

Manuscript body

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 [2]. 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. 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 [3].

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[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 \[1,7\]. 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 \[2,3,8\]. These methods typically offer improved spatial resolution compared to real-time imaging.](#)

[Another approach used in earlier studies is cine phase contrast MRI \[9,10\]. This method directly encodes velocity information into the MRI signal, allowing for quantitative measurements of tissue motion. It has been applied to study both patellofemoral and tibiofemoral kinematics.](#)

[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 \[6\]. Such approaches are particularly valuable for understanding the](#)

[biomechanical changes associated with conditions like osteoarthritis and ligament injuries.](#)

To analyze tibiofemoral kinematics effectively, precise segmentation of the tibia and femur in medical imaging is essential. Segmentation can allow for the extraction of key kinematic parameters, such as the relative positions and orientations of these bones during knee motion. This process becomes particularly challenging when dealing with dynamic imaging sequences that capture knee motion over time, as it requires consistent and accurate segmentation across multiple image frames.

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To overcome these challenges, we developed a semi-automated segmentation pipeline specifically designed for dynamic 2D sagittal images of the knee during flexion-extension cycles. and compared its performance against traditional manual segmentation. Our results demonstrates that a semi-automated approach not only significantly reduces processing time but also yields more consistent and smoother tracking of bone angles throughout the motion cycle.

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2. Material and Methods

2.1 Image acquisition and reconstruction

Five healthy volunteers (three males and two females, ages 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).

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A custom MRI-safe device [4] 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 [5] with the following parameters: echo time (TE) of 2.51 ms, flip angle of 8 degrees, and repetition time (TR) of 5.8 ms. During each 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. This process was repeated for the entire range of motion, ensuring comprehensive coverage. 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:

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(I) Edge Detection: The Canny edge detection algorithm was applied to each frame to identify the boundaries of the tibia and femur [6]. 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 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.

(III) Reference Point Extraction: A set of reference points was manually 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. These sorted points were then downsampled to 50-80 equidistant points using cubic spline interpolation. 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:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \mathbf{R}(\phi) \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} \Delta x \\ \Delta y \end{bmatrix}$$

Where ϕ is the angle of rotation, (x, y) and (x', y') are the points in the target frame and reference frame, respectively, $(\Delta x, \Delta y)$ are the frame-to-frame translations within the measured sagittal plane and

$\mathbf{R}(\phi)$ is the 2D in-plane rotation matrix given by

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$$R(\phi) = \begin{bmatrix} \cos \phi & -\sin \phi \\ \sin \phi & \cos \phi \end{bmatrix}$$

To determine the optimal transformation parameters $(\phi, \Delta x, \Delta y)$ that best align the reference points from one frame to the next, a cost function that minimizes

$$C(\Delta x, \Delta y, \phi) = \sum_{p=1}^N \min_{q \in Q} \left(\sqrt{(x_q - x'_p)^2 + (y_q - y'_p)^2} \right)$$

was used, where (x_q, y_q) are the points in the target frame and (x'_p, y'_p) 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 q to its nearest point in the target frame p 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 $(\Delta x, \Delta y)$ 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. 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

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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 ranges 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

In **Figure 3**, the angle between the tibia and femur is plotted as a function of flexion percentage for each of the five datasets for both the manual segmentation (orange) and semi-automatic segmentation (blue) methods. Across all datasets, both methods exhibit consistent angular trajectories, characterized by a pronounced "V"-shaped pattern that peaks at maximum flexion and reaches its lowest point around full extension. The range of angles correlate with the range of motion inside the scanner for each dataset.

Despite the similar trends, the manual segmentation results appear to have more local fluctuations compared to the semi-automatic method. To visualize these differences in trajectory smoothness, the rate of change of the angle with respect to the flexion percentage was computed. This derivative analysis, as shown in **Figure 4**, plots the angular velocity (in degrees per flexion percentage) against the flexion percentage for each dataset and segmentation method. For both manual and semi-automatic methods, the values generally cluster around -0.25 degrees per flexion percentage for the first half of the motion cycle (-100% -0%) and 0.25 degrees per flexion percentage for the second half (0%-100%). The semi-automatic method shows a more consistent distribution of values within these values across all datasets. In contrast, the manual method exhibits greater variability, with more frequent and pronounced deviations from these values.

To provide an overview of the segmentation methods' performance across all datasets, **Figure 5** presents the aggregated results. This graph shows the average angle between the long axis of tibia and femur segments, plotted against the flexion percentage, with the shaded regions representing the standard deviation. Both methods maintain the characteristic V-shaped pattern observed in the individual datasets. Notably, the standard deviation, as indicated by the shaded area, is consistently larger for the manual segmentation compared to the semi-

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automatic method throughout the entire motion cycle. This difference in variability is particularly evident at the maximum extension phase.

4. Discussion

The results show that the semi-automated segmentation algorithm behaves more smoothly, and hence more in line with reality than the manual segmentation. Also, the semi-automated segmentation only involves segmentation of a single frame, and a few interventions like picking out the relevant label edges, which makes it significantly faster than segmentation of all the datasets and frames manually. This strongly suggests that the new approach is a more efficient and accurate method to segment the tibia and femur, provided that the movement of the leg is restricted to a single plane.

This assumption was largely true, but one has to be really careful with positioning the leg in the device. If the straps are loose, then it could allow the tibia to rotate internally. If this happens, then the computation of transformation matrices will not give accurate results because the assumption of movement in a single plane fails. This problem is more pronounced for the tibia as compared to the femur because of the design of the device as well as on anatomy. During the experiments, it was observed that this problem was more apparent in subjects with shorter legs. This was identified as one of the limitations of the device.

5. Conclusion

This study introduces a novel semi-automated segmentation pipeline for analyzing tibiofemoral kinematics using dynamic MRI. Our findings demonstrate that this method offers significant advantages over traditional manual segmentation, including improved efficiency, consistency, and smoothness of kinematic measurements. The semi-automated approach requires minimal user intervention, significantly reducing processing time while maintaining accuracy comparable to manual methods. Results show reduced variability and smoother trajectories in angle measurements across the motion cycle, likely reflecting more accurate knee joint kinematics. However, the method's reliance on single-plane movement highlights areas for future improvement, such as accounting for out-of-plane motion and optimizing subject positioning. Despite these limitations, the proposed pipeline shows promise as a valuable tool for both research and clinical applications in knee biomechanics. Future work should focus on extending the

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method to 3D imaging techniques, validating it against established kinematic measurement methods, and exploring its utility in studying pathological knee conditions.