INTRODUCTION

Conventional radiography remains widely used in imaging to assess osteoarthritis in a clinical setting. Radiography is limited by its inability to non-invasively visualize cartilage, to provide insight into structural and functional changes of cartilage, and to stage cartilage degeneration before cartilage damage is thought to be irreversible.

Magnetic resonance imaging (MRI) provides a non-invasive means to quantitatively assess articular cartilage morphology and biochemistry in three dimensions. There is a growing interest in using quantitative MRI (qMRI) to identify degenerative changes in cartilage. One large multicentered study, the Osteoarthritis Initiative (OAI), has collected qMRI cartilage data using double echo steady state (DESS) and T2 MRI. DESS imaging provides volumetric information while quantitative T2 MRI probes aspects of tissue hydration and collagen structure [1-3]. There is a need for freely available software to register multiple MRI sequences and perform semi-automated segmentation on images like those obtained by the OAI study.

The objective of this study was to describe and validate the open-source, freely available image analysis software, ImageK, that segments and registers MRI sequences. As a proof of concept, DESS and T2 sequences were registered and semi-automated segmentation of DESS images were completed. The software can perform identical analysis on similar sequences. The software executable files, source code, and example files will be made freely available at www.ImageK.org.

METHODS

MRI Sequences: DESS and T2 relaxation MR images were collected using sequences approved for the NIH sponsored OAI study. Subjects provided informed consent and the studies were IRB approved.

Image Analysis: Femoral condyle articular cartilage was segmented from MRI sequences using the following strategy. DESS and T2 sequences were registered using a mutual information metric as defined by Mattes [4]. Semi-automated computer segmentation of the cartilage was completed using the following approach. The approximate anatomic center of the femoral condyle is user defined, and a radial search is completed identifying bone-cartilage and cartilage-soft tissue edge points. These edges can be redefined by the user. A path framework is used to connect these points. Image analysis and visualization software design was completed using the Insight Toolkit and the Visualization Toolkit, respectively.

Validation: Registration was validated using two separate approaches. First, a checkerboard overlap of the registered images was used to qualitatively verify the accuracy of the results. Second, MRI lucent fiduciary markers placed in a cadaver knee were used to quantify differences between the two registered image sections. These were completed on three separate cadaveric knees. Segmentation was validated by comparing differences in segmentation between expert manual user segmented slices and computer segmented slices. The DESS sequences from three separate patients were used, and twenty five images from each patient were randomly selected for comparison.

RESULTS

Registration: Figure 1 is a representative image of the fine checker board layout of overlaid DESS and T2 images after Mattes multimodality registration. In the figure, note the excellent alignment of the femoral and tibial cartilage. The accuracy of the registration was quantified using MRI lucent fiduciary markers and measuring alignment across both MRI sequences. Across the x and y axis, alignment was less than one pixel of difference. In the z-axis, alignment was perfect within the precision of the measurement in the z-axis which is limited by the resolution of MRI sequences. T2 resolution was 2mm as compared to 0.7mm for the DESS sequences.

Segmentation: Figure 2 displays a comparison between expert user and computer segmented femoral condyle cartilage. Here, agreement is highlighted using purple pixels, and red pixels denote areas of disagreement. The arrow highlights the largest area of disagreement. Overall, across three separate data sets, expert user and computer segmented slices were within 94 ± 1% (SEM) agreement.

DISCUSSION

With the growing interest in qMRI analysis to identify cartilage degeneration, such as the OAI study, there is a need for freely available image analysis software to support qMRI analysis. Here, we introduce free, open-source image analysis software that easily and accurately segments knee articular cartilage. Registration validation demonstrated an agreement between MRI sequences of less than one pixel. Semi-automated segmentation was 94% accurate compared to expert segmentation. The segmented images can be used in assessment of MRI parameter mapping sequences such as T2, T1p and dGEMRIC.

The software, source code, and example image files used to generate the data presented will be made available for downloaded from the archival site: www.ImageK.org.

Here, we use femoral condyle articular cartilage to validate the software on DESS and T2 data sets. However, the software can easily be used to segment the tibial articular cartilage or modified to segment the cartilage of other joint articular interfaces using sequences similar to DESS.

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