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Brief Report

Three-dimensional hip cartilage quality assessment of morphology and dGEMRIC by planar maps and automated segmentation

C. Siversson † ‡ *, A. Akhondi-Asl †, S. Bixby §, Y.-J. Kim ||, S.K. Warfield †

† *Computational Radiology Laboratory, Department of Radiology, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA*
‡ *Department of Medical Radiation Physics, Lund University, Malmö, Sweden*
§ *Department of Radiology, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA*
|| *Department of Orthopaedic Surgery, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA*

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SUMMARY

Objective: The quantitative interpretation of hip cartilage magnetic resonance imaging (MRI) has been limited by the difficulty of identifying and delineating the cartilage in a three-dimensional (3D) dataset, thereby reducing its routine usage. In this paper a solution is suggested by unfolding the cartilage to planar two-dimensional (2D) maps on which both morphology and biochemical degeneration patterns can be investigated across the entire hip joint.

Design: Morphological TrueFISP and biochemical delayed gadolinium enhanced MRI of cartilage (dGEMRIC) hip images were acquired isotropically for 15 symptomatic subjects with mild or no radiographic osteoarthritis (OA). A multi-template based label fusion technique was used to automatically segment the cartilage tissue, followed by a geometric projection algorithm to generate the planar maps. The segmentation performance was investigated through a leave-one-out study, for two different fusion methods and as a function of the number of utilized templates.

Results: For each of the generated planar maps, various patterns could be seen, indicating areas of healthy and degenerated cartilage. Dice coefficients for cartilage segmentation varied from 0.76 with four templates to 0.82 with 14 templates. Regional analysis suggests even higher segmentation performance in the superior half of the cartilage.

Conclusions: The proposed technique is the first of its kind to provide planar maps that enable straightforward quantitative assessment of hip cartilage morphology and dGEMRIC values. This technique may have important clinical applications for patient selection for hip preservation surgery, as well as for epidemiological studies of cartilage degeneration patterns. It is also shown that 10–15 templates are sufficient for accurate segmentation in this application.

Introduction

At early stages of osteoarthritis (OA) the glycosaminoglycan (GAG) content in the cartilage has been shown to decrease[1]. The delayed gadolinium enhanced magnetic resonance imaging (MRI) of cartilage (dGEMRIC) method is a validated imaging technique for estimation of the GAG content, based on the principle that the intravenously injected contrast agent gadopentetate dimeglumine [$Gd(DTPA)^{2-}$] (Magnevist®, Bayer Schering Pharma) distributes in the cartilage in an inverse relationship to the GAG content[1]. A quantitative measurement of T1 in the cartilage is then performed, which correlates to the distributed amount of $Gd(DTPA)^{2-}$.

Although three-dimensional (3D) volumetric hip-dGEMRIC is often used, the complexity of manually segmenting and visualizing the cartilage typically restricts the routine evaluation to just a few select slices. One of the few innovative attempts to date at evaluating the full 3D volume in a clinically useful way is a scheme presented by Domayer *et al.*[2], where an isotropic 3D T1 dataset is manually reformatted to evaluate the cartilage quality at multiple locations around the femoral head.

This paper describes a new method for straightforward quantitative whole-joint assessment of both morphology and dGEMRIC

* Address correspondence and reprint requests to: C. Siversson, Computational Radiology Laboratory, Department of Radiology, Boston Children's Hospital, 02115 Boston, MA, USA. Tel: 1-857-218-5172.
E-mail addresses: carl.siversson@childrens.harvard.edu, carl.siversson@med.lu.se (C. Siversson), alireza.akhondi-asl@childrens.harvard.edu (A. Akhondi-Asl), sarah.bixby@childrens.harvard.edu (S. Bixby), young-jo.kim@childrens.harvard.edu (Y.-J. Kim), simon.warfield@childrens.harvard.edu (S.K. Warfield).

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values in hip cartilage, using novel two-dimensional (2D) planar maps. This work also includes the implementation and verification of an automated segmentation technique that has never previously been utilized with hip cartilage.

Method

A multi-template based label fusion technique is used to automatically segment the cartilage from the acquired 3D data. The segmented cartilage is then unfolded using a projection algorithm, resulting in two planar maps showing the T1 variation and cartilage thickness across the joint. In addition, a leave-one-out cross validation study was performed to verify the segmentation technique and its dependence on the included number of templates.

Image acquisition

A retrospective analysis was performed on data from 15 hip dGEMRIC patients (2 males and 13 females, 13–45 years old). The cohort consisted of patients who were sent for a dGEMRIC examination by an orthopedic specialist, either as a part of a pre-surgical examination or as part of a clinical workup for hip pain. All subjects were symptomatic with mild or no radiographic OA. Hence, sufficient cartilage tissue was present for assessment using MRI and the patients were deemed representative of the typical dGEMRIC population. The study was approved by the local Institutional Review Board.

All imaging was performed on a 1.5 T Siemens Avanto scanner at 45 min after intravenous injection of a double dose (0.4 mL/kg) $Gd(DTPA)^{2-}$. T1 maps were generated using the 3D-Variable Flip Angle (3D-VFA) method[3], acquired in the oblique sagittal plane along the axis of the femoral neck using isotropic 0.8^3 mm^3 voxels and an acquisition matrix of $192 \times 192 \times 100$. Excitation pulse flip angles were 5° and 28°[4]. repetition time (TR) was 15 ms and echo time (TE) was 4.8 ms. Scan time was 7 min and 26 s. The subsequent TrueFISP sequence was acquired in the same plane using 0.6^3 mm^3 voxels and an acquisition matrix of $256 \times 256 \times 144$, covering the same region as the 3D-VFA acquisition. TR was 12.6 ms and TE was 5.5 ms. Scan time was 7 min and 47 s. Parallel imaging acceleration factor was 2, for both sequences.

The bulk cartilage inside of the acetabular rim (i.e., the combined femoral and acetabular cartilage, excluding the area around fovea), the femur and the acetabulum were segmented manually in all 15 TrueFISP datasets in order to serve as a library of template segmentations to guide the automated segmentation algorithm.

Automated segmentation

Automated segmentation was performed using a method referred to as multi-template based label fusion[5]. First, all template images are registered to a target image (i.e., a TrueFISP image on which automated segmentation is to be performed), using a combined seven-parameter (rigid plus global scaling) and non-rigid block matching registration[6]. By then applying the deformation field retrieved from these registrations to the associated template segmentations, a set of segmentation candidates for the target image are constructed. Finally, the segmentation candidates are fused into a consensus segmentation estimate using the Local MAP STAPLE (LS) algorithm[7]. For comparison, fusion was also performed using standard majority voting (MV)[5]. Total processing time was typically around 3 h using 20 Intel Xeon cores.

In this work, each of the 15 cases were automatically segmented through a leave-one-out scheme, using all or a subset of the remaining cases as templates, thus keeping target and template volumes completely disjoint.

Unfolding to planar maps

The automatically generated segmentations were used to mask out the cartilage from the T1 volume. This was followed by a sphere fitting routine[8] to find the center of the spherical cartilage structure. Finally, the Lambert azimuthal equal area projection algorithm[9] was applied to unfold the radially averaged acetabular cartilage to a T1 planar map (Fig. 1). The bulk cartilage morphological planar map and the acetabular surface area were also retrieved.

Leave-one-out cross validation

The impact of the number of templates on segmentation performance was investigated by repeatedly selecting n random cases from the 14 possible ($n = 4, 6, 8, 10, 12, 14$) and using them as templates for the segmentation pipeline. By repeating this 50 times, for each case and for each $n < 14$, average Dice's similarity coefficients[5] were calculated, for which the effect of individual template selection was averaged out. From these average Dice coefficients, the influence of the number of templates on segmentation performance can be determined. As an additional measurement to investigate regional variations in segmentation accuracy, the average Dice coefficient was also calculated only involving cartilage segmented superior to the fovea (i.e., the superior hemisphere of the femoral head cartilage).

Results

Automated segmentation

From the leave-one-out studies it was shown that LS performs better than MV for any number of templates and for all of the segmented structures (Fig. 2). In cartilage segmentation using four templates, average Dice coefficients (±SD between subjects) were 0.788 (±0.053) and 0.761 (±0.069) for LS and MV, respectively. Corresponding values using 14 templates were 0.824 (±0.052) and 0.82 (±0.056) [Fig. 2(a)]. Similar tendencies were seen in segmentations of femur and acetabulum, with a Dice coefficient in the approximate range of 0.94–0.96 in femur and 0.86–0.91 in acetabulum, as the number of templates was increased from four to 14 [Fig. 2(b) and (c)]. The separately calculated average Dice coefficient, only involving cartilage superior to the fovea, was 0.87 (±0.039) when segmented using LS and 14 templates.

Planar maps

Various patterns of cartilage degeneration and morphology are readily demonstrated by the different color patterns on the planar maps (Fig. 1). T1 values range between 200 and 800 ms and bulk cartilage thickness mostly ranges between 1.0 and 3.5 mm. Cartilage surface area varies between 2359 and 3727 mm^2 for the different cases.

Discussion

The primary purpose of this work is to introduce a method for assessing cartilage quality throughout the entire hip joint that is readily useful in clinical applications. As an important step, this work also verifies the performance of the segmentation method for use in this application. Although there are prior work done on automated segmentation of hip cartilage[10], to our best knowledge,