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1 Introduction

The study of tibiofemoral kinematics, i.e. the relative motion between the femur and tibia during knee joint movement, is crucial for understanding normal knee function and identifying pathological conditions [1]. Accurate assessment of these movement patterns can provide valuable insights into the diagnosis and treatment of various knee disorders, including osteoarthritis (OA) and ligament injuries [2,3, 4]. For instance, alterations in tibiofemoral kinematics have been associated with the progression of knee OA, one of the most common joint disorders affecting a significant portion of the global population [5].Also, it has been found that the three-dimensional kinematics of anterior cruciate ligament-deficient knees are changed even during low-stress activities, such as walking. [6, 7]

Dynamic MRI has proven to be a valuable tool for studying tibiofemoral kinematics in vivo, offering insights into both normal and pathological knee function. Various MRI techniques have been employed to capture knee motion under different conditions.

Real-time MRI is one approach that allows for rapid image acquisition during continuous joint movement, offering true real-time visualization of knee motion. This technique has been employed to study knee deep-flexion kinematics and patellofemoral joint motion [8,9]. While these methods excel at capturing dynamic events, they may be limited in spatial resolution.

CINE MRI techniques, which involve reconstructing multiple motion phases into a single representative cycle, have been used to investigate patellar tracking patterns and tibiofemoral kinematics [10,11,12]. These methods typically offer improved spatial resolution compared to real-time imaging.

Another approach to study joint kinematics is cine phase contrast MRI [13,14]. This method directly encodes velocity information into the MRI signal, allowing for quantitative measurements of tissue motion.

Many of these dynamic MRI studies have incorporated specialized devices to guide knee motion and apply controlled loading conditions during imaging. These devices allow for the investigation of load-dependent variations in knee kinematics, providing insights into how the joint responds to different mechanical stresses [15]. Such approaches are particularly valuable for understanding the biomechanical changes associated with conditions like osteoarthritis and ligament injuries.

In these dynamic MRI studies of knee kinematics, researchers have employed various methods to extract kinematic parameters from the acquired data. Some studies use high-resolution static MRI scans to create detailed 3D models of the bones, which are then registered to lower-resolution dynamic MRI frames [8, 10]. This approach allows for tracking of bone movement throughout the motion cycle. Other studies utilize cine phase contrast MRI techniques, which directly encode velocity information into the MRI signal [14]. Kinematic parameters are then derived by integrating this velocity data over time. Additionally, some researchers opt for identifying and tracking specific anatomical landmarks in each frame of the dynamic sequence [9].

To enhance the physiological relevance of these studies, many researchers have incorporated custom MRI-compatible knee loading devices [11]. These devices allow for controlled knee motion and the application of specific loads during imaging, simulating more realistic joint conditions. Such setups have enabled the investigation of knee kinematics under various loading scenarios, providing valuable insights into joint behavior during functional activities.

In light of these advancements in dynamic MRI techniques and loading devices, we recognized the need for an efficient method to analyze the resulting image data. To address this, we developed a semi-automated algorithm for segmenting the tibia and femur in 2D sagittal images of the knee during flexion-extension cycles. This segmentation serves as the basis for tracking specific kinematic parameters throughout the motion cycle. By employing this method in conjunction with a custom MRI-compatible knee loading device, we seek to contribute to the growing body of knowledge on in vivo knee mechanics. This combination of imaging technique, loading device, and analysis method offers a promising tool for both research and clinical applications in understanding normal and pathological knee function.

2. Material and Methods

2.1 Image acquisition and reconstruction

Five healthy volunteers (three males and two females, age 24-39, body weight 55-90 kg) participated in this study. Dynamic MRI scans were conducted on the left leg of each participant using a 3 T clinical whole-body MRI scanner (MAGNETOM Prisma, Siemens Healthineers).

A custom MRI-safe device [16] was used to guide knee motion and ensure consistent, planar movement during flexion-extension cycles. Participants were positioned supine in the scanner with their thigh secured on a wedge positioner using a strap. The lower leg was attached to an ankle support just above the malleoli using Velcro straps to minimize lateral movement. The knee was aligned with the device's axis of rotation, allowing only up and down movement in a single plane.Two flexible 16-channel multifunctional coils (Variety, Noras MRI products GmbH) were used with one coil was wrapped around the top of the knee, covering the distal femur, while the other was placed underneath the knee, supporting the proximal tibia.

During the scan, participants performed controlled flexion-extension cycles of the knee joint guided by a 60-bpm metronome. The range of motion varied among subjects, spanning from 30 to 46 degrees. Each cycle consisted of an eight-beat extension-to-flexion movement, with the leg being flexed at the first beat and fully extended by the fourth, resulting in 7.5 cycles per minute. The total scan duration was 160 seconds, allowing for approximately 20 full flexion-extension-flexion cycles.

MRI data was acquired using a 2D radial golden-angle gradient echo FLASH sequence [17,18] with the following parameters: echo time of 2.51 ms, flip angle of 8 degrees, FOV of [192×192×3] mm, matrix size of [176×176×1], voxel size of [1.09×1.09×1] mm and repetition time of 5.8 ms. During reach repetition, 276 spokes were acquired, with each spoke consisting of 352 data points. A total of 100 k-space repetitions were acquired during the scan session.

Image reconstruction was facilitated using an optical fiber position sensor (MR338-Y10C10, Micronor, Camarillo, CA, USA) integrated into the knee device. This optical sensor precisely measured the knee rotation angle which was then converted to an electrical signal that was sampled simultaneously with the MRI scanner's trigger signal using a RedLab 1208LS USB-based data acquisition module (Meihaus Electronic GmbH). By synchronizing the knee rotation angles with the start of each k-space repetition the radial golden-angle k-space data was then sorted into 2-degree intervals of knee rotation [19]. This process was repeated for the entire range of motion, ensuring comprehensive coverage. Image reconstruction was carried out using the RIESLING (Radial Interstices Enable Speedy Low-volume imagING) toolbox [20]. This open-source software package is specifically designed for reconstructing non-Cartesian MRI data, employing advanced algorithms to handle the radially sampled k-space data efficiently. Image reconstruction was performed separately for flexion (downward leg movement) and extension (upward leg movement) to account for potential differences in biokinematics.

The final reconstructed 2D-CINE datasets had a varying number of frames based on each participant's achievable range of motion. **Figure 1** shows a series of reconstructed frames from a single dataset, showcasing the progression of knee motion during flexion-extension cycles and the available input data for subsequent segmentation and tracking.

2.2 Semi-automated bone tracking

For semi-automatic bone tracking of the tibia and femur the following tracking algorithm was implemented in Python programming language (v.3.11.5):

(I) Edge Detection: The Canny edge detection algorithm was applied to each frame to identify the boundaries of the tibia and femur [21]. Parameters such as gradient thresholds and Gaussian blur strength were manually optimized to effectively isolate the bone edges. This step resulted in binary images highlighting the detected edges, including the interior cortical bone boundaries.

(II) Edge Labeling: Connected-component labeling [22] was then performed on the binary edge images to isolate specific structural features and distinguish the desired interior cortical bone edges from other detected edges. The labeling algorithm's connectivity parameters were carefully selected to ensure that each bone's interior edge was assigned a consistent label across the entire image stack. In Steps I and II, the edge detection and labeling parameters were optimized once for the given image contrast and resolution, then applied consistently across all datasets and frames.

(III) Reference Point Extraction: A set of reference points was established along the labeled edges of the tibia and femur in the initial frame (fully flexed position). The process began by identifying the most distal point of each bone and then sorting the edge points using a greedy nearest neighbor algorithm [23]. Thee sorted points were then downsampled to 50-80 equidistant points using cubic spline interpolation [24]. By establishing these reference points in the initial frame, a template of equidistant points along the bone edges was created that could be transformed to match the bone positions in subsequent frames, facilitating the tracking of bone movement throughout the motion sequence.

(IV) Transformation Computation: Transformation matrices were computed to align the equidistant reference points of the bones edges from one frame to the next. This process assumed rigid body motion, considering only translations in the sagittal plane and rotations about the transverse axis perpendicular to the sagittal plane. Mathematically, the transformation of each point from one frame to the next can be expressed as:

Where ϕ is the angle of rotation, and are the points in the target frame and reference frame, respectively, are the frame-to-frame translations within the measured sagittal plane and **R**(ϕ) is the 2D in-plane rotation matrix given by

To determine the optimal transformation parameters that best align the reference points from one frame to the next, a cost function that minimizes

was used, where are the points in the target frame and are the points in the reference frame after transformation. Set P is the set of points in the reference frame and Set Q is set of points in the target frame. This function computes the distance between the transformed point to its nearest point in the target frame and sums all the distances for each point in the reference frame. For perfect alignment, the sum would be zero.

Starting from the first frame the Nelder-mead method was used to minimize this cost function and obtain the frame-to-frame transformation parameters, whereas the transformation was only calculated from one frame to next with applied reasonable initial parameters and tight parameter boundaries that could be applied from a priori knowledge about the type of motion (i.e. ϕ should be in the range of the frame to frame angle increment used during reconstruction and being relatively small considering a continuous motion). Finally, by using the frame-to-frame edge tracking transformations any manual segmentation drawn in the first frame, could be automatically transformed to all other frames.

A schematic overview of the algorithm is shown in **Figure 2**.

2.3 Manual Segmentation and parameter estimation

To compare the accuracy and reliability of the proposed bone tracking algorithm, segmentation was performed for all frames and datasets manually using the Napari (v.4.16) image processing software [25]. For this purpose, the bone segmentation obtained in the first frame was manually aligned (translated and rotated) to match the new bone positions in subsequent frames.

To compare the performance of the tracking algorithm to the manual segmentation, the angle between the long axis of the femur with respect to the tibia was extracted from the bone segmentations. Principal component analysis [26] was used to obtain the unit vectors that define the long axis. Because the number of frames reconstructed for each dataset varied between subjects due to differences in the achievable range of motion, a normalization of the knee flexion angle was performed as a fraction of the ‘flexion percentage’, where -100% represents the point of maximum flexion, 0% corresponds to full extension, and +100% marks the return to maximal flexion.

3. Results

**Figure 3** presents a comparison of kinematic parameters derived from manual and semi-automated segmentation methods for an exemplary dataset during a knee flexion-extension cycle. The left panel shows the angle between the long axes of tibia and femur plotted against flexion cycle percentage. Both methods exhibit the characteristic V-shaped pattern, with the angle decreasing as the knee extends (from -100% to 0%) and increasing as it flexes again (from 0% to +100%). Notably, the semi-automated method (blue) demonstrates a smoother trajectory compared to the manual method (orange).

The right panel of Figure 3 displays the rate of change of the angle (angular velocity) over the flexion cycle. This derivative analysis reveals more pronounced differences between the two methods. The semi-automated method shows a more consistent pattern, with negative values (indicating flexion) in the first half of the cycle and positive values (indicating extension) in the second half. In contrast, the manual method exhibits greater variability and more frequent fluctuations in angular velocity.

To assess the overall trend and variability across all datasets, **Figure 4** presents the rate of change of the tibiofemoral angle throughout the knee flexion-extension cycle for both segmentation methods. The shaded areas represent one standard deviation from the mean. Consistent with the single dataset analysis, the automatic method (blue) demonstrates less variability compared to the manual method (orange).

**Figure 5** provides a quantitative comparison of the consistency in frame-to-frame angle changes between the two methods. The Coefficient of Variation (CV) is calculated for each dataset and method, with lower values indicating more consistent tracking. Across all five datasets, the automatic method consistently shows lower CV values compared to the manual method.

4. Discussion

Our study introduces a semi-automated segmentation pipeline for analyzing tibiofemoral kinematics using dynamic MRI. The results demonstrate that this method offers significant advantages over the manual segmentation approach used for comparison in this study, particularly in terms of efficiency and consistency in tracking knee joint motion throughout flexion-extension cycles.

In the context of current literature on dynamic MRI of the knee, our approach offers a unique balance between efficiency and accuracy. Unlike methods that rely on registering dynamic frames to high-resolution 3D static scans [8, 10], our technique directly utilizes the dynamic frames without the need for additional static imaging. This not only reduces total scan time but also eliminates potential errors that could arise from registering images acquired in different joint positions.

Our technique offers several advancements compared to previous landmark-based tracking methods, such as the one described by Draper et al. [9]. While their approach relies on manually selecting anatomical landmarks and using image registration to track these points across frames, our method utilizes the full contour of the bone edges. Draper's method creates templates around manually identified landmarks and searches for these templates in subsequent frames. In contrast, our semi-automated approach detects and tracks the entire bone edge, potentially providing more robust and comprehensive motion tracking. By using the full bone contour rather than discrete points, our method may be less susceptible to errors that could arise from landmark misidentification or local image artifacts.

A key strength of our method is its efficiency. By requiring manual segmentation of only a single frame, with minimal user interventions thereafter, our approach significantly reduces processing time compared to full manual segmentation of all frames. The consistency in frame-to-frame angle changes, as evidenced by the lower coefficients of variation, suggests that our semi-automated method may better capture the continuous nature of knee motion.

However, our study has limitations. The current implementation is restricted to 2D sagittal plane analysis, capturing primarily flexion-extension and anterior-posterior translation. This limits our ability to quantify out-of-plane motions such as internal-external rotation or abduction-adduction, which are important components of full 3D knee kinematics. Additionally, the accuracy of our method relies on movement being confined to a single plane, which can be challenging to achieve perfectly in vivo.

Despite these limitations, our method shows promise for clinical applications. The ability to quickly and consistently quantify tibiofemoral kinematics could be valuable for assessing knee function in various patient populations. For instance, this technique could be applied to study altered kinematics in patients with ACL reconstruction, who are known to exhibit changes in knee motion patterns. The method could also be extended to analyze patellofemoral kinematics, potentially aiding in the assessment of conditions like patellar maltracking.

Moreover, the integration of our segmentation pipeline with the custom MRI-compatible knee loading device offers a unique opportunity to study load-dependent changes in knee kinematics. This could provide insights into how joint mechanics are altered under physiological loading conditions, which is crucial for understanding the biomechanics of both healthy and pathological knees.

Future work should focus on extending this method to 3D analysis, which would allow for a more comprehensive assessment of knee joint kinematics. This could involve adapting the segmentation algorithm to work with multi-planar dynamic MRI acquisitions or exploring ways to infer 3D motion from 2D projections.

Improvements in subject positioning and fixation within the knee loading device could help minimize unintended out-of-plane motions, particularly tibial internal-external rotation. This would enhance the accuracy of the 2D analysis and make the technique more robust across a wider range of subjects.

Validation studies comparing our method to established gold standards for knee kinematic measurement, such as biplane fluoroscopy or marker-based motion capture, would be valuable in further establishing the accuracy and reliability of this technique.

5. Conclusion

This study presents a novel semi-automated approach for analyzing tibiofemoral kinematics using dynamic MRI, offering a balance of efficiency and accuracy in knee motion analysis. By leveraging direct analysis of dynamic frames and full contour tracking, our method provides consistent and smooth kinematic measurements with minimal user intervention.

While current limitations include 2D analysis and reliance on single-plane movement, the proposed approach shows significant promise for both research and clinical applications in knee biomechanics. The integration with a custom MRI-compatible knee loading device further enhances its potential for studying load-dependent changes in knee kinematics.

This comprehensive approach to studying in vivo knee mechanics under physiological loads represents a significant step forward in dynamic MRI analysis of joint function. As we continue to refine and extend this method, it has the potential to enhance our understanding of both normal and pathological knee function, ultimately contributing to improved diagnosis, treatment, and rehabilitation strategies for knee disorders.