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Quantitative Three-dimensional Ultrashort Echo Time Cones (3D UTE-Cones) Imaging of the Knee Joint with Motion Correction

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Abstract

Knee degeneration involves all the major tissues in the joint. However, conventional MRI sequences can only detect signals from long T2 tissues such as the superficial cartilage, with little signal from the deep cartilage, menisci, ligaments, tendons, and bone. It is highly desirable to develop new sequences which can detect signal from all major tissues in the knee.

We aimed to develop a comprehensive quantitative three dimensional Ultrashort Echo Time (3D UTE) Cones imaging protocol for a truly “whole joint” evaluation of knee degeneration. The protocol included 3D UTE-Cones actual flip angle imaging (3D UTE-Cones-AFI) for T₁ mapping, multi-echo UTE-Cones with fat suppression for T₂* mapping, UTE-Cones with adiabatic T_{1ρ} (AdiabT_{1ρ}) preparation for AdiabT_{1ρ} mapping, and UTE-Cones magnetization transfer (UTE-Cones-MT) for MT ratio (MTR) and modeling of macromolecular proton fraction (f). An elastix registration technique was used to compensate for motion during scans. Quantitative data analyses were performed on the registered data. Three knee specimens and 15 volunteers were evaluated at 3T.

The elastix motion correction algorithm worked well in correcting motion artifacts associated with relatively long scan times. Much improved curve fitting was achieved for all UTE-Cones biomarkers with greatly reduced root mean square errors (RMSE). The averaged T₁, T₂*, AdiabT_{1ρ}, MTR, and f for knee joint tissues of 15 healthy volunteers were reported.

The 3D UTE-Cones quantitative imaging techniques (i.e. T₁, T₂*, AdiabT_{1ρ}, MTR, and MT modeling) together with elastix motion correction provide robust volumetric measurement of relaxation times, MTR, and f of both short and long T₂ tissues in the knee joint.

Keywords

ultrashort echo time; T₁; T₂*; AdiabT_{1ρ}; MT; motion correction; knee; quantitative analyses

Introduction

It is well understood that knee joint degeneration involves all the major tissues or tissue components, including both the superficial and deep layers of articular cartilage, menisci, ligaments, tendons, and bone (1–4). However, conventional clinical MRI sequences can only detect signals from long T_2 tissues such as the superficial layers of articular cartilage, with little or no signal detected from the deep layers of articular cartilage, menisci, ligaments, tendons, and bone (5). It is highly desirable to develop new sequences such as ultrashort echo time (UTE) sequences to detect signal from all the major tissue components in the knee joint for a truly “whole joint” evaluation of knee degeneration.

Quantitative MRI is preferable for evaluation of early joint degeneration since morphological changes are typically associated with late stage degeneration (6). Most researchers have focused on T_2 and continuous wave $T_{1\rho}$ (CW- $T_{1\rho}$) measurements of the superficial layers of articular cartilage (7–9). Recently, we developed UTE with variable flip angles (VFA) for T_1 measurement (10), UTE with clusters of adiabatic full passage (AFP) pulses for reliable measurement of adiabatic $T_{1\rho}$ (Adiab $T_{1\rho}$) (11), and UTE with magnetization transfer (UTE-MT) imaging and signal modeling for quantitative assessment of water and macromolecular proton fractions (f) and exchange rates (12). Additionally, we developed the UTE actual flip angle (UTE-AFI) sequence for volumetric B_1 mapping for correction of quantitative T_1 , Adiab $T_{1\rho}$, and MT modeling of both short and long T_2 tissues (10, 13). Moreover, UTE acquisitions with variable TE delays were used to map T_2^* of all tissues in the knee joint (14). Those UTE sequences can be combined into a single protocol for comprehensive quantitative evaluation of various knee joint tissues *in vivo*. Specially, previous studies have reported that T_1 , Adiab $T_{1\rho}$, and f are much less sensitive to the magic angle effect than T_2 , which is extremely important for the study of collagen-rich tissues (15–17). Thus, this comprehensive quantitative UTE technique can likely help to evaluate knee joint degeneration more robustly than conventional clinical sequences.

However, quantitative imaging typically involves multiple acquisitions, leading to much longer scan time over morphological imaging. The above quantitative UTE sequences involve UTE-AFI, UTE-VFA, UTE-Adiab $T_{1\rho}$, UTE- T_2^* , and UTE-MT imaging, and are therefore time-consuming. The long acquisition process may lead to substantial subject motion, causing potential errors in quantitative measurements. One approach to resolve this challenge is to perform image registration to minimize motion artifacts before any quantitative data analysis.

In this study, we aimed to develop a comprehensive quantitative UTE-Cones imaging protocol for evaluation of various knee joint tissues *in vivo* with motion correction. Specifically, UTE-Cones-AFI, UTE-Cones-VFA, multi-echo UTE-Cones with fat suppression, UTE-Cones-Adiab $T_{1\rho}$, and UTE-Cones-MT data were acquired for each knee joint. This is the first study to apply UTE-Cones-MT modeling in the study of whole knee joint tissues, including articular cartilage, menisci, anterior cruciate ligament (ACL), posterior cruciate ligament (PCL), tendon, and muscle. The elastix registration toolbox, a registration library developed by Insight Segmentation and Registration Toolkit (ITK) to

address medical image registration problems, was used to compensate for inter-scan motion (18, 19). Quantitative data analyses were then performed on the registered data. To evaluate the robustness of the new approach, three knee joint specimens with and without manually introduced motion were scanned with the same protocol, and the measured values were compared. Then, the protocol was applied to 15 healthy volunteers to evaluate the robustness of the proposed techniques in quantitative imaging of knee joint tissues *in vivo* at 3T.

Method

The study protocol was approved by the local Ethics Committee. Informed consent was obtained from all subjects in accordance with guidelines of the institutional review board (IRB). The 3D UTE-Cones sequences were implemented on a 3T MR750 scanner (GE Healthcare Technologies, Milwaukee, WI) (Figure 1) (20). An 8-channel knee coil that is a transmit/receive coil was used for signal excitation and reception. To compensate for B_1 inhomogeneity regarding quantitative T_1 , Adiab $T_{1\rho}$, and MT modeling, we implemented a UTE-Cones-AFI scheme for volumetric B_1 mapping, where two UTE datasets were acquired with different TRs (Figure 1A) (10, 13). 3D UTE-Cones-VFA data acquisitions were used for T_1 measurement (10). MTR and MT modeling were performed based on UTE-Cones-MT data acquired with a series of MT powers and frequency offsets (Figure 1B). The details on two-pool MT modeling were reported in prior publications (12, 21–23). 3D UTE-Cones-Adiab $T_{1\rho}$ was used for volumetric $T_{1\rho}$ assessment of both short and long T_2 tissues in the knee joint, where identical non-selective AFP pulses with a duration of 6.048 ms, bandwidth of 1.643 kHz, and maximum B_1 amplitude of 17 μ T were used to generate $T_{1\rho}$ contrast (Figure 1C) (11). Multispoke acquisition after each MT or Adiab $T_{1\rho}$ preparation was incorporated for improved time-efficiency (e.g., N_{sp} spokes were acquired per MT or adiabatic $T_{1\rho}$ preparation). T_2^* was quantified by acquiring multi-echo UTE-Cones data with chemical shift-based fat suppression (24). The basic 3D UTE-Cones sequence employed a short rectangular pulse for signal excitation (Figure 1D), followed by k-space data acquisition along twisted spiral trajectories ordered in the form of multiple cones (Figure 1E) (20).

The quantitative 3D UTE-Cones imaging protocol was applied to three cadaveric human knee specimens (aged 31–54 years, mean age 43.3 ± 11.6 years; 2 males, 1 female) and 15 healthy volunteers (aged 20–49 years, mean age 33.2 ± 8.9 years; 6 males, 9 females). The 3D UTE-Cones sequences used to scan these knee joints employed the same field of view (FOV) of $15 \times 15 \times 10.8$ cm³ and receiver bandwidth of 166 kHz. Other sequence parameters were: 1) 3D UTE-Cones-AFI: $TR_1/TR_2 = 20/100$ ms, flip angle = 45° , matrix = $128 \times 128 \times 18$ and a total scan time = 4 min 57 sec; 2) 3D UTE-Cones-VFA: TR = 20 ms; flip angle = 5° , 10° , 20° , and 30° ; matrix = $256 \times 256 \times 36$; and total scan time = 9 min 28 sec; 3) 3D UTE-Cones-Adiab $T_{1\rho}$: TR = 500 ms; FA = 10° ; matrix = $256 \times 256 \times 36$; $N_{sp} = 25$, spin-locking time (TSL) = 0, 12, 24, 36, 48, 72, and 96 ms; number of AFP pulses $N_{AFP} = 0, 2, 4, 6, 8, 12$, and 16; each with a scan time of 2 min 34 sec; 4) 3D UTE-Cones- T_2^* : TR = 45 ms; FA = 10° ; matrix = $256 \times 256 \times 36$; fat saturation; multi-echo of 0.032, 4.4, 8.8, 13.2, 17.6, and 22 ms; and scan time = 3 min 40 sec; 5) 3D UTE-Cones-MT: TR = 100 ms; TE = 32 μ s; flip angle = 7° ; $N_{sp} = 11$; three MT powers = 500° , 1000° , and 1500° ; and five MT frequency

offsets = 2, 5, 10, 20, and 50 kHz; with scan time of 58 seconds per acquisition. The total acquisition time for the five types of UTE sequences was around 50 minutes.

All the quantitative UTE data, including 3D UTE-Cones-AFI, 3D UTE-Cones-VFA, 3D UTE-Cones-AdiabT_{1ρ}, 3D UTE-Cones-T₂^{*}, and 3D UTE-Cones-MT, were acquired. First, we scanned the knee specimens without any motion. Then, during pre-selected time points, we introduced random motion (i.e., translational and rotational motion, as well as flexion and extension) to simulate inter-scan motion. The translational range was around 20 millimeters. The degree of rotational motion, flexion, and extension was about 15°. Quantitative UTE processing was performed for all biomarkers before and after elastix motion registration, which was based on ITK (19). The elastix software consists of a collection of algorithms that are commonly used to solve medical image registration problems. In this paper, UTE-Cones-VFA images with TR = 20 ms and FA = 5° were treated as the fixed images, and the remaining sets of data (AdiabT_{1ρ}, T₂^{*}, and MT) were treated as moving images. 3D non-rigid registration was applied to register the moving images to fixed images. In the 3D non-rigid registration, both rigid (affine) and non-rigid (B-spline) were applied in a two-staged approach to register the images. All registrations were driven by Advanced Mattes mutual information (25). The transformations were obtained by registration of the grayscale images (source: UTE images), then applied to the labeled images. Adaptive stochastic gradient descent optimizer was used to optimize both the affine and B-spline registration. Quantitative UTE values before and after motion correction were compared.

For the 15 healthy volunteers, the degree of motion differed for each volunteer. We did not control the degree of motion. The degree of rotational motion, flexion, and extension was about 0–10°. The elastix motion registration was applied to the 3D UTE-Cones data before quantification. Rigid registration was first carried out to correct for translations and rotations, subsequently followed by non-rigid registration for further fine adjustment (such as scaling and shearing). The Levenberg-Marquardt algorithm was used for non-linear fitting of UTE-Cones data based on prior reported equations. The analysis algorithms written in Matlab (The Mathworks, Inc., Natick, MA) were applied to the DICOM images obtained using the 3D UTE-Cones protocol described above. Manually drawn regions-of-interest for the 15 *in vivo* knees were used to measure the mean and standard deviation for T₁, T_{1ρ}, T₂^{*}, MTR, and f of various tissues, including the articular cartilage (including femoral cartilage, tibial cartilage, and patellar cartilage), meniscus, quadriceps tendon, patellar tendon, ACL, PCL, and muscle. After fitting was completed, goodness of fit statistics (i.e., root mean squared error (RMSE)) was computed.

The impact of B₁ inhomogeneity on quantitative magnetic resonance imaging is well known (26). Since the 3D UTE-Cones-AFI technique provides accurate B₁ measurement for both short and long T₂ tissues, it allows the investigation of the impact of B₁ inhomogeneity on various quantitative 3D UTE-Cones measurements including T₁, T_{1ρ}, and f. The impact of B₁ inhomogeneity on quantitative 3D UTE-Cones imaging was investigated on the knee specimen and 15 healthy volunteers with motion correction.

Results

Figure 2 demonstrates the effectiveness of the elastix motion correction algorithm when applied to representative 3D UTE-Cones-AdiabT_{1ρ} images of a cadaveric knee joint before and after manually induced motion. We observed that the difference images with motion correction achieved near noise level, demonstrating that near perfect registration was achieved. Moreover, we observed significant residual signals in the difference images without motion correction.

Figure 3 shows 3D UTE-Cones-AdiabT_{1ρ} fitting before and after motion for the same cadaveric knee joint. Without motion, AdiabT_{1ρ} values were achieved with a T_{1ρ} of 13.5 ± 0.9 ms for the quadriceps tendon, 38.2 ± 4.3 ms for the PCL, 21.0 ± 1.1 ms for the meniscus, and 56.4 ± 4.0 ms for the patellar cartilage. When motion was introduced during the scans, RMSE increased to 20.71% for the quadriceps tendon, 8.71% for the PCL, 19.12% for the meniscus, and 10.33% for the patellar cartilage. However, after elastix motion registration, very similar AdiabT_{1ρ} values were achieved for the quadriceps tendon (T_{1ρ} = 13.0 ± 0.7 ms), the PCL (T_{1ρ} = 39.2 ± 5.2 ms), the meniscus (T_{1ρ} = 24.4 ± 1.6 ms), and the patellar cartilage (T_{1ρ} = 61.3 ± 5.2 ms) when compared to the non-motion condition. RMSE decreased to 3.30%, 3.80%, 3.77%, and 4.54% respectively. Supporting Table S1 summarizes RMSE measurements for T₁, T_{1ρ}, and f fitting for various tissues of the cadaveric knee joint. Overall, RMSE was greatly reduced for all the UTE biomarkers of all knee joint tissues following elastix motion correction.

Figure 4 shows 3D UTE-Cones-MT modeling before and after motion for the cadaveric knee joint. Without motion, f values were measured for the quadriceps tendon (f = $20.7 \pm 1.6\%$), the PCL (f = $15.2 \pm 1.0\%$), the meniscus (f = $22.9 \pm 1.2\%$), and the patellar cartilage (f = $10.3 \pm 0.5\%$). When motion was introduced during the scans, RMSE increased to 39.78% for the quadriceps tendon, 24.57% for the PCL, 28.82% for the meniscus, and 19.98% for the patellar cartilage. After elastix motion registration, very similar macromolecular fractions were achieved for the quadriceps tendon (f = $20.4 \pm 1.5\%$), the PCL (f = $15.0 \pm 0.9\%$), the meniscus (f = $21.6 \pm 1.4\%$), and the patellar cartilage (f = $9.7 \pm 0.7\%$) when compared with the non-motion condition. RMSE decreased to 1.83%, 1.36%, 1.61%, and 1.14%, respectively.

Table 1 summarizes mean and standard deviation values of T₁, T_{1ρ}, f, and MTR for articular cartilage, menisci, PCL, ACL, tendon, and muscle over three cadaveric knee joint specimens before and after elastix motion registration. The results demonstrate the efficiency of the elastix motion registration algorithm.

Figure 5 shows representative 3D UTE-AdiabT_{1ρ} fitting as well as 3D UTE-Cones-MT modeling of the femoral condyle for a 32-year-old female volunteer before and after elastix motion registration. Before elastix motion registration, the femoral condyle showed AdiabT_{1ρ} and f values of 20.7 ± 4.7 ms and $39.7 \pm 13.3\%$, with RMSE of 6.22% and 2.36%, respectively. After elastix motion registration, AdiabT_{1ρ} and f values changed to 39.1 ± 3.9 ms and $9.8 \pm 0.9\%$, with RMSE decreased to 3.28% and 0.70%, respectively. The elastix motion registration reduced the MT fitting error by more than four-fold.

Table 2 summarizes mean and standard deviation of T_1 , T_2^* , $\text{Adiab}T_{1\rho}$, MTR, and f for articular cartilage, menisci, quadriceps tendon, patellar tendon, ACL, PCL, and muscle of 15 healthy volunteers before and after elastix motion registration. Some values are significantly different between the postprocessing with and without image co-registration, even though only a few volunteers moved during the scan.

The impact of B_1 inhomogeneity on quantitative 3D UTE-Cones imaging is shown in Supporting Table S2 for the *ex vivo* study and in S3 for the *in vivo* study.

Discussion

We have demonstrated that the 3D UTE-Cones sequences provide high SNRs for all the major tissues in the knee joint. Together with the elastix motion registration algorithm, the proposed sequences can quantitatively measure T_1 , T_2^* , $\text{Adiab}T_{1\rho}$, MTR, and f for both short and long T_2 tissues in the knee joint including articular cartilage, menisci, ACL, PCL, quadriceps tendon, patellar tendon, and muscle. The elastix motion registration method can reliably correct motion which occurs between the repeated UTE measurements. Those UTE measurements allow for the first comprehensive quantitative evaluation of the knee joint using a truly “whole joint” approach (27). This new protocol may provide more sensitive evaluation of knee degeneration in its early stages than conventional clinical imaging sequences, which are largely focused on the superficial layers of articular cartilage and provide little or no quantitative information regarding the short T_2 tissues or tissue components (6).

UTE-Cones biomarkers including T_1 , T_2^* , $\text{Adiab}T_{1\rho}$, MTR, and f for all the soft tissues in the human knee joint are largely consistent with previously reported 3T studies. For example, our 3D UTE-Cones T_1 values for long T_2 tissues such as cartilage (944~1152 ms) and muscle (~1385 ms) were close to those reported by Jordan et al., who reported a mean T_1 of 1016 ms for cartilage and 1256 ms for muscle (28), and to those reported by Stanisz et al., who reported a T_1 value of 1156 ms for cartilage and 1412 ms for muscle (29). Neither Jordan et al. nor Stanisz et al. reported T_1 values for menisci, ligaments, and tendons, as their sequences had too long TEs to detect enough signal from those short T_2 tissues. Our 3D UTE-Cones T_2^* values for cartilage (20~39 ms) were also largely consistent with those reported by Williams et al. (20~30 ms) (30, 31). The measured $\text{Adiab}T_{1\rho}$ values for cartilage (33~46 ms), meniscus (~21 ms), quadriceps tendon (~13 ms), patellar tendon (~10 ms), ACL (~26 ms), PCL (~17 ms), and muscle (~43 ms) were also consistent with previous reports of 36–45 ms for cartilage, 18~23 ms for meniscus, 13 ms for quadriceps tendon, 10 ms for patellar tendon, 35 ms for ACL, 22 ms for PCL, and 43 ms for muscle (11).

Although cones acquisitions are often believed to be less sensitive to motion artifact than cartesian acquisitions, the motion artifacts may still impact quantitative measures. The elastix motion registration is critical for robust quantitative evaluation of various knee joint tissues (25). Our preliminary studies suggest that knee joint motion occurring during the relatively long scan time involved in these sequences could be well compensated for, as demonstrated by the near noise level signal in the difference image between original and motion-corrected images. In the specimen study, significantly different measurements were

derived for the knee joint tissues with and without manually induced motion. However, consistent measurements were achieved when the elastix motion registration was applied before data analyses compared with the non-motion results, demonstrating the accuracy of the motion correction and further supporting the feasibility of comprehensive quantitative 3D UTE-Cones evaluation of knee joint tissues *in vivo*.

We observed greater errors for thinner tissues such as articular cartilage and fewer errors for thicker tissues such as muscle. It is therefore likely that the elastix motion registration algorithm is less robust for 3D anisotropic imaging (e.g., our 3D UTE imaging protocol used an in-plane resolution of 0.586 mm with a much thicker slice of 3 mm). A more robust motion registration algorithm, as well as more isotropic imaging (e.g., a thinner slice), would help in reducing quantification errors associated with motion. However, the errors are smaller than changes produced by knee joint degeneration, which are typically in the range of 10–30% (7). Notably, the elastix motion registration cannot correct intra-scan motion, which leads to degradation of the UTE image quality and to errors in quantification. UTE data acquisition with incorporated motion navigation is needed to correct for this type of motion and to further improve the quantification accuracy.

Degeneration of the knee joint or osteoarthritis (OA) is a heterogeneous and multifactorial disease associated with progressive loss of articular cartilage. It is much more than a cartilage disease, however, as it involves multiple joint tissues, including short T_2 tissues (27,32–37). When one tissue begins to deteriorate, it often affects surrounding tissues, contributing to overall failure of the joint (2). From this point of view, UTE sequences have the potential to resolve a major problem for conventional clinical MRI evaluation of abnormalities in the early stages of OA.

Another advantage of the new protocol is the fact that many of the UTE biomarkers are less sensitive to fiber orientation relative to the B_0 field, i.e. the magic angle effect. Conventional T_2 and CW- $T_{1\rho}$ measurements have been shown to be sensitive to the magic angle effect (38–41). When the fibers are re-oriented near 55° relative to the B_0 field, T_2 and CW- $T_{1\rho}$ can increase by more than 100%, which can be higher than the increase attributed to tissue degeneration (42). This is a major limitation in employing clinical T_2 and CW- $T_{1\rho}$ measurements to detect early OA. On the other hand, most of our UTE biomarkers, such as T_1 (10), Adiab $T_{1\rho}$ (11), MTR, and MT modeling of f (12, 21–23), are much less sensitive to the magic angle effect. The proposed 3D UTE-Cones-AFI-VFA technique allows, for the first time, robust evaluation of T_1 for short T_2 tissues in the knee joint without compromise from RF inhomogeneity. Prior studies have shown that T_1 is nearly magic angle-independent (15). The derived T_1 value is an important input for both quantification of Adiab $T_{1\rho}$ and MT modeling (11, 12). 3D UTE-Cones-Adiab $T_{1\rho}$ has also shown reduced sensitivity to the magic angle effect (11, 16). 3D UTE-Cones-MTR and particularly UTE-Cones-MT modeling of water and macromolecular proton fractions and exchange rates are insensitive to the magic angle effect (17, 21).

There are several limitations of this study. First, only cadaveric knee joint specimens and healthy volunteers were recruited. OA patients, with whom motion is more likely to occur, were not scanned; therefore, the clinical significance of our proposed technique remains to

be demonstrated. However, the preliminary results from this study clearly demonstrate the feasibility of *in vivo* studies of the knee joint, and we expect no technical difficulty running the same comprehensive UTE imaging protocol on OA patients. Second, the quantitative 3D UTE-Cones imaging protocol is relatively long, taking about 50 minutes in total. Further optimization of the protocol, especially the combination of parallel imaging, compressed sensing, and/or deep learning, may significantly reduce the total scan time (e.g., 25 minutes when using an acceleration factor of 2), thus facilitating clinical translation of those techniques (43, 44). Third, the advantages of the comprehensive quantitative UTE imaging protocol over a conventional clinical imaging protocol remain to be demonstrated, although our preliminary findings suggest obvious benefits, as UTE sequences can be used to evaluate both short and long T_2 tissues and they are less sensitive to the magic angle effect. Fourth, only inter-scan motion correction was performed in our study. Intra-scan motion was not considered, as most of the quantitative UTE scans were around 3 minutes or shorter (e.g., 58 seconds for each UTE-MT acquisition, 2 minutes 22 seconds for each UTE-Cones-VFA acquisition). The whole quantitative UTE protocol lasts around 50 minutes, which is much longer than each single scan, and is thus more prone to inter-scan motion artifacts. As a result, intra-motion is expected to be much smaller than inter-scan motion. More advanced techniques incorporating motion registration in UTE-Cones data acquisition would allow intra-scan motion correction, further improving the robustness of these quantitative UTE techniques. Fifth, we only performed the first order eddy currents correction by running calibration on a homogenous water phantom to calculate the constant delay in Gx, Gy, and Gz. Correction of higher order eddy currents, including the distortion of kx, ky, and kz can be performed by measuring the k-space trajectory with techniques such as the Duyn's method (45). This remains to be implemented for more accurate quantitative 3D UTE-Cones imaging.

Conclusion

The 3D UTE-Cones quantitative imaging techniques (i.e. T_1 , T_2^* , $\text{Adiab}T_{1\rho}$, MTR, and MT modeling) together with elastix motion correction provide robust volumetric measurement of relaxation times, MTR, and f of both short and long T_2 tissues in the knee joint.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations

3D	three dimensional
UTE	ultrashort echo time
AFI	actual flip angle

AdiabT_{1ρ}	adiabatic T _{1ρ}
MT	magnetization transfer
MTR	magnetization transfer ratio
f	macromolecular proton fraction
RMSE	root mean square errors
CW-T_{1ρ}	continuous wave T _{1ρ}
VFA	variable flip angles
AFP	adiabatic full passage
ACL	anterior cruciate ligament
PCL	posterior cruciate ligament
ITK	Insight Segmentation and Registration Toolkit
IRB	institutional review board
FOV	field of view
TSL	spin-locking time
OA	osteoarthritis
ROI	regions of interest

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Figure 1.

The quantitative 3D UTE-Cones sequences. (A) is the UTE-Cones-AFI sequence with dual-TR acquisitions for B1 mapping. (B) and (C) are the MT- and Adiab $T_{1\rho}$ -prepared UTE-Cones sequences for MTR/MT modeling and $T_{1\rho}$ measurement, respectively. To speed up data acquisition, multiple spokes (N_{sp}) were sampled after both MT and adiabatic $T_{1\rho}$ preparation. In the basic 3D UTE-Cones sequence (D), a short rectangular pulse was used for signal excitation followed by 3D spiral sampling with a minimal nominal TE of 32 μs . The spiral trajectories were arranged with conical view ordering (E).

Figure 2. 3D UTE-Cones AdiabT_{1ρ} imaging of a cadaveric human knee joint (31-year-old male donor) without motion (A), the signal differences between static and moved images without elastix motion correction (B) and with elastix motion correction (C). Near noise level signal was observed after motion correction, suggesting the accuracy of the motion correction technique.

Figure 3. 3D UTE-Cones-AdiabT_{1ρ} imaging of a cadaveric knee joint with representative regions of interest (ROI) (A-D), along with the corresponding fitting curves for quadriceps tendon, PCL, meniscus, and patellar cartilage before motion (E-H), after motion without elastix motion correction (I-L), and with elastix motion correction (M-P). AdiabT_{1ρ} values obtained using elastix motion correction are comparable to the non-motion condition.

Figure 4.

3D UTE-Cones-MT imaging of a cadaveric knee joint with representative ROI (A-D), the corresponding fitting curves for quadriceps tendon, PCL, meniscus, and patellar cartilage before motion (E-H), after motion without elastix motion correction (I-L), and with elastix motion correction (M-P). UTE-MT modeling parameters obtained using elastix motion correction are comparable to the non-motion condition.

Figure 5.

A representative slice from 3D UTE-Cones-AdiabT_{1ρ} (A) and UTE-Cones-MT (B) imaging of the knee joint of a 32 year-old female volunteer, and an ROI in the femoral condyle cartilage used for AdiabT_{1ρ} fitting before (C) and after (D) elastix motion registration as well as MT modeling before (E) and after (F) elastix motion registration. RMSE values were much higher for the fitting curves before motion correction, and much lower after motion correction. More reasonable AdiabT_{1ρ} of 39.1 ± 3.9 ms and f of 9.8 ± 0.9 % were achieved for articular cartilage in the femoral condyle after elastix motion registration.

Table 1.

Mean T_1 , $T_{1\rho}$, macromolecular fraction (f), and MTR values for various cadaveric human knee joint tissues including cartilage, menisci, ligaments, tendons, and muscle before and after elastix motion registration. The values in parentheses are percentage changes relative to the quantitative values before motion.

	T_1 (ms)			$T_{1\rho}$ (ms)			f (%)			MTR (%)		
	Before motion	After motion	After registration	Before motion	After motion	After registration	Before motion	After motion	After registration	Before motion	After motion	After registration
Meniscus	596.4±1.9	707.8±7.1 (18.68%)	626.8±10.2 (5.10%)	22.4±1.1	40.3±13.6 (79.91%)	24.4±1.7 (8.93%)	21.6±1.0	28.5±20.2 (31.94%)	21.0±0.6 (2.78%)	52.5±0.3	23.9±17.7 (54.48%)	53.0±0.3 (0.00%)
Femoral Cartilage	723.8±16.2	990.9±286.5 (36.90%)	652.2±10.1 (9.89%)	42.7±1.2	21.6±1.3 (49.41%)	38.5±0.2 (9.84%)	16.3±1.8	18.2±12.3 (11.66%)	15.2±1.1 (6.75%)	40.6±1.3	13.8±7.1 (66.01%)	43.7±1.3 (7.00%)
Tibial Cartilage	713.5±27.4	1246.2±360.2 (74.66%)	643.3±5.3 (9.84%)	36.9±3.8	31.2±7.0 (15.45%)	34.1±5.5 (7.59%)	16.1±1.2	20.7±12.7 (28.57%)	14.6±0.4 (9.32%)	43.0±1.1	15.5±1.9 (63.95%)	45.0±1.1 (4.00%)
Patellar Cartilage	898.3±9.9	658.5±26.5 (26.69%)	815.6±11.2 (9.21%)	57.3±4.1	34.5±3.9 (39.79%)	53.6±6.0 (6.46%)	12.3±1.4	23.7±20.9 (92.68%)	11.2±0.5 (8.94%)	42.1±1.7	2.6±3.1 (93.82%)	44.4±1.7 (4.00%)
Quadriceps tendon	555.8±11.2	457.9±2.2 (17.61%)	502.3±2.1 (9.63%)	14.6±0.9	11.2±0.4 (23.29%)	14.0±0.7 (4.11%)	19.5±0.9	23.2±0.9 (18.97%)	19.8±1.0 (1.54%)	48.3±5.8	85.7±1.4 (77.43%)	51.6±1.4 (6.00%)
Patellar Tendon	506.1±16.8	109.0±187.6 (78.46%)	531.9±16.2 (5.10%)	19.7±1.0	13.3±0.5 (32.49%)	17.8±0.3 (9.64%)	25.1±2.4	10.2±0.0 (59.36%)	27.5±3.8 (9.56%)	43.1±2.1	79.6±1.8 (84.69%)	47.9±1.8 (9.00%)
ACL	736.2±82.6	507.1±32.1 (31.12%)	665.1±8.2 (9.66%)	29.6±3.9	26.8±4.1 (9.46%)	29.0±3.7 (2.03%)	14.6±2.3	9.9±5.7 (32.19%)	13.3±1.3 (8.90%)	45.8±5.3	43.9±10.9 (4.15%)	48.6±5.3 (6.00%)
PCL	710.7±46.8	495.9±3.0 (30.22%)	648.5±13.1 (8.75%)	33.9±4.2	26.8±2.0 (20.94%)	34.7±5.8 (2.36%)	16.7±0.8	6.7±6.5 (59.88%)	15.4±0.7 (7.78%)	46.5±0.3	35.7±13.3 (23.23%)	48.3±1.3 (3.00%)
Muscle	1058.9±4.7	1168.7±31.7 (10.37%)	993.1±15.3 (6.21%)	63.3±1.3	45.0±10.3 (28.91%)	63.2±4.5 (0.16%)	7.9±0.3	6.0±2.5 (24.05%)	7.9±0.3 (0.00%)	37.0±0.1	9.9±8.2 (73.24%)	40.8±0.1 (8.00%)

Table 2.

Mean T_1 , $AdiabT_{1\rho}$, MTR, MT modeling of macromolecular fraction (f), and T_2^* for various knee joint tissues including meniscus, femoral cartilage, tibial cartilage, patellar cartilage, quadriceps tendon, patellar tendon, ACL, PCL, and muscle of 15 healthy volunteers before and after elastix motion registration.

	T_1 (ms)		$T_{1\rho}$ (ms)		MTR (%)		f (%)		T_2^* (ms)	
	Before registration	After registration	Before registration	After registration	Before registration	After registration	Before registration	After registration	Before registration	After registration
Meniscus	820.1±56.7	820.1±57.9	20.1±2.1	20.9±1.5 ^{*1}	57.0±4.6	58.1±3.1	19.1±2.0	18.9±1.5	11.1±7.9	9.1±1.5
Femoral Cartilage	1118.1±129.4	1152.1±116.0	42.5±8.3	44.2±7.1	47.3±7.0	46.7±5.7	11.3±1.5	10.7±1.6 ^{*5}	33.3±8.9	39.1±1.5
Tibial Cartilage	957.2±114.9	943.8±93.2	33.8±5.3	32.6±4.6	48.6±4.4	49.7±4.0	15.5±6.2	14.3±2.7	24.0±7.2	20.1±1.5
Patellar Cartilage	1094.7±110.5	1105.2±117.0	46.1±5.8	46.2±5.1	39.3±8.1	41.1±5.3	9.5±2.0	10.1±1.8 ^{*6}	34.6±8.8	36.1±1.5
Quadriceps tendon	800.5±62.3	802.6±59.6	13.2±2.3	13.3±2.1	47.6±8.8	52.6±7.3 ^{*2}	18.9±6.2	17.3±2.1	10.5±2.8	11.1±1.5
Patellar Tendon	646.6±53.1	641.6±54.7	9.9±1.6	9.9±1.5	43.5±8.7	46.3±6.1	23.7±9.3	20.2±2.7	5.8±2.3	5.1±1.5
ACL	942.6±138.6	922.3±119.1	25.5±4.2	25.8±3.9	47.1±6.6	48.4±6.5 ^{*3}	13.7±2.2	14.1±2.2	16.4±4.0	11.1±1.5
PCL	838.6±57.6	839.4±54.0	17.2±3.2	17.4±3.0	53.8±5.9	55.6±5.3 ^{*4}	16.1±3.6	17.1±1.8	9.2±1.5	8.1±1.5
Muscle	1389.9±71.2	1385.0±69.9	43.3±2.9	43.3±2.9	47.1±2.0	47.3±2.0	7.7±0.6	7.8±0.6	31.2±3.4	31.1±1.5

^{*1} p=0.026;

^{*2} p=0.000;

^{*3} p=0.035;

^{*4} p=0.010;

^{*5} p=0.029;

^{*6} p=0.007;

^{*7} p=0.007;

^{*8} p=0.004;

^{*9} p=0.006.