Manuscript body

1.1 Introduction

Tibiofemoral kinematics refers to the relative motion between the femur and tibia during knee joint movement. It encompasses six degrees of freedom: three translations (anterior-posterior, medial-lateral, and proximal-distal) and three rotations (flexion-extension, internal-external, and varus-valgus) [1]. The study of tibiofemoral kinematics 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].

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.

To overcome these challenges, we developed a semi-automated segmentation pipeline specifically designed for 2D CINE sagittal images of the knee during flexion-extension cycles. Our approach utilizes a custom MRI-safe device that facilitates controlled, repetitive knee flexion-extension movements within a 3T Siemens Prisma scanner.

To validate our method, we compared its performance against traditional manual segmentation. Our results demonstrate that the semi-automated approach not only significantly reduces processing time but also yields more consistent and smoother tracking of bone angles throughout the motion cycle. Specifically, when analyzing the angle between the long axes of the tibia and femur segments, the segmentation algorithm showed reduced variability and fewer local fluctuations in angle measurements compared to manual segmentation.

2.1 Methods (Image acquisition and reconstruction)

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

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.

To enhance signal-to-noise ratio and provide comprehensive coverage of the knee joint, two flexible 16-channel multifunctional coils (Variety, Noras MRI products GmbH) were employed. 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. This arrangement ensured optimal signal capture throughout the range of motion.

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. For each k-space, 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 by the use of an optical fiber position sensor (MR338-Y10C10, Micronor, Camarillo, CA, USA) integrated into the knee device. This sensor precisely measured the knee rotation angle with a resolution of 0.025°. The sensor data was transmitted via fiber optic cabling to an MR330 controller outside the MRI room, which converted the optical signals to electrical signals. A RedLab 1208LS USB-based data acquisition module (Meihaus Electronic GmbH) simultaneously sampled both the knee rotation signals and the MRI scanner's trigger signals. These signals were then transmitted to an acquisition computer and converted into binary data.

During reconstruction, the binary data was parsed to extract the knee rotation angles and MRI trigger signals. The start of each k-space repetition was identified using the trigger signals, allowing the knee rotation angles to be grouped according to each k-space repetition. This resulted in 100 groups, each containing knee rotation angle information for a specific k-space repetition.

The k-space data was then sorted into 2-degree intervals based on the knee rotation angles. 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 frames had dimensions of 528 x 528 pixels, with the number of frames varying based on each participant's achieved range of motion.

2.2 Methods (Segmentation algorithm)

The semi-automatic segmentation of the tibia and femur was performed using a custom algorithm implemented in Python. The process consisted of four main steps:

(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 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. This process distinguished the 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 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 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 reference points 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,

* **p** is the position vector of the point in its current frame
* **p**′ is the position vector of the point after transformation to the next frame
* ϕ is the angle of rotation
* **R**(ϕ) is the rotation matrix, given by
* **t** is the translation vector,
* and are the translations in the sagittal plane given in Cartesian coordinate system.

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

where, are the points in the target frame and are the points in the reference frame after having undergone transformation. Set P is the set of points in the reference frame and Set Q is set of points in the target frame.

For a given set of transformation parameters, 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.

The Nelder-mead method was used to minimize this cost function and obtain the transformation parameters for the first and second frame. This whole process was repeated again, this time considering the transformed second frame as the reference frame. And, by doing so, parameters for all the frames in the motion cycle was determined. Finally, by using these parameters, any segment drawn on the first frame, could be automatically used to segment the bones in rest of the frames.

2.3 Manual Segmentation and Angle measurement

To compare the accuracy and reliability of this algorithm, segmentation was performed for all frames and datasets manually as well. The napari (v.4.16) image processing software was used. Segmentation was done by a single user by adding fine points along the boundary of the interior cortical bone.

To make a comparison between the two methods, the angle between the long axis of the bones were extracted from the segments and tracked over the motion cycle. Principal component analysis was used to obtain the unit vectors that define the long axis.

3. Results

Following the calculation of the angle between the tibia and femur segments for each frame of the motion cycle, the focus was placed on visualizing the dynamic changes in this angle throughout the flexion-extension cycle. Since the number of frames reconstructed for each dataset varied between subjects due to their different ranges of motion, it necessitated the normalization of the time axis for visualization. This was done by defining the time axis as ‘flexion percentage’, where -100% represents the point of maximum flexion, 0% corresponds to full extension, and +100% marks the return to maximal flexion.

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