottom CCW. It depends on the position of bone region, i.e., the region of interest (ROI) in the respective contour. In the left (right) contour traversal, ROI should be on the right (left) side of the contour path. Our contour traversal algorithm checks the intensity values of neighboring pixels and selects the next pixel position whenever it encounters a pixel whose intensity value exceeds the adaptive threshold value of the present pixel. After selection of a new pixel position, the algorithm checks whether or not the pixel is already visited. If the pixel is found visited, then the algorithm starts searching from a new position; otherwise it adds the current pixel in the visited list and decides the direction for the next move. The use of adaptive thresholding rectifies most of the false discontinuities which appear in the outputs of other contour generation algorithms like Sobel's or Canny's method [see Fig. 3(k), Fig. 3(l)]. This happens because the adaptive thresholding algorithm works on a small pixel window and performs the thresh-

Fig. 2. Traversal Direction (a) Traverse-0, (b) Traverse-1, (c) Traverse-2, (d) Traverse-3 and (e) Traverse-4

olding with respect to the local maximum intensity. Hence, it produces the image contour correctly and also reduces the appearance of false edges.

Selection of New Start Point: In many cases, contour traversal ends with a pixel position which is already visited. In such situations, a new start point is selected based on the mode of traversal. For left-to-right (right-to-left) traversal, the search for a new start point is initiated from the left (right) end of next row. The process is repeated until no new start point is required. Finally, we connect the missing contour pixels in the boundary and generate the final boundary.

3.2 Experimental Results

We have used several *X-ray* images of long bone and generated the contour using the proposed algorithm. In first phase of the algorithm, we generate segmented bone image from input *X-ray* image (Fig. 3(b)). This segmented bone image ($I_i = LE \times LS$ image) becomes the input image for second phase of the algorithm. We traverse the segmented image and run the proposed adaptive thresholding based contour detection approach to generate the bone contour (Fig. 3(c)). The bone contour generated by this approach may have some short (false) discontinuities. The final pass of proposed algorithm connects the intermediate missing pixels of the bone contour (Fig. 3(d)).

We have run our algorithm on several input *X-ray* images and observed very good performance especially for long-bone *X-ray* images compared to Sobel and Canny edge detectors (see Fig. 3). In most of the images, the bone regions are clearly segmented and false discontinuities are removed. In some images, however, (e.g., the foot image of Fig. 3 (m)) in which the contrast is very poor at the transition region, complete reconstruction could not have been possible (Fig. 3 (p)). On the other hand, for a fractured bone image, it clearly shows the outline of the fracture in the contour as desired (Fig. 3 (s) - Fig. 3 (v)).

We quantify the performance of segmentation by using the SEQA measure [14]. The segmentation entropy $E(S)$ measures how much the image entropy has changed during segmentation. Better segmented regions are more homogeneous in nature and thus will exhibit lower region entropy. Table 1 shows that the $E(S)$ value of the bone contour generated by the proposed method is lower than that of the input *X-ray* image. Also, it produces improved results compared to Sobel's and Canny's not only in terms of $E(S)$ value, but also with respect to appearance of false discontinuities.

Fig. 3. Elbow X-ray (a) X-ray image (b) *Entropy × Standard deviation* image of (a) (c) Contour of (a) (d) Final Contour of (a) (e) Contour of (a) using Sobel (f) Contour of (a) using Canny (g) X-ray image (h) *Entropy × Standard deviation* image of (g) (i) Contour of (g) (j) Final Contour of (g) (k) Contour of (g) using Sobel (l) Contour of (g) using Canny (m) Leg X-ray image (n) *Entropy × Standard deviation* image of (m) (o) Contour of (m) (p) Final Contour of (m) (q) Contour of (m) using Sobel (r) Contour of (m) using Canny (s) Broken Tumor X-ray image (t) *Entropy × Standard deviation* image of (s) (u) Contour of (s) (v) Final Contour of (s) (w) Contour of (s) using Sobel (x) Contour of (s) using Canny

Table 1. PERFORMANCE MEASURE OF SEGMENTED X-RAY IMAGES

$E(S)$ of input image	$E(S)$ (Sobel)	$E(S)$ (Canny)	$E(S)$ (proposed method)
5.09 (Fig. 3(a))	1.03	1.85	1.02
3.09 (Fig. 3(g))	1.05	1.65	1.04
4.51 (Fig. 3(m))	1.18	1.77	0.84
20.75 (Fig. 3(s))	0.66	1.63	0.63

4 Discussion and Conclusion

We have developed a new contour generation technique from gray-level bone X-ray images based on adaptive thresholding. This approach favorably overcomes the problem associated with the classical edge detectors like Canny's or Sobel's, particularly when the flesh boundaries appear as false bone edges. Contour generation approaches like deformable model based algorithms need good initialization of model contour. Our proposed method is fully automated and can generate the bone contour without any user intervention. Use of adaptive thresholding improves segmentation quality and expands the scope of its usefulness to more complex images. Bone contours thus generated from an X-ray image, can next be used for automatic fracture detection. Any non-uniformity present in the contour of a fractured bone image can also be identified by the algorithm while tracing the contour.

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