Localized inter-subject comparison of knee cartilage thickness, T2 and T1ρ: generating an atlas of the knee

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Introduction and Motivation. In osteoarthritis of the knee (knee OA), different morphological, molecular, and biochemical biomarkers for predicting or evaluating the degree of knee OA have been investigated. It has been observed that with progression of knee OA morphometric parameters such as cartilage thickness and volume decrease; and that molecular and biochemical cartilage properties such as T2, T1ρ, and uptake of contrast agent Gd-DTPA in the cartilage matrix (dGEMRIC) increase. In intra- and inter-subject follow-up studies of knee OA it is common to divide the cartilage into few compartments (e.g. medial, trochlea, and lateral for femoral cartilage) and report means and standard deviations of their morphometric and relaxometry properties. However, in knee OA matching identical regions of interest, so the exact same cartilage region can be evaluated longitudinally and between different subjects is of utmost importance. In addition the study of localized cartilage changes of potential knee OA biomarkers across different subjects could lead to a better understanding of the pathology. Thus image processing techniques that enable such localized analysis and comparisons are needed. For the brain, considerable amount of work has been done in this field; however few efforts have been done for knee cartilage. In terms of localized inter-subject comparisons of cartilage, only the 2D patellar work of Dardzinski et al. has been reported for T2 [1]; and two different 3D approaches have been reported for thickness [2, 3]. The technique presented in [3] was based on shape-matching and its application to build an atlas of femoral cartilage thicknesses was presented in [4]. A key point of that technique was the registration of cartilage surfaces based on the registration of bone shapes. Cartilage was represented as a sheet with each point having a thickness value assigned to it. The purpose of this work was then twofold: to enable localized inter-subject comparisons of knee cartilage T2 and T1ρ relaxation times, and to build femoral atlases for cartilage thickness, T2 and T1ρ relaxation times.

Materials and Methods. Sagittal MR images of the knee joint of 6 human subjects were acquired at 3T on a GE scanner. Images included anatomic high-spatial resolution scans with fat-suppression for good cartilage delineation, and scans to compute T2 and T1ρ maps. Femoral bones and cartilage were segmented semi-automatically from the high-spatial resolution scans using a semi-automatic segmentation technique based on Bezier splines and edge detection [3]. T2 and T1ρ relaxation time maps were computed on a pixel by pixel basis by mono-exponential fitting, and bone and cartilage regions of interest were mapped to them.

The localized inter-subject comparison of cartilage thickness measurements was previously described in [3]. Basically, corresponding anatomic landmarks are computed on bone structures based on 3D *shape contexts*. These common landmarks are then used to compute affine and non-linear registration parameters, which are later applied to the corresponding cartilage surfaces. In this way, based on minimum Euclidean distances, a point to point matching could be performed to compare cartilage properties and/or to compute additional landmarks to build an atlas [4]. The inter-subject comparison of MR cartilage relaxation times proposed in this work is also based on the registration of corresponding bone structures. In order to do so, a single sheet of cartilage representing T2 or T1ρ relaxation time measurements was needed. This was accomplished in the following way. Bezier splines representing the bone-cartilage interfaces were evaluated and perpendicular vectors originating at each point on these splines and ending in the articular surfaces were computed. Along these perpendicular vectors and by using bicubic interpolation equally spaced points were selected with their corresponding relaxation time values. In this way, we were able to represent femoral cartilage as a single sheet (the bone-cartilage interface) and assign a line profile of T2 or T1ρ values to each point in the sheet. Because current morphometric and relaxometry MR cartilage scans have in-plane resolution much higher than the slice thickness, we performed shape-based interpolation based on distance fields to get isotropic voxels for the bone and cartilage structures to improve the registration and 3D visualization. Line profiles of T2 and T1ρ were then assigned to each point in the shape-interpolated bone-cartilage interface based on interpolation of the line profiles of the splines. At this stage we were able to perform localized inter-subject comparisons of cartilage thickness, T2, and T1ρ and obtain cartilage maps representing the localized differences, or to generate atlases of these morphometric and relaxometry parameters as described in [4]. Basically, the atlases were generated in the following way. After computing corresponding anatomic landmarks on the 6 bone structures as described above, the original femora (non-warped) were aligned to create a mean shape as suggested by Cootes et al. in [5], and PCA was performed to compute the modes of variation. The alignment of cartilage surfaces followed that of the femora and a mean cartilage thickness map, and mean cartilage T2 and T1ρ maps were generated.

Results. Successful localized inter-subject comparisons of cartilage thickness, T2 and T1ρ were obtained as is shown in Fig. 1i and 1j for T1ρ. By having line profiles of relaxation time measurements at each point in the bone-cartilage interface, quantitative comparisons at different cartilage depths were possible as is illustrated in Figs. 1c and 1g, and Figs. 1d and 1h for T1ρ maps of 2 different subjects. A qualitative advantage resulting from the line profile representation of cartilage relaxation times is that 3D maps of T2 and T1ρ values can be displayed. Successful mean cartilage thickness maps, mean cartilage T2 maps, and mean cartilage T1ρ maps were also generated (not shown).

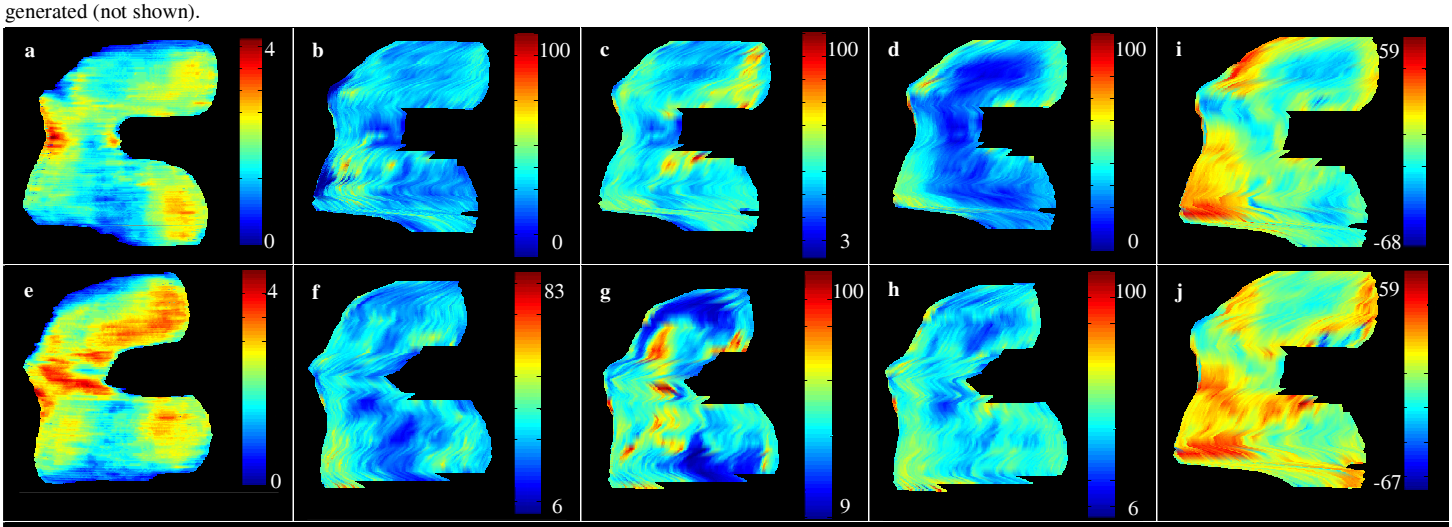

Fig. 1. (a) Thickness map of subject 1. (b) T2 map of subject 1 at 75% depth from the bone-cartilage interface. (c) T1ρ map of subject 1 at 75% depth. (d) T1ρ map of subject 1 at 25% depth. (e) Thickness map of subject 2. (f) T2 map of subject 2 at 75% depth. (g) T1ρ map of subject 2 at 75% depth. (h) T1ρ map of subject 2 at 25% depth. (i) T1ρ difference map at 25% depth: map (d) minus map (h). (j) T1ρ difference map at 75% depth: map (c) minus map (g). Scales are in [mm] and [ms].

Discussion. The analysis of exactly the same cartilage regions across different subjects in longitudinal studies of knee OA is of great importance. The generation of atlases representing mean bone shapes, and mean cartilage morphometric and relaxometry properties could be a valuable tool for the consistent localized inter-subject comparison of such parameters. In this work we have presented the feasibility of creating those tools. Future work requires a larger training set as well as the construction of different atlases based on gender, age, or level of OA.

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References. 1. Dardzinski, et al., 2002. 2. Williams, et al., 2003. 3. Carballido-Gamio, et al., 2005. 4. Carballido-Gamio, et al., 2006. 5. Cootes, et al., 2004.