Automatic Segmentation of Articular Cartilage from MRI: A Multi-Contrast and Multi-Dimensional Approach

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Introduction

The regional variation in the morphology (thickness or volume) of articular cartilage is frequently used for evaluating the initiation and progression of osteoarthritis [1]. Quantifying regional cartilage thickness or volume requires MR image segmentation (classification) and three-dimensional reconstruction [2]. A number of computational methods have been used to automate the segmentation of articular cartilage from a gray scale MR images taken with a single sequence. Yet, fully automatic segmentation seems to be a difficult goal to achieve. There exist many different MR sequences that utilize tissue properties such as T1 and T2 relaxation times to increase the contrast between cartilage and its surrounding soft tissues in joints. Multiple sets of MR images taken with different sequences provide different contrast mechanisms between tissues and will help separate different tissues [3]. The purpose of this study was to evaluate segmentation of knee articular cartilage automatically from multiple sets of MR images using a support vector machine (SVM) method [4], a kernel-based machine learning algorithm.

Methods

Data acquisition: Four 3D MR sequences, SPGR, GRE, 3D FSE "XETA" and IDEAL-balanced-SSFP "FIESTA", were run on the knee of a healthy subject to get five sets of MR images (three sets from each SPGR, GRE and 3D FSE "XETA", and two sets (water and fat images) from IDEAL-balanced-SSFP "FIESTA") within 30 minutes. The MR images were spatially registered using the mutual information based multi-modal registration algorithm in Insight Segmentation and Registration Toolkit [5]. The even and odd numbered slices were used for training and testing of SVM, respectively. We also developed a method to automatically segment bone from multiple sets of MR images in the similar manner described here but it will be assumed without explanation to focus on cartilage segmentation. Each pixel in the image could be regarded as a vector with five intensity values obtained from five sets of MR images. For each pixel the distance between the pixel and the bone boundary was appended to its vector to account for the geometric information of the articular cartilage which always exists at the end of the bone. Training of SVM: The pixels that consist of the articular cartilage were manually identified using the SPGR MR images in the even numbered slices. Both the cartilage and non-cartilage pixels were input to a SVM. The SVM, conceptually speaking, mapped each pixel to a six-dimensional vector space and calculated an optimal hyperplane that separates the cartilage pixels from non-cartilage pixels as shown in Figure 1. For the calculation of the hyperplane, the SVM-light was used [6]. Segmentation with trained SVM: As with the pixels in the even numbered slices for training, the pixels in the odd numbered slices also had six components in the same order. Each pixel was tested by the trained SVM to determine whether the pixel was inside or outside of the hyperplane representing the boundary of cartilage pixels in the six-dimensional space. To assess the performance of the SVM, the cartilage in the odd numbered slices were manually segmented as a gold standard, and the sensitivity and specificity of the classification results were calculated.

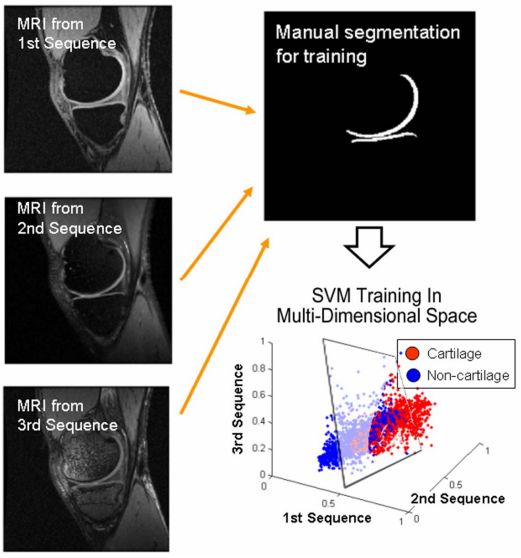

Figure 1. Training of SVM: Calculation of an optimal hyperplane that separates cartilage and non-cartilage pixels in a multi-dimensional signal intensity space

Results

True positive, false posive, true negative and false negative pixels were counted from the classification result (Figure 2 (a)). The sensitivity and specificity were 93.8 % and 99.3 %, respectively. Three-dimensional models were created from the classfication result and the manual segmentation for qualitative comparision as shown in Figure 2 (b) and (c). The muscle pixels in the posterior regions of the femoral condyles and the tibia were frequently misclassified as cartilage.

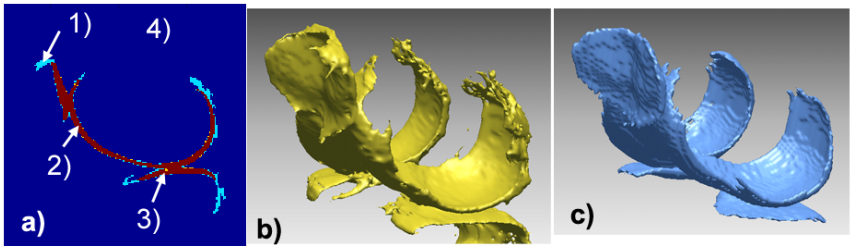

Figure 2. a) Classification result of a slice – 1) false positive, 2) true positive, 3) false negative and 4) true negative, b) 3D model from the classification results, c) 3D model from the manual segmentation (gold standard)

Discussion

The results show that for all true cartilage pixels, 93.8% of them were classified as cartilage pixels. The sensitivity in this study was higher than the sensitivity reported in a recent study using another machine learning method [7]. This study showed the possibility of using the signal intensities from multiple MR images along with minimal geometric information as features for SVM to automatically segment articular cartilage. Ideally, the training is required only once to determine the hyperplane of SVM and then, the hyperplane can be used to automatically segment articular cartilage from new data sets from the joints from other subjects. Next steps include finding best sets of sequences to reduce scan time, improving the spatial alignment between sequences, normalizing the signal intensities between subjects and accounting for coil sensitivity profiles to apply this method between different subjects.

References

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