Interactive Segmentation of Hip Joint Cartilage

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Abstract— This work deals with hip joint cartilage segmentation, which is an important task in joint diseases diagnosis. Since the manual segmentation commonly used nowadays, is a tedious and lengthy task, this work brings a new idea into its automation and simplification of the medical expert work. The proposed method is an interactive algorithm for hip joint cartilage segmentation, and hence it requires some user interaction, which is common and usually desired in medical image processing. The first step of the method is a selection of several points in several slices lying inside the cartilage. The purpose is a rough delimitation of the cartilage area. This delimitation is based on the assumption that the femoral head has approximately circular shape. The cartilage is then segmented using the combination of Graph Cut segmentation and K-means clustering techniques. The algorithm was tested on 3D isotropic True-FISP volumes of patients with femoroacetabular impingement and the results were evaluated by commonly used Dice Similarity Coefficient (0.62). The results of the segmentation will be prospectively used for the segmentation of quantitative MR maps (T1 and T2) in femoro-acetabular impingement (FAI) investigation.

1. INTRODUCTION

This work deals with hip joint cartilage segmentation, which is an important task in joint diseases diagnosis. Since the manual segmentation commonly used nowadays, is a tedious and lengthy task, this work brings a new idea into its automation and simplification of the medical expert work.

General image segmentation is still an unsolved problem, therefore specific methods have to be applied for particular types of images. A general method that could be applied for all kinds of images has not been developed so far and in the near future the situation will probably remain the same. For MR image segmentation, the classic techniques such as thresholding, region growing, active contour, etc. can be used [1]. Another type of segmentation used in MRI is pixel classification into several classes. This can be either supervised using algorithms such as SVM [2] used e.g., in [3], or unsupervised using clustering algorithms. Such algorithms can be based on data space division such as k-means algorithm [4] or they can respect the noise distribution such as Gaussian Mixture Model using the Expectation-Maximization algorithm for determination of model parameters [5]. Since tissues of a user's interest may reach similar intensities as other tissues present in image, more sophisticated algorithm has to be used.

Only few algorithms were proposed for hip joint cartilage segmentation task. Sato et al. [6] proposed a method based on automatic determination of approximate center of femoral head and subsequent determination of cartilage using a radial directional derivatives. The method proposed by Khanmohammadi et al. [7] is based on automatic determination of femoral center by Hough transform. Femoral head and acetabulum are detected, and segmented and the cartilage is found as the space between these two bones.

The method proposed in this paper is semi-automated and expects manual determination of several starting points lying inside the hip joint cartilage. Users have higher control on the segmentation process since they can manually correct the partial segmentation, which can improve the overall result of the segmentation process. Even though this leads to higher demands on users, it can achieve the accuracy according the user's expectation.

2. PROPOSED METHOD

The flow diagram of the proposed method is depicted in Figure 1. The algorithm is based on 2D segmentation of selected axial slice and subsequent propagation in both directions with possible manual correction. It uses graph cut segmentation algorithm with subsequent automatic correction by Bayesian Quadratic Discriminant Analysis (Bayesian QDA) for the segmentation of selected slice. In propagation, only Bayesian QDA is employed.

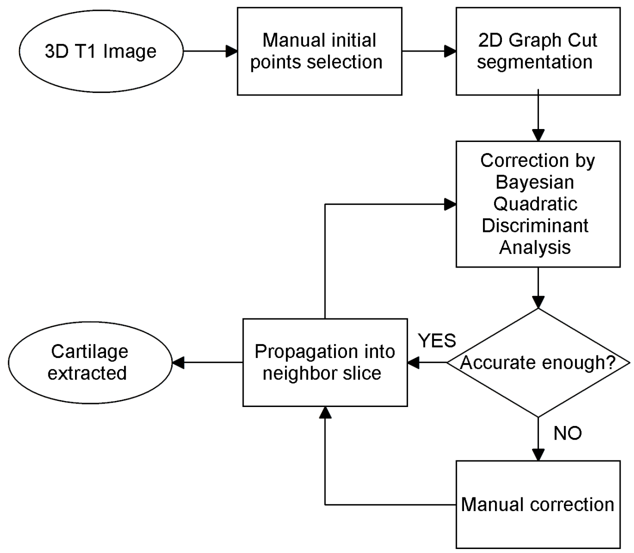

Figure 1: Flow diagram of the proposed method.

2.1. ROI Delimitation

The first step of the method is a manual selection of several points not lying in a plane. The purpose is a rough delimitation of the cartilage area using a sphere fitting to these points. This delimitation is based on the assumption that the femoral head has approximately a circular shape. The next step consists of the manual selection of the suitable axial slice and the subsequent several reference point selection. These points are interpolated by a cubic spline in clock-wise order with respect to the center of the circle that best fits the points. The spline creates the foreground mask for subsequent segmentation. The background mask is created as inverted morphological dilation of the spline with particular dilation size dependent on the image resolution.

2.2. Graph Cut Segmentation

The labels for points in between foreground and background are computed by Graph Cut segmentation technique [8]. The input of this method, except the image itself, is a map of labels. Each pixel is labeled as foreground, background or unknown. The optimal border between foreground and background is found in the area of unknown labels.

2.3. Correction

The result of the Graph Cut segmentation is corrected by Bayesian Quadratic Discriminant Analysis (Bayesian QDA) [9], where the training data consists of pixels inside and outside the segmentation result with respect to their label in the mask. The new label is assigned again to the pixels with previously unknown label and isolated ones are eliminated.

Bayesian QDA is a supervised classification technique using a Gaussian distribution for modeling the likelihood of each class. The Gaussian parameters are estimated by maximum likelihood estimation from training points.

As a next step, the segmentation result can be corrected or confirmed by user and it is used as reference segmentation for neighbor slices.

2.4. Propagation

The resulting mask of 2D segmentation is used as a reference segmentation in the propagation process into the neighbor slices.

The points from the neighbor slice lying inside the dilated reference mask are classified by Bayesian Quadratic Discriminant Analysis, where pixels from the previous slice are used for training. Isolated pixels are eliminated and the result can be again corrected by user, because its precision plays a significant role in the subsequent segmentation in further slices. The result is again used as a reference for the next slice segmentation.

3. EXPERIMENTS AND RESULTS

3.1. Evaluation Criteria

The results were evaluated by commonly used Dice Coefficient (DC) and Accuracy Coefficient (AC), where only the space inside the bounding box for enlarged fitted sphere was considered. If the whole volume had been considered, the DSC would reach the same value, but the accuracy would be very close to 1 and would not reflect the algorithm performance. No interaction or manual correction was performed during this testing procedure.

The Dice Coefficient (DC), in some works called Similarity Index, is computed according to the equation

$$\mathrm{DC} = \frac{2\left|A \bigcap B\right|}{|A| + |B|}, \tag{1}$$

where A and B denotes the ground truth and the result masks of the segmentation, respectively. This criterion compares the intersection of two sets with their union. The range of values of DC is $\langle 0; 1 \rangle$, where the value 1 expresses the perfect segmentation. According to [10], the DC > 0.7 indicates an excellent similarity.

Another measure widely employed for segmentation evaluation is Accuracy (A), used e.g., in [3] and defined by the equation:

$$A = \frac{TP + TN}{TP + FP + TN + FN}, \tag{2}$$

where TP, FP, FN and TN stand for "True Positive", "False Positive", "False Negative", and "True Negative", respectively. Both measures are in the same range as DC and the higher value indicates the better performance as well.

3.2. Results

The algorithm was tested on 20 3D isotropic True-FISP volumes of patients with femoroacetabular impingement. All MR images were obtained using a 1.5 T system (Avanto, Siemens Healthcare, Erlangen, Germany) with the voxel size of $0.63 \times 0.63 \times 0.63$ mm and the volume size of $512 \times 512 \times 321$ px. The ground truth performed by a medical expert was available. More information about the data can be found in [11]. The results are summarized in Table 1 using the both coefficients for initial selected slice and the whole 3D volume. For each of 20 cases, the algorithm was repeated three times with different initial slice, where 10 points were chosen in the initial slice. An average example of the result for an initial slice is shown in Figure 2.

Table 1: Segmentation evaluation by dice coefficient and accuracy for both planes.

	DC	Accuracy
Initial slice	0.81 ± 0.05	0.94 ± 0.02
3D volume	0.62 ± 0.07	0.96 ± 0.01

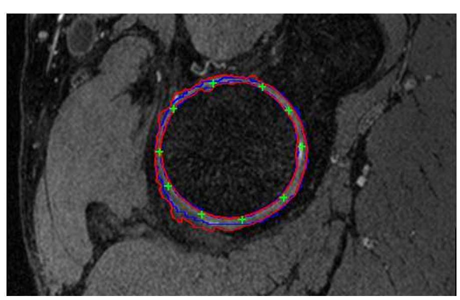

Figure 2: Average result (DC = 0.82) of an initial slice segmentation (red) compared to ground truth (blue) for manually selected 10 points (green).

4. CONCLUSION AND FUTURE WORK

This work describes the initial research in the automation of the hip joint cartilage segmentation task. The result of this work is a tool for the automated interactive segmentation, which speeds up this tedious task in the diseases diagnosis and research. There are only a few papers dealing with this particular problem (e.g., [6]), and these do not contain quantitative results; therefore the proposed method cannot be compared with them. The future research will focus on improving the accuracy of the automated segmentation of the hip cartilage, especially in the most problematic area of femoral neck, and will be prospectively used for the segmentation of quantitative MR maps (T1 and T2) in femoro-acetabular impingement (FAI) investigation.

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