Automated Segmentation for Patella from Lateral Knee X-ray Images

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Abstract—X-ray image segmentation is an important issue in medical image analysis. Due to inconsistent X-ray absorption, the intensities are usually unevenly distributed and noisy in the processed organ, thus the object segmentation becomes difficult. In this paper we propose a new segmentation method for patella from the lateral knee X-ray images based on the active shape model (ASM). At first, a patella shape model is constructed by principal component analysis (PCA) of corresponding landmarks obtained from a set of training shape. As the knee X-ray image usually contains many anatomical structures, we design a strategy based on edge tracing to place the initial shape model as close to the patella boundary as possible. Then, the shape model is deformed and fitted to the patella boundary by using a dual-optimization approach that includes a genetic algorithm (GA) to get the global geometric transform and ASM to deform the shape model iteratively. Consequently, the proposed method can cope with different knee X-ray images and can segment the patella in an automatic procedure. In the experiment, 20 images were tested and promising results are obtained by the proposed method. This method is found useful for the clinical evaluation and biomechanical study of knee.

I. INTRODUCTION

X-RAY imaging is one of the common techniques for non-invasively examining human internal organs because of its low cost, convenience, fast imaging speed and high contrast for bone tissues. The lateral view image is commonly used in clinical diagnosis and assessment of patella diseases. To facilitate the pathological observation and assessment of patella from X-ray image, patella segmentation is very important. However, due to the inconsistent absorption of X-ray, the image intensities are usually unevenly distributed and noisy in the processed areas of target organ and make the patella segmentation complicated.

Image segmentations have been intensively investigated in medical image analysis. Pixel classification-based, region-based and deformable model-based methods are the three main categories. Pixel classification-based methods, such as Otsu's optimal threshold [1], are usually sensitive to

uneven intensity distribution, and the region-based methods, such as region growing, are weak in differentiating objects with similar intensity. According to our trials, the two methods cannot achieve reliable patella segmentation. Active shape model (ASM) proposed by Cootes *et al.* is one of the most popular deformable model-based segmentation methods [2]. Although ASM is excellent in handling large variability of object shape [3][4], it requires a good initial model for avoiding being trapped in local optima. If using a pure ASM method to segment patella from lateral knee X-ray images, manual intervention is definitely necessary. However, it also makes the processing inconvenient and operator dependent.

In this paper we propose a new framework of patella segmentation from lateral knee X-ray images. The proposed method includes two parts: one is feature point localization and the other is boundary segmentation. In the localization part, a specific patella feature point is automatically extracted and used to determine the position of initial model on the knee X-ray image. The patella feature point is determined by the geometrical relationship between the patella and femur dominant axis. The femur axis is estimated based on femur edges, which are extracted by the proposed Rolling-Ball Algorithm (RBA). In the segmentation part, a dual-optimization strategy is utilized to delineate the boundary of patella. At first, the model pose is adjusted by the global optimization of genetic algorithm (GA) based on a measurement of edge strength at the model landmarks. Next, the local optimization of ASM is used to refine the model pose and shape such that an improved boundary fitting of the model and image is obtained. As a result, the proposed method can automatically segment the patella from the lateral knee X-ray images. The experiments achieve good results from a number of X-ray images.

II. PATELLA FEATURE POINT LOCALIZATION

In this section, the Rolling-Ball Algorithm (RBA) that is used in the extraction procedure of patella feature is firstly introduced. This algorithm extracts a contour from a clutter of edge points. Starting with a seed point beside a target edge point, the seed point rolls (or pivots) around the target edge point clockwise or counter clockwise until it touches the other edge point. The touched edge point is the new t point and added to the shape list. The process is repeated until the rolling seed point cannot meet any other untouched edge point. To simplify the algorithm, a mask is used to easily indicate the rolling direction of the seed point '*s*' around the

target edge point '*t*', as shown in Fig. 1. The pseudo code of this algorithm is in Fig. 2.
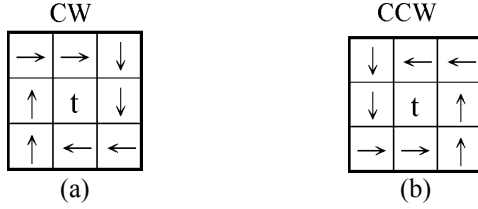
CW   CCW

(a)   (b)

Fig. 1. Rolling mask, (a) clockwise, and (b) counterclockwise.

Set point *t* to an initial position (an edge point)
Set point *s* to be an arbitrary neighbor of *t*
Set *temp* to the neighbor of *s* along the rolling direction of
    s in the rolling mask
Initialize *i* to zero
While *i* is less than a user-defined tracing length
    If *temp* is not on the edge
        Set *s* to *temp*
    Else
        Set *t* to *temp*
        Add *t* to the shape list
        Increment *i*
    End if
    Set *temp* to the neighbor of *s* along the rolling direction of
        s in the rolling mask
End while

Fig. 2. Pseudo code of Rolling Ball Contour Tracing.

In general, a suitable feature point should be with certain characteristics for identification. According to our observations, the point situated at the transition corner of patella frontal boundary with very high curvature, as indicated by the red point on Fig. 3a, is recognizable. In the proposed method, the feature point with high curvature is searched nearby the point, which is the farthest point away from the femur dominant axis.

To derive the femur dominant axis, several preprocessing steps are performed sequentially. We firstly apply the Asterisk-region filter, which is based on a mask of image-contrast measure, to convolve with the input image [5]. Then, an edge image is obtained. Next, the edge image is thresholded with value 17 and then small regions are removed. The femur anterior and posterior contours are then traced by RBA. The initial tracing edge points for RBA are at the 1/5 height of image from top image margin. The horizontal searching range starts from and ends at the 1/8 of image width from the left and right margins of image and the searching directions are toward to the center of each horizontal line. The first met edge points in both left and right directions are the starting edge points of both left and right femoral edges which are shown as the red points in Fig. 3b. In RBA, the clockwise rolling mask is applied on the right femur edge points, and the counterclockwise mask is applied on the left femur edge points. As a result, two femoral edges are extracted which are the anterior and posterior femoral contours (yellow contours in Fig. 3b). The midline of the two contours is calculated by the least square error approximation as the femur dominant axis. The resulting axis is indicated by the green line in Fig. 3b.

Next, the original X-ray image is also preprocessed by contrast enhancement, canny edge filtering and small edge regions removal [6]. After the anterior femur edge is found in the previous step, we trace along the Canny edge map, which coincides with this femur edge and connects the patella contour, to find the feature point on the upper right corner of patella. The corner point is the maximal curvature point in the region which is the farthest from the femur dominant axis. Fig. 3c demonstrates the resulting feature point (red point).

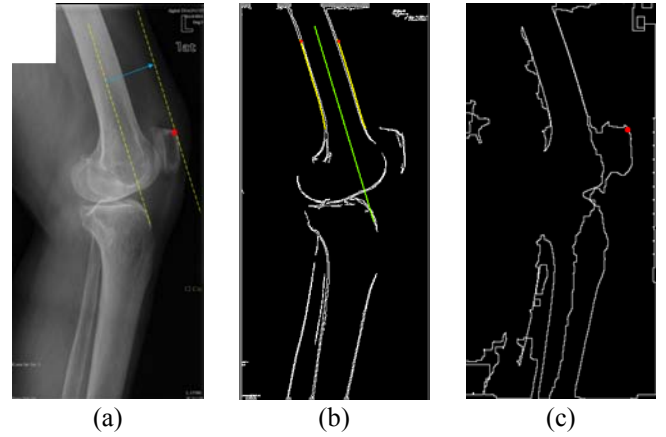(a)   (b)   (c)

Fig. 3. Patella feature point localization.

III. PATELLA SEGMENTATION

In the segmentation part, we utilize a fitting strategy, which incorporates the ASM framework with GA, for delineating the patella boundary.

A. Active Shape Model (ASM)

The ASM framework is driven by a PDM, which is a kind of flexible representation for the shape of a specific object [2]. At the beginning, *M* training images are selected and *N* landmarks that form a training shape are manually annotated from each training image. Note that *M* and *N* are assigned with 21 and 11, respectively in our experiment. In order to build the PDM, the pose differences of these training shapes are eliminated by Procrustes analysis [7]. A mean shape $\mathbf{x_0}$ is obtained by averaging the positions of corresponding landmarks of aligned training shapes. Then, a covariance matrix that characterizes the patella shape variability between each training shape and the mean shape is formed as

$$\mathbf{x}_0 = \sum_{i=1}^{M} \mathbf{x}_i \qquad \mathbf{C} = \frac{1}{M} \sum_{i=1}^{M} (\mathbf{x}_i - \mathbf{x_0})(\mathbf{x}_i - \mathbf{x_0})^T . \qquad (1)$$

By applying the principal component analysis (PCA) to covariance matrix **C**, the representation domain of a geometrical shape can be transformed from Euclidean space

to a reduced Eigen space. Consequently, any shape in the training data can be approximated by

$$\mathbf{x} \approx \mathbf{x_0} + \sum_{i=1}^{t} b_i \mathbf{p}_i , \qquad (2)$$

where $\mathbf{x_0}$ is the mean shape, $\mathbf{p}_i$ is the principal component vector that corresponds to the *i-th* significant component, and b_i is the shape parameter that is the weighting value of $\mathbf{p}_i$. The PDM in (2) can be used as a local optimizer to elastically adjust the model to fit with the object boundary on the test image. An important point is that the shape parameters b_i is usually constrained by the training data so that unreasonable deformations are avoided. The local optimization of ASM is achieved as follows. Step 1: Give an initial pose of model including the four parameters, scaling s, orientation θ, and model center C_x and C_y. Step 2: Search for the best fitting point of model landmark along its normal direction as shown in Fig. 4. Step 3: Update the pose and shape parameters (s, θ, C_x, C_y, b_i) based on the displacements between the detected fitting points and model landmarks. Step 4: Refine the shape parameters b_i based on the shape constraints of PDM, Step 5: if the difference of parameters between the current and previous iterations is smaller than a predefined threshold, then the optimization converges and stops; otherwise go to step 2. As ASM convergence is sensitive to the pose of initial model and user-guided initialization is tedious, we also design the following process to get the initial pose of shape model.
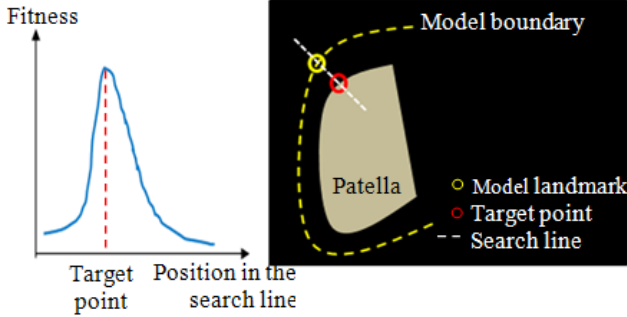

Fig. 4. Target point search in normal line of model boundary

B. Genetic Algorithm (GA)

Here, GA is employed for automatic initialization of ASM. We utilize GA to locate the model close to the object of interest so that the correct solution can be reached by PDM after some local searching steps [8]. GA is a kind of global optimization strategy based on the concept of natural selection. In this algorithm, each parameter to be optimized is viewed as a gene, and all the desired parameters are encoded in a chromosome. We also define the population size and a problem-specific function of fitness. The following evolution steps are utilized to optimize the chromosomes. Step 1: Randomly generate the population. Step 2: Evaluate fitness for each chromosome. Step 3: Select a pair of chromosome to reproduce from the population. Step 4: Crossover of the selected pair with a predefined crossover probability. Step 5:

Mutate the new offspring at one or more positions in chromosome with a predefined mutation probability. Step 6: Repeat step 3-5 until n new chromosomes are generated. Step 7: Population replacement. Step 8: Go to step 2 until the number of generation or the fitness reaches the predefined values.

C. The Segmentation Procedure

The proposed segmentation procedure is based on a strategy. After using GA to get the initial pose of shape model, the next step of the proposed dual-optimization is to refine the pose and shape of model by using ASM. In other words, we place the mean shape $\mathbf{x_0}$ to the feature location of patella and then apply GA to obtain the best fitting parameters of affine transform for the shape model. In the proposed system, each chromosome of GA encodes the transform parameters of model, and the population size is set as 200. Roulette Wheel Selection is used in the selection step. Each chromosome is given a probability of selection that is proportional to its fitness value. Moreover, we adopt 0.8 as the crossover probability. The mutation probability is set as 0.2 and the population replacement is based on the elitist method. The fitness function f is defined as:

$$f = \kappa - \frac{1}{G_0} \sum_{i=1}^{N} \left\{ \left| \frac{p_i}{L} \right| + \left| \frac{G_i}{G_0} - 1 \right| \right\}, \qquad (3)$$

$$G_0 = \sum_{i=1}^{N} G_i , \qquad (4)$$

$$G_i = \nabla I(x_i + p_i) - \nabla I(x_i + p_i + 1), \qquad (5)$$

$$p_i = \arg\max_{s_i \in [\frac{-L}{2}, \frac{L}{2}]} \left\{ (\nabla I(x_i + s_i) - \nabla I(x_i + s_i + 1)) \right\}, \qquad (6)$$

where κ is a positive large constant. L is the length of search line of model landmark i, x_i is the position of i-th landmark of model, and G_i is the maximal directed gradient at the search line of x_i. After the initial pose of shape model is obtained, the boundary fitness between the model and the patella in the image is refined by using the iterative deformation of ASM. In the deformation, the fitness function of ASM (Fig. 4) is indicated in (5). After the ASM converges, the segmentation of patella boundary is accomplished.

IV. Results and Discussion

In our experiment, 20 lateral knee X-ray images are tested. Fig. 5 shows six of these cases, the segmented contours were overlapped with the X-ray images and were shown in the first two rows. In the last two rows, we zoomed the resulting contours for detailed inspection. There are different kinds of artifacts in X-ray images, such as the overlapping edges of different bone contours, fuzzy bone boundary, and confusing pathological structures (e.g., spur), which are indicated by the green arrows in Fig. 5g, 5i, and 5j, respectively. In the

proposed method, the statistical model provides the shape information of patella to constrain the deformation process so that stable segmentation can be obtained even with these image artifacts. The patella localization strategy using RBA and the utilization of knee features also successfully resolve the difficult problem of determining the initial position of patella model. As a result, the proposed method can cope with different artifacts of X-ray image and achieve good patella segmentation in an automatic process.

V. Conclusion

The patella segmentation on lateral knee X-ray images is an important issue in clinical diagnosis, and however, few researches have been reported. In this paper we proposed a new segmentation framework to handle this problem based on ASM. At first, a feature point localization procedure is designed to locate the patella shape model automatically. Then, we used a dual-optimization strategy including GA and ASM to fit the shape model to the patella boundary. For GA initialization, the placement of shape model is first given by the feature position, and then refined by using the global optimization of GA. At last, the model boundary is elastically adjusted by ASM deformation. Since the proposed method is constrained by the shape distribution of training data, the resulting contours can be kept as similar to the real shape of patella as possible even in the presence of image artifacts. The experimental results show good detections that are consistent with experts' expectations. As the proposed method is stable and efficient, it is valuable for both clinical diagnosis and biomechanical evaluation. The proposed system will be extended to investigate patella pathology and disease assessment in the future research.

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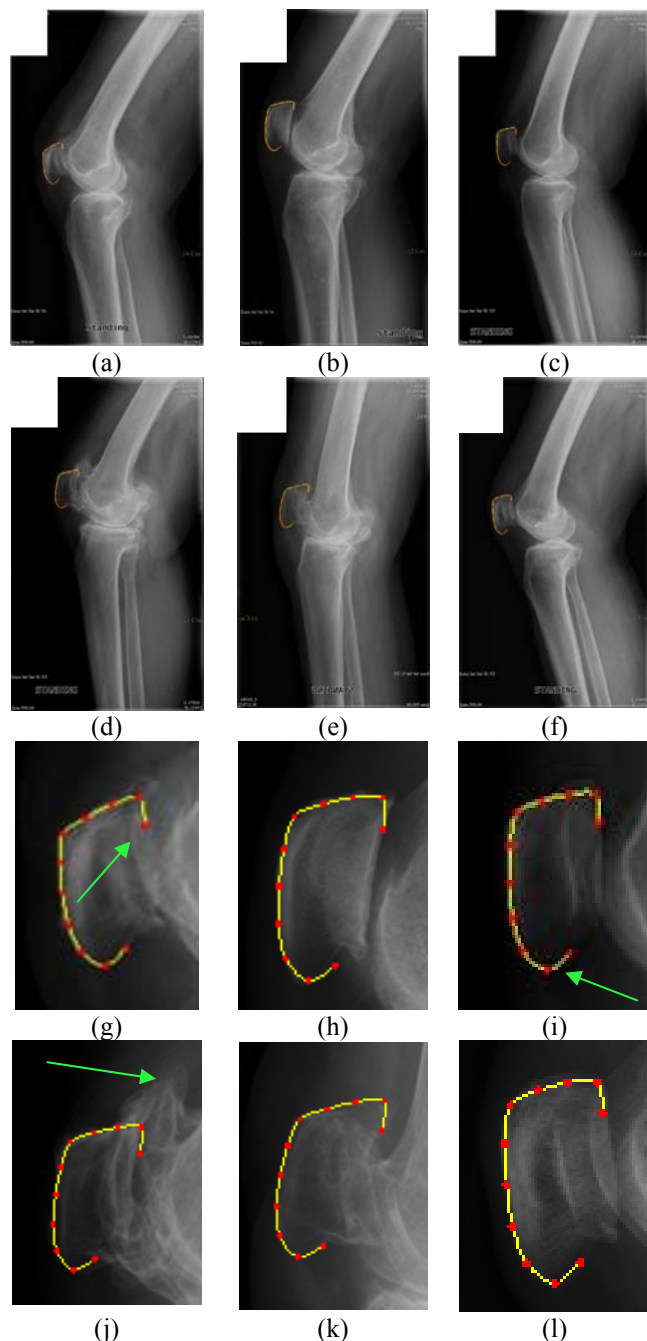
Fig. 5. Segmentation results. (a)-(f) The yellow curves are resulting contours and the red points represent the model landmarks. (g)-(l) are enlarged images corresponding to (a)-(f), respectively. The green arrows indicate artifact conditions that may cause difficulties in segmentation.