Abstract

Dynamic MRI enables in vivo analysis of relative bone motion during knee movement, but quantifying this motion from imaging data remains challenging due to the trade-offs between temporal and spatial resolution. This study aimed to develop and validate a semi-automated pipeline to track femoral and tibial motion and extract motion parameters from sagittal plane CINE MRI during flexion-extension cycles. Our method combines Canny edge detection and connected-component labeling with frame-to-frame transformation optimization to track bone boundaries. The approach was validated in five healthy volunteers performing controlled knee motion using an MRI-compatible device, with results compared to manual segmentation. The semi-automated tracking achieved an average alignment error of 0.40 ± 0.02 mm for both bones, with processing time reduced from approximately 15 minutes for manual segmentation to less than 5 minutes per dataset. Both approaches showed similar motion patterns, with horizontal displacement ranging from 8 to 28 mm and vertical displacement remaining relatively constant around 57 mm with approximately 2 mm variation through the motion cycle. All displacements were defined in the 2D image coordinate system, with the centroid of the tibial segment tracked relative to the centroid of the femoral segment. The semi-automated method demonstrated higher precision through consistently smaller standard deviations in displacement measurements. This approach enables efficient and reliable quantification of relative bone positions during knee motion in dynamic MRI sequences without requiring additional high-resolution reference scans, making it suitable for both research and clinical applications.

Keywords: Dynamic MRI; Bone tracking; Semi-automated segmentation; Motion analysis; Knee osteokinematics

Manuscript Body

1 Introduction

Studying the relative motion between the femur and tibia (osteokinematics) during knee joint movement is essential for understanding normal knee function, diagnosing pathological conditions, and improving prosthetic design [1–3]. It also helps optimize surgical techniques for ligament reconstruction, developing rehabilitation protocols, and evaluating treatment outcomes [4–6] . Accurate assessment of osteokinematics aids in diagnosing and treating various knee disorders involving altered joint biomechanics, including ligament injuries which can lead to altered gait mechanics and cartilage degradation, post-traumatic osteoarthritis, and joint instability syndromes [7–9]. These conditions often result from joint malalignment, increased joint laxity and altered congruency of articulating surfaces, which can all be better understood through detailed analysis of bone motion patterns [10–12].

Dynamic MRI has emerged as a promising tool for studying in vivo knee motion [13]. While several dynamic imaging techniques including real-time MRI [14,15], CINE MRI [16,17], and cine phase contrast MRI [18,19] can effectively visualize knee movement, extracting quantitative motion parameters from these scans presents significant challenges. Dynamic sequences necessarily trade off spatial resolution and image quality to achieve temporal resolution suitable for motion capture. For methods aiming to track bone motion across frames, one common approach is to use high-resolution static reference scans that must be manually segmented to create detailed bone models, which are then registered to the lower-resolution dynamic frames [18–20], though this adds complexity to the workflow and increases processing time.

In this work, we present a semi-automated pipeline to measure the relative motion between the distal femur and proximal tibia in the sagittal plane from CINE MRI images acquired during controlled knee flexion and extension using a custom MRI-compatible knee motion and loading device. The primary objective is to reliably track the bone segments so that clinically relevant motion parameters can be derived. Our approach combines Canny edge detection [21] and connected-component labeling [22] with frame-to-frame transformation optimization to track the bone segments across frames, enabling quantification of their relative horizontal and vertical displacements. Unlike methods requiring 3D bone models, our technique operates directly on dynamic MRI data without the need for additional static scans, streamlining the analysis process. We also evaluate measurement precision and processing time by comparing our pipeline with manual segmentation approaches. Overall, this semi-automated method has the potential to serve as an efficient tool for analyzing relative bone motion from dynamic MRI data, with potential applications in both research and clinical settings.

2. Material and Methods

2.1 Image Acquisition and Reconstruction

Five healthy volunteers (three males and two females, 24-39 years old, 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 [23] 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 surface of the knee resting directly on it. The second coil was wrapped around the anterior surface 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 [24,25] 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 enabled CINE MRI, which continuously acquired 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 was created, effectively producing a ‘cinema’ of the joint motion.

Image reconstruction was based on 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°.The optical signals were first converted to electrical signals by a controller unit (MR330, Micronor), which were then sampled simultaneously with the electrical MRI scanner's sequence 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 [26]. This process was repeated for the entire range of motion, ensuring complete coverage of the knee’s range of motion. Image reconstruction was performed using the RIESLING (Radial Interstices Enable Speedy Low-volume imagING) toolbox [27]. This open-source software package is specifically designed for reconstructing non-Cartesian MRI data, employing advanced algorithms to efficiently reconstruct the radially sampled k-space data. Specifically, the “Alternating Direction Method of Multipliers” algorithm within RIESLING was used, with “Total Generalized Variation” regularization [28,29]. 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 after reconstruction as compared to participants with a 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). **Figure 2** provides a schematic overview of this tracking pipeline, which consists of the following steps:

(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 groups adjacent pixels into distinct regions or "components". Full 3D connectivity was used, meaning pixels could be considered part of the same component if they were adjacent (including diagonally) either within a frame or across consecutive frames. This approach ensured that the same bone edge maintained a consistent label throughout the motion sequence, facilitating tracking across frames. 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 [30]. The sorted points were then downsampled to 80 equidistant points using cubic spline interpolation [31]. 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 described by three parameters: two translations in the sagittal plane and one rotation about the axis perpendicular to the sagittal plane. As illustrated in the final panel of **Figure 2** using the tibia as an example, this involved transforming the initial reference points (orange dots) to match the bone edges in a new position. When the transformation parameters are optimally computed, the transformed points (green dots) should align perfectly with the binary edge (shown in white) in the new position.

To compute the optimal set of these three parameters, a cost function was defined. This function quantified the total distance between the transformed reference points (established along the bone edges in the initial frame) and the detected bone edges in the target frame, with a perfect alignment resulting in an output of 0. The goal was to find the combination of transformation parameters that minimize 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 [32]. 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.

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 [33]. 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.

For both manual and semi-automated segmentations, relative bone positions were quantified using centroid-based measurements. The centroid position was calculated for both the tibial and femoral segmentations in each frame. In the sagittal plane view, the relative displacement between the femoral and tibial centroids was measured in two directions: horizontal and vertical in the image plane, with the origin at the top-left corner, increasing downward and to the right.

To enable comparison across datasets with different ranges of motion, the device arm angle measured by the rotary encoder was normalized to a 'flexion percentage' scale, where -100% represents the minimum device arm angle (maximum knee flexion position), and +100% marks the return to the minimum device arm angle (return to maximum flexion position).

The tracking accuracy was evaluated using the cost function described in section 2.2, which quantifies the distance between the transformed reference points and the detected bone edges. The cost function value divided by the total number of reference points provided an average alignment error in millimeters for each bone in each frame.

3. Results and Discussion

The semi-automated tracking algorithm successfully tracked both the tibia and femur edges throughout the motion cycle for all five subjects, with a combined average alignment error of 0.40 ± 0.02 mm for both bones. **Figure 3** demonstrates the tracking results at different points in the motion cycle, showing the segmented bone contours overlaid on the original CINE frames. The semi-automated method required less than 5 minutes of processing time per dataset, compared to approximately 15 minutes needed for manual segmentation of all frames in a single dataset.

The relative bone motion (osteokinematics) of the tibia with respect to the femur using both manual and semi-automated segmentation methods is shown in **Figure 4**. The horizontal displacement showed a consistent linear trend across both extension and flexion phases, ranging from approximately 8 mm to 28 mm through the motion cycle. The vertical displacement remained relatively constant around 57 mm, with total variation of approximately 2 mm across the cycle. Both manual and semi-automated methods demonstrated similar motion patterns, with the semi-automated method showing consistently smaller standard deviations across all measurements, indicating higher precision and measurement reliability.

The ability to precisely quantify relative bone positions in healthy volunteers (n=5) demonstrates the technical feasibility of our bone tracking approach. As this study focused on algorithm development, establishing normative bone motion parameters and their variations across populations would be the subject of future dedicated studies. This capability could be particularly valuable for studying conditions that alter normal knee mechanics. Ligament injuries can affect joint stability, leading to increased laxity [34]. Additionally, these injuries can result in altered movement patterns during functional activities, as demonstrated in studies of ACL deficiency showing changes in tibial motion [35]. Our method's precision could potentially detect such subtle deviations from normal motion patterns. While the clinical interpretation of such differences would require careful validation in future studies with specific patient cohorts, the precision and efficiency of our tracking method makes it a promising tool for comparative analyses between normal and pathological joint motion patterns.

4. Conclusion

This study presents a novel semi-automated method for tracking bone motion in 2D sagittal CINE MRI sequences during controlled knee flexion-extension movements. The method significantly reduces processing time compared to manual segmentation while improving measurement reliability. The ability to efficiently quantify relative femoral and tibial positions during motion makes this approach valuable for analyzing joint movement patterns. This technical advancement contributes to the broader goal of understanding normal and pathological knee function through dynamic MRI analysis.

5. References

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