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 high-resolution dynamic imaging data and applies edge detection, connected-component labelling, and frame-to-frame transformation computation to track bone movement 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. While currently limited to 2D analysis, the method shows promise for extension to 3D data and application for studying various knee pathologies.

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, 3, 4]. For instance, .Additionally, alterations in tibiofemoral kinematics have been associated with the progression of knee osteoarthritis, one of the most common joint disorders affecting a significant portion of the global population [5].

Dynamic MRI has proven to be a valuable tool for studying tibiofemoral kinematics in vivo, offering insights into both normal and pathological knee function under realistic conditions. Recent advancements have led to various dynamic imaging techniques, including real-time MRI [8,9], CINE MRI [10,11,12], and cine phase contrast MRI [13,14], each offering unique capabilities for capturing in vivo knee motion. Many of these studies have incorporated specialized devices to guide knee motion and apply controlled loading conditions during imaging, allowing for the investigation of load-dependent variations in knee kinematics [15].

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 [8, 10]. Other approaches involved tracking specific anatomical landmarks across dynamic image frames using image registration techniques [9]. While these methods have provided valuable insights into knee kinematics, they often rely on dynamic scans with lower spatial resolution.

In this work, we present a novel semi-automated segmentation pipeline for analyzing tibiofemoral kinematics from high-resolution dynamic MRI data. Our method leverages advanced 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 imaging 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 [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 malleolus using Velcro straps to minimize lateral movement. The knee joint center 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 wrapped around the top of the knee, covering the distal femur, and the other placed underneath the knee, supporting 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 [17,18] 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.

Image reconstruction was done 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 USB-based data acquisition module (RedLab 1208LS, 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 intervals of knee rotation [19]. This process was repeated for the entire range of motion, ensuring comprehensive coverage. Image reconstruction was performed 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 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. **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 [21]. 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 [22] 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'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, 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 [23]. The 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 bone 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 XXX 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 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 [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 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 changes 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

**Figure 3** illustrates the result of applying the semi-automated segmentation algorithm to an example dynamic MRI dataset. The tibia and femur masks are overlaid on the original MRI image, showing how the algorithm identifies and outlines the bone boundaries. This segmentation provides the basis for tracking bone movement and calculating kinematic parameters throughout the flexion-extension cycle

**Figure 4** presents a comparison of kinematic parameters derived from manual and semi-automated segmentation 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 4 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.

**Figure 5** presents a comparison of kinematic analysis results between the automatic and manual segmentation methods. The left panel shows the rate of change of the tibiofemoral angle throughout the knee flexion-extension cycle, aggregated across all datasets. The x-axis represents the flexion percentage, where -100% indicates maximum flexion, 0% represents full extension, and +100% indicates return to maximum flexion. Shaded areas represent one standard deviation from the mean. Consistent with the single dataset analysis shown in Figure 4, the automatic method (blue) demonstrates less variability compared to the manual method (orange).

The right panel of Figure 5 provides a quantitative comparison of the consistency in frame-to-frame angle changes between the automatic and manual methods. The coefficient of variation (CV) was calculated for each dataset and method, with lower values indicating more consistent tracking. The mean CV for the automatic method was 34.0%, lower than the manual method, which had a mean CV of 59.5%. Each point in the plot represents the CV for one dataset.

4. Discussion

This study introduces a semi-automated segmentation pipeline for analyzing tibiofemoral kinematics using dynamic MRI. The results demonstrate that the presented approach offers significant advantages over manual segmentation in terms of efficiency and consistency in tracking knee joint flexion and extension.

In the context of current literature on dynamic MRI of the knee, the proposed 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], this 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. Furthermore, the presented method utilizes the full contours of the bones rather than relying on specific anatomical landmarks [9, 27]. By tracking entire bone edges instead of discrete points, it may offer improved robustness against errors that can arise from landmark misidentification or local image artifacts.

A key strength of the described method is its efficiency. By requiring manual segmentation of only a single frame, with minimal user intervention thereafter, this approach significantly reduces processing time compared to full manual segmentation of all frames. The significantly lower CVs observed for the automatic method across all datasets shows higher consistency in tracking knee motion compared to manual segmentation. This improved consistency suggests that the automatic method may be better suited for detecting subtle changes in knee kinematics.

However, the presented tracking algorithm has limitations. The current implementation is restricted to 2D sagittal plane analysis, capturing primarily flexion-extension and anterior-posterior translation. This limits the 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 the method relies on movement being confined to a single plane, which can be challenging to achieve perfectly in vivo.

Despite these limitations, the method shows promise for application in clinical studies. The ability to quickly and consistently quantify tibiofemoral kinematics could be valuable for assessing knee function in the context of various knee injuries and mechanically driven musculoskeletal conditions [7]. The method could also be extended to the patellofemoral joint, enabling kinematic analysis [27] to support clinical decision making for conditions such as patellofemoral instability and patellofemoral pain syndrome [28]

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.~~

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, the proposed method provides consistent and smooth kinematic measurements with minimal user intervention.

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.