Abstract

This study introduces a semi-automated segmentation pipeline for analyzing tibiofemoral kinematics using dynamic magnetic resonance imaging (MRI) data. While dynamic MRI offers valuable insights into knee function, current analysis methods often require time-consuming manual segmentation or rely on registering low-resolution dynamic images to high-resolution static scans. We present an efficient approach that directly utilizes the dynamic imaging data and applies edge detection, connected-component labelling, and frame-to-frame transformation computation to track the movement of the tibia and femur throughout knee flexion-extension cycles. The method was validated against manual segmentation using data from five healthy volunteers who performed guided active knee motion in a 3T MRI scanner. Results demonstrated that the semi-automated approach achieved greater consistency in tracking knee motion, with a mean coefficient of variation of 34.0% compared to 59.5% for manual segmentation. The semi-automated segmentation pipeline increased efficiency and accuracy compared to manual segmentation, potentially streamlining the analysis of knee joint kinematics using MRI data.

Manuscript Body

1 Introduction

The study of tibiofemoral kinematics, which describes 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 knee movement patterns can provide valuable insights for the diagnosis and treatment of various knee disorders, including ligament injuries and osteoarthritis [2–4]. For instance, studies have shown that the kinematics of anterior cruciate ligament-deficient knees are altered under various conditions. During walking, ACL-deficient knees demonstrated changes in tibial rotation patterns [5]. In a controlled knee extension exercise, these knees exhibited increased anterior tibial translation compared to healthy knees [6].

These alterations in knee kinematics observed in ACL-deficient knees exemplify how ligament injuries can lead to increased joint laxity and instability [7]. Such instability can result in higher tissue strains and abnormal loading patterns throughout the joint [8]. Over time, these biomechanical changes may contribute to the development and progression of osteoarthritis. Indeed, specific alterations in tibiofemoral kinematics, such as increased adduction moment and altered load bearing patterns have been associated with the progression of knee osteoarthritis, one of the most common joint disorders affecting a significant portion of the global population [9].

Dynamic MRI has emerged as a promising tool for studying tibiofemoral kinematics in vivo, offering insights into both normal and pathological knee function under realistic conditions. While not yet widely adopted as a standard approach, several studies have demonstrated its utility in capturing knee motion. These studies have employed various dynamic imaging techniques, including real-time MRI [10,11], CINE MRI [12,13], and cine phase contrast MRI [14,15], and methods incorporating specialized devices for controlled loading conditions [16,17] each offering unique capabilities for capturing in vivo knee motion.

In these dynamic MRI studies of knee motion, researchers have employed various methods to extract kinematic parameters. Some studies used high-resolution static MRI scans to create detailed 3D models of the bones, which were then registered to lower-resolution dynamic MRI frames [10,16]. Alternatively, some studies have employed landmark-based tracking methods, such as using a semi-automatic tracking algorithm where bony landmarks are manually identified in the first dynamic frame and then tracked across subsequent frames using normalized cross-correlation [11], or manually defining landmarks on bones in each frame and tracking their 2D coordinates throughout the motion sequence [13].

In this work, we present a semi-automated segmentation pipeline for analyzing tibiofemoral kinematics from dynamic MRI data. Our method leverages edge detection and tracking to segment and follow the contours of the tibia and femur throughout the flexion-extension movement cycle. Unlike previous approaches, our technique operates directly on the dynamic frames without requiring additional static scans, potentially streamlining the overall analysis process. By computing frame-to-frame transformations, we can efficiently track bone movement while minimizing manual input to just the initial frame. This approach allows for robust extraction of kinematic parameters, such as the tibiofemoral angle, throughout the motion sequence. We implemented this method to analyze data acquired with a custom MRI-compatible knee motion and loading device, enabling the study of knee kinematics under controlled, physiological loading conditions. The primary objective of this work was the development of the bone tracking algorithm and its validation against manual segmentation, demonstrating its potential as an efficient and accurate tool for investigating in vivo knee mechanics.

2. Material and Methods

2.1 Image Acquisition and Reconstruction

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

A custom MRI-safe knee motion and loading device [18] 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 secured to an ankle support positioned just proximal to the malleolus using Velcro straps to attach the leg to the device arm. Additional straps were applied around the thigh to minimize unwanted lateral movement. The knee joint center was carefully aligned with the device's axis of rotation, allowing only flexion and extension movements in the sagittal plane. Two flexible 16-channel multifunctional coils (Variety, Noras MRI products GmbH) were used to ensure comprehensive coverage of the knee region. One coil was positioned beneath the knee, with the posterior aspect of the knee resting directly on it. The second coil was wrapped around the anterior aspect of the knee, covering the proximal tibia.

During the scan, participants performed controlled extension-flexion cycles of the knee joint to the beat of a metronome (60 beats per minute). Each knee extension-flexion movement cycle was guided by eight metronome beats, with the knee fully flexed at the first beat, fully extended by the fourth beat and fully flexed again by the eighth beat, resulting in 7.5 cycles per minute. The knee range of motion achieved by the participants varied between 30 and 46 degrees. The total scan duration was 160 seconds, allowing for the acquisition of approximately 20 full knee extension-flexion cycles.

MRI data were acquired using a 2D radial golden-angle gradient echo FLASH sequence [19,20] with the following parameters: echo time of 2.51 ms, flip angle of 8 degrees, field of view 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.

This acquisition method enables CINE MRI, which continuously acquires k-space data throughout the knee motion cycle. By retrospectively sorting the k-space data into discrete knee angle intervals, a series of images or frames representing the knee at different flexion-extension positions is created, effectively producing a ‘cinema’ of the joint motion.

Image reconstruction was done using an optical fiber position sensor (MR338-Y10C10, Micronor, Camarillo, CA, USA) integrated into the knee device. This optical sensor measured the knee rotation angle with a precision of 0.025° using optical signals. The optical signals were first converted to electrical signals by a controller (MR330, Micronor), which were then sampled simultaneously with the MRI scanner's trigger signal using a USB-based data acquisition module (RedLab 1208FS Meihaus Electronic GmbH). By synchronizing the knee rotation angles with the start of each k-space repetition, the radial golden-angle k-space data were then sorted into two degree windows of knee rotation [21]. This process was repeated for the entire range of motion, ensuring comprehensive coverage of the knee’s range of motion. Image reconstruction was performed using the RIESLING (Radial Interstices Enable Speedy Low-volume imagING) toolbox [22]. This open-source software package is specifically designed for reconstructing non-Cartesian MRI data, employing advanced algorithms to efficiently handle the radially sampled k-space data. Specifically, the “Alternating Direction Method of Multipliers” algorithm within RIESLING was used, with “Total Generalized Variation” regularization. A regularization strength of 0.05 was used, which was empirically determined to balance noise suppression and edge sharpness. Image reconstruction was performed separately for knee extension (upward leg movement) and knee flexion (downward leg movement) to account for biomechanical differences.

The final reconstructed 2D-CINE datasets had a varying number of frames based on each participant's achievable range of motion. Participants with a larger range of motion had more frames available for reconstruction as compared to participants with lower range of motion. **Figure 1** shows a series of reconstructed frames from a single dataset, showcasing the progression of knee motion from a flexed position, to extended position, back to flexed position, which are used subsequently as the input data for bone segmentation and tracking.

2.2 Semi-Automated Bone Tracking

For semi-automated tracking of the tibia and femur, the following tracking algorithm was implemented in Python (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 [23]. Parameters such as gradient thresholds and Gaussian blur strength were optimized manually to 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 [24] was 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 groups adjacent pixels into distinct regions or "components". The algorithm’s connectivity settings were adjusted to define how pixels are considered connected (e.g., diagonally adjacent pixels were considered to be part of the same component). These settings were carefully tuned to ensure that each bone's interior edge was consistently identified as a single, continuous component 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, and 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 [25]. The sorted points were then downsampled to 80 equidistant points using cubic spline interpolation [26]. 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: Frame to frame transformations were computed to align the equidistant reference points of the bone edges. This process assumed rigid body motion, considering only translations in the sagittal plane and rotations about the transverse axis perpendicular to the sagittal plane. As such, the transformation was described using three parameters: two translations in the inferior-superior and anterior-posterior directions and one rotation in the axis perpendicular to the sagittal plane.

To compute the optimal set of these three parameters, a cost function was defined. This function quantifies the total non-overlapping distance between the target frame and transformed frame, with a perfect alignment resulting in an output of 0. The goal was to find the combination of transformation parameters that minimizes the output of this cost function. The minimization of this cost function effectively identifies the optimal way to track the bone edges between consecutive frames.

The Nelder-Mead method was used to minimize the cost function and obtain the frame-to-frame transformation parameters [27]. To guide the search, constraints were applied based on a priori knowledge of the motion characteristics. For instance, the rotation was restricted to the expected range of frame-to-frame angle increments used during reconstruction, while the translations were limited to relatively small values to account for the continuous nature of the motion.

Once the parameters were obtained for all the frames, any manual segmentation of the bones drawn in the first frame, could be automatically transformed to all other frames.

A schematic overview of the tracking 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 manually for all frames and datasets using the Napari (v.4.16) image processing software [28]. 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 [29] 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 knee range of motion, the flexion angle was normalized to the ‘flexion percentage’, where -100% represents the point of maximum flexion, 0% corresponds to maximum extension, and +100% marks the return to maximum flexion.

To quantitatively assess the consistency of both the semi-automated and manual segmentation methods, the coefficient of variation (CV) for the frame-to-frame angle differences was calculated. The CV was computed for each dataset and method by dividing the standard deviation of the frame-to-frame angle changes by their mean. Lower CVs indicate more consistent tracking of knee motion.

3. Results and Discussion

The semi-automated segmentation pipeline developed in this study demonstrated the ability to track tibiofemoral kinematics from dynamic MRI data with improved consistency compared to manual segmentation. Figure 3 illustrates the outcome of applying the algorithm to an example dataset, showing the segmented tibia and femur overlaid on the original MRI image. This segmentation forms the basis for subsequent kinematic analysis throughout the flexion-extension cycle.

When comparing the kinematics derived from the semi-automated and manual methods (Figure 4), both approaches captured the characteristic patterns of tibiofemoral angle changes and their rates during knee flexion and extension. However, the semi-automated method produced noticeably smoother trajectories for both angle and angular velocity measures. The smoother trajectories produced by the semi-automated method more accurately represent the expected continuous nature of knee motion during the controlled flexion-extension task. This continuity in angle change and angular velocity aligns with the actual movement performed by the subject - a repeated, metronome-guided open chain knee flexion-extension while secured in the MRI-compatible device. The fluctuations seen in manual segmentation likely reflect frame-to-frame inconsistencies in analysis rather than true variations in the subject's smooth, rhythmic leg movement. To quantify this improved consistency, we calculated the coefficient of variation (CV) for frame-to-frame angle changes across all datasets (Figure 5). The semi-automated method achieved a mean CV of 34.0%, compared to 59.5% for manual segmentation, indicating more consistent tracking of knee motion.

The semi-automated approach offers significant advantages in terms of efficiency and reproducibility. By requiring manual input for only the initial frame, it substantially reduces processing time compared to full manual segmentation of all frames. This efficiency, combined with the improved consistency in tracking, makes the method promising for both research and clinical applications in knee biomechanics.

In the context of existing literature, our method offers a streamlined approach to analyzing knee kinematics from dynamic MRI data. Unlike techniques that rely on registering dynamic frames to high-resolution static scans [16,17], our approach directly utilizes the dynamic frames. This can potentially reduce total scan time and eliminate errors that might arise from registering images acquired in different joint positions. However, it's important to note that our method is currently limited to 2D analysis in the sagittal plane, which restricts the kinematic information that can be extracted.

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.

4. Conclusion