

## Semi-Automated Profile Generation for Functional Cartilage Imaging

D. R. Thedens<sup>1</sup>, N. F. Klocke<sup>2</sup>, A. Amendola<sup>2</sup>, and D. R. Pedersen<sup>2</sup>

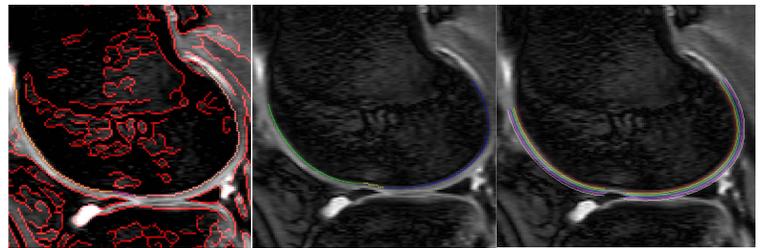
<sup>1</sup>Radiology, University of Iowa, Iowa City, IA, United States, <sup>2</sup>Orthopaedics and Rehabilitation, University of Iowa, Iowa City, IA, United States

**Introduction:** Early stages of osteoarthritis (OA) are associated with collagen matrix changes and proteoglycan (PG) loss, increasing susceptibility of the cartilage to further mechanical damage, but these changes are not detectable on standard morphological imaging. The need for imaging biomarkers of early degenerative changes has led to the development of several MRI cartilage imaging techniques, such as T1 $\rho$ , T2 mapping, and delayed gadolinium-enhanced imaging of cartilage (dGEMRIC). These techniques are sensitive to biochemical changes and may be useful as indicators of the presence of early processes of OA. Each technique provides complementary information on the state of cartilage, with T2 depending primarily on water content and collagen matrix, dGEMRIC on glycosaminoglycan content, and T1 $\rho$  relaxation on proteoglycans (PG) and their interactions with free water. Consequently, a comprehensive assessment of cartilage condition may utilize two or more of these techniques.

Proper collation of the information contained in each of the protocols at a single time point (which may originate from two separate sessions in the case of dGEMRIC) as well as over time requires that the anatomy from each acquisition be brought into correspondence. Previous studies have largely relied on dividing the cartilage into zones (anterior/posterior, superficial/deep) for quantitative assessment. It is desirable generate correspondence nearer to a pixel-by-pixel level which would permit correlation of focal changes in cartilage and the development of multiparameter maps of cartilage condition at a similar level of detail as the source images. The purpose of this study was to develop a semi-automated technique to generate accurate and reproducible line profiles along the joint surface of the knee for T2, T1 $\rho$ , and dGEMRIC to permit direct registration, comparison, and correlation between functional cartilage imaging methods.

**Methods:** The line profiling algorithm begins with two user-identified points encompassing the femoral sulcus groove, which serves as a separator between anterior and posterior regions. The midpoint of the sulcus is estimated from edge information within the user-selected region, and an ellipse is fit to the anatomy within this region to refine the location of the sulcus and reduce interobserver variability. A Canny edge detection operator is applied to the image to generate the objective function for a line growing search in each of the anterior and posterior directions from the sulcus. This process continues to a preset angle to cover the entire boundary between bone and cartilage. The result is a full description of the bone/cartilage interface.

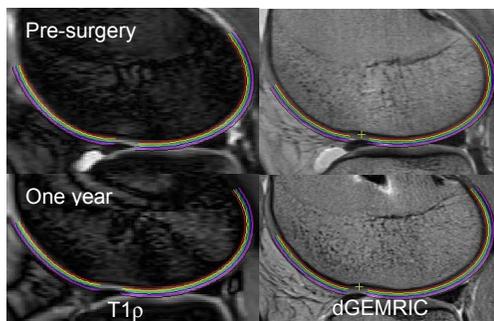
Next, contours for subsequent profiling within different layers of the cartilage are generated from the "raw" bone/cartilage interface (Figure 1, left panel). Ellipses are fit separately to all points along the anterior and posterior regions of the surface to smooth out pixelation in the raw boundaries. This is followed by a resampling of the smoothed curve at 0.5mm intervals along each surface (Figure 1, center). At each of the resampled locations, a local search determines the perpendicular direction to the cartilage surface based on a circle fit to the bone/cartilage interface for anterior and posterior surfaces. Additional parallel profile lines are then created (separated by 0.5mm thickness) to create matching contours at different layers of the cartilage (Figure 1, right panel). The result is a family of contours precisely matched to the anatomy with constant geometric spacing between locations from the anatomical landmarks. Matching the anatomically generated contours between T2, T1 $\rho$ , and dGEMRIC data sets yields a direct correspondence of their values at each location and layer. The algorithm described was applied to T2, T1 $\rho$ , and dGEMRIC acquisitions from nine ACL-injured subjects, as well as T2 and T1 $\rho$  data from five healthy volunteers imaged in three separate sessions.



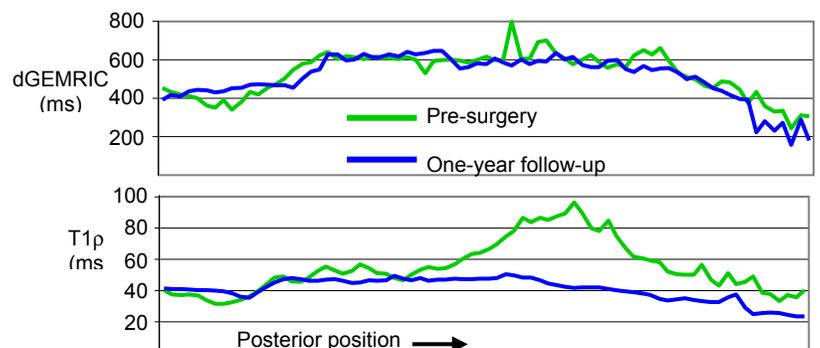
**Figure 1:** Refinement of raw edges. Initial edge detection (left) is refined by fitting anterior and posterior regions to an ellipse to smooth (middle) for subsequent resampling and generation of multiple contour layers for anterior and posterior regions (right).

**Results:** Figure 2 shows the automatically generated family of contours for an ACL-injured subject at two imaging time points for T1 $\rho$  and dGEMRIC images. The cross shows the identified sulcus location on the dGEMRIC image. Variability in the refined sulcus location was within 2 pixels over all observers. Figure 3 shows the corresponding relaxation profiles for T1 $\rho$  and dGEMRIC in the superficial zone of the posterior femoral cartilage surface prior to reconstructive surgery and at one year after surgery. The correspondence of features in the relaxation profile in unaffected areas suggests good correspondence of the anatomical regions displayed in the maps, while both measures demonstrate anomalous changes at the time of surgery, which has resolved by the time of followup, suggesting resolution of acute cartilage injury.

**Discussion:** Assessment and interpretation of MR-derived indices of cartilage health requires objective and robust processing and analysis tools to accurately and reproducibly track changes in these indices to follow cartilage healing or degeneration over time. Such tools are also needed to amalgamate the complementary information available in T2, T1 $\rho$ , and dGEMRIC. This work demonstrates the feasibility of an edge-based line growing technique to generate the needed anatomical correspondence between multiple modalities and time points to directly correlate and contrast the measurements from each. The developed tools may serve as the first step in a pipeline for functional assessment of cartilage health with MRI.



**Figure 2:** Generated contours for two time points and imaging methods for an ACL-injured subject. The anatomically-derived objective contours are reproducible and suitable for direct location-by-location comparison of maps of the two indices.



**Figure 3:** Matched contours along superficial zone femoral cartilage for time points shown in Figure 2 for ACL-injured subject. Contours show corresponding features along with anomalies in the presurgical assessment that resolved at one year.