Abstract

Dynamic magnetic resonance imaging (MRI) enables in vivo imaging of bone motion during knee movement, but quantifying this joint motion from imaging data remains challenging. This study aimed to develop and validate a semi-automated pipeline to track relative femoral and tibial motion, and extract motion parameters from sagittal plane CINE MRI scans during active knee flexion-extension movement. The presented 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 flexion and extension using a dedicated MRI-compatible device. Results of the [XXX analysis – what parameters specifically?] obtained using the semi-automated approach were compared to manual segmentation. The semi-automated tracking method 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 for semi-automated segmentation per dataset. Both approaches showed similar relative bone motion patterns, with horizontal displacement ranging between 8 and 28 mm and vertical displacement remaining relatively constant around 57 mm with approximately 2 mm variation through the knee motion cycle. All bone displacements were defined in the two-dimensional image coordinate system, with the centroid of the tibial segment tracked relative to the centroid of the femoral segment. The semi-automated method demonstrated consistently smaller standard deviations in displacement measurements. The developed semi-automated approach enables efficient and reliable quantification of relative bone positions during knee motion in dynamic MRI protocols 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

Osteokinematics is the study of gross movement of bony segments, typically characterized by the displacement of bony shafts [1] . Studying the relative motion between the femur and tibia (osteokinematics) during gross knee joint movement is essential for understanding normal knee function, diagnosing pathological conditions, and improving prosthetic design [2–4]. An enhanced understanding of arthrokinematics can also help in optimizing surgical techniques for ligament reconstruction, developing rehabilitation protocols, and evaluating treatment outcomes [5–7] . Accurate assessment of arthrokinematics aids in diagnosing and treating various knee disorders involving altered joint biomechanics, including ligament injuries which can lead to joint instability syndromes, altered ambulatory mechanics, and joint tissue degradation (e.g., osteoarthritis)[8–10]. These conditions often result from joint malalignment, altered congruency of articulating surfaces, increased joint laxity and/or decreased dynamic joint stability, which can all be better understood through detailed analysis of bone motion patterns [11–13].

Dynamic MRI represents a promising tool for studying in vivo knee motion [14]. While several dynamic MRI techniques, including real-time MRI [15,16], CINE MRI [17,18], and cine phase contrast MRI [19,20], can effectively visualize knee movement, quantifying the arthrokinematics from these scans presents significant challenges. Dynamic MRI sequences necessarily trade off spatial resolution and image quality to achieve temporal resolution suitable for time resolved (4D) images of joint motion. For methods aiming to track bone motion across MRI 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 [19–21]. However, this method increases workflow complexity and data processing time. [Similarly, another common method is …XXX], which allows for YY, but necessitates complex registration methods and ZZZ…]

The primary aim of this work was to develop a semi-automated pipeline to consistently track the bones of the knee joint (tibia and femur) using sagittal plane CINE MRI images acquired during controlled, active knee flexion and extension using a custom MRI-compatible knee motion and loading device. A secondary aim was to subsequently use the processed data to measure arthrokinematics, more specifically, the relative motion between the proximal tibia and distal femur during the knee flexion-extension movement. Our approach combines Canny edge detection [22] and connected-component labeling [23] 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 three-dimensional bone models [or complex XXX], 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 a manual segmentation approach. ~~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 [24] was used to guide planar knee movement during flexion-extension cycles. Participants were positioned supine with their thigh upon a wedge and secured using a strap in such a way that the knee joint center was aligned with the device's axis of rotation, allowing only flexion and extension. The lower leg was fastened to the ankle rest of the leg support using straps attached just proximal to the malleolus. Additional straps were applied around the thigh to minimize unwanted movement. Two flexible 16-channel multifunctional coils (Variety, Noras MRI products GmbH) were positioned around the knee to enable coverage of the entire joint. One coil was positioned beneath the knee, with the posterior surface of the knee resting directly on it. The other 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 two-dimensional (2D) radial golden-angle gradient echo FLASH sequence [25,26] with the following parameters: echo time of 2.51 ms, flip angle of 8°, 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 by retrospectively sorting the k-space data into discrete knee angle intervals to create a series of images or frames representing the knee at different flexion positions, effectively producing a series of images (or ‘cinema’) showing the joint motion.

Image reconstruction was based on angular data measured using an optical fiber position sensor (MR338-Y10C10, Micronor, Camarillo, CA, USA) integrated into the dedicated knee motion device. This optical sensor measured the knee rotation angle with a precision of 0.025°. The optical signals were converted to electrical signals by a controller unit (MR330, Micronor), and 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 sequence trigger signal, the acquired radial golden-angle k-space data were then sorted into two degree windows of knee rotation [27]. This procedure ensured full coverage of the knee’s range of motion. Image reconstruction was performed using the RIESLING (Radial Interstices Enable Speedy Low-volume imagING) toolbox [28]. 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 [29,30]. 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 resulted in more reconstructed frames 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 were 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 the tracking pipeline, consisting 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 [22]. 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 [23] 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". Through-frame connectivity was used, meaning pixels could be considered part of the same component if they were adjacent (including diagonally) either spatially 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 only 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) by identifying the most distal point of each bone, sorting the edge points using a greedy nearest neighbor algorithm [31] and downsampling the sorted points to 80 equidistant points using cubic spline interpolation [32]. 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 to effectively identify 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 [33]. To guide the parameter 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 incremental 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 Relative Bone Motion Analysis

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 [34]. For this purpose, the bone segmentation obtained in the first frame was aligned (translated and rotated) manually to match the new bone positions in subsequent frames.

For both semi-automated and manual segmentations, relative bone positions were quantified using centroid-based measurements. [MORE METHODS DESCRIPTION NEEDED]. [This approach was selected as a basic way to quantify the relative motion between bones]. 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 and the coordinates increasing downward and to the right.

To enable comparison across datasets with different knee ranges of motion, the joint positions (knee flexion angles) measured by the dynamic MRI knee motion device’s optical sensor 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

The semi-automated tracking algorithm successfully tracked both the tibia and femur edges throughout the motion cycle for all five subjects. When averaged across both bones, all frames, and all datasets, the alignment error between the transformed reference points and detected bone edges was 0.40 ± 0.02 mm. 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. **Figure 3** demonstrates the tracking results at different points in the motion cycle, showing the segmented bone contours overlaid on the original CINE frames.

**Figure 4** shows the quantitative analysis of relative bone motion, which revealed consistent patterns across all subjects. The horizontal displacement of the tibial centroid relative to the femoral centroid showed a linear trend during 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.

4. Discussion

The results demonstrate the technical feasibility of our semi-automated bone tracking approach for analyzing knee motion during flexion-extension movements. The method achieved sub-millimeter alignment accuracy (0.40 ± 0.02 mm) while significantly reducing processing time compared to manual segmentation. The smaller standard deviations observed with the semi-automated method suggest improved measurement consistency compared to manual tracking, likely due to the algorithmic approach being less susceptible to human variability in frame-to-frame segmentation.

The method successfully quantified two-dimensional motion patterns in the sagittal plane across all subjects. The measurements revealed consistent trends: a systematic change in horizontal displacement (8-28 mm) through the flexion-extension cycle, and a relatively stable vertical displacement (57 ± 2 mm). The consistency of these measurements across repeated motion cycles and between subjects demonstrates the method's ability to capture reproducible motion patterns, though establishing normative ranges would require larger population studies.

This method's ability to precisely track bone motion could be particularly valuable for studying conditions that alter normal knee mechanics. Ligament injuries can affect joint stability and lead to increased laxity [35], potentially resulting in altered movement patterns during functional activities. This has been demonstrated in studies of ACL deficiency showing changes in tibial motion [36]. While the clinical interpretation of such differences would require careful validation in future studies with specific patient cohorts, our method's precision and efficiency make it a promising tool for comparative analyses between normal and pathological joint motion patterns.

Several technical aspects of our approach contribute to its potential clinical utility. The method operates directly on dynamic MRI data without requiring additional static reference scans, streamlining the workflow. The semi-automated nature of the tracking reduces processing time while maintaining high precision, making it more practical for both research and clinical applications. Additionally, the ability to process sagittal plane CINE MRI data provides a balance between acquisition speed, spatial resolution, and motion information that is particularly relevant for analyzing knee flexion-extension patterns.

5. 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. Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

6. Funding Information

This research was funded by the German Research Foundation (DFG – Deutsche Forschungsgemeinschaft, BR 6698/1-1, KR 4783/2-1). The funding source had no role in the design of this study; in the collection, analysis and interpretation of data; in the writing of the article; and in the decision to submit the article for publication.

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