



Evaluation of fast approximate inverse kinematics for digital twin models of human movement

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Abstract: Digital twin models of human movement can be used to enhance physical performance, improve health, and reduce injury risk. Non-invasive motion capture can be used to measure body dimensions and body movement. When combined with biomechanical modelling and domain specific analyses, such as for ergonomics, these models can be used to estimate how changes to activity and workplace design correlate to performance and injury risk.

We have developed a prototype digital twin system called Ergomechanic that measures body movement and body segment loading but not all features are currently available in a real-time application. Joint angles are used in biomechanics to compare between study participants and evaluate differences from mean results. This is because these angles are relatively invariant between the population, despite large variations in height and weight. Inverse kinematics (IK) is the process of fitting a biomechanical model to measured movements of a person, though which joint angles can be calculated. As this process relies on a large sequence of recursive equations and a least-squares optimisation approach, it takes too long to converge, and can be too slow for real-time system applications. Here we call this method the “SlowIK” approach.

Here we propose a simple and fast approximation to the IK problem (called “FastIK”). It reduces the complexity of the applied equations and is explicit in formulation, thus avoids the optimisation formulation. The method is implemented in the Ergomechanic pipeline and tested with both a simple walking motion and a more complex workout activity. The FastIK method is more than 100x faster than the SlowIK method for both test activities. The knee joint angles calculated by the FastIK approach are found to be within a suitable accuracy in comparison to the SlowIK method, for most biomechanics applications. The elbow joint angle is reproduced well for the FastIK case in two of four cases but has a systematic offset in one instance and incorrectly identifies the sign of the angle in a second instance. This method shows good potential for reasonable accuracy of digital twin outputs when subject to the challenges of real-time applications.

Keywords: *Biomechanics, motion capture, computer vision, inverse kinematics*

1. INTRODUCTION

A digital twin (DT) is a virtual representation of an object or collection of objects that may provide real time visualisation of important features and simulation capabilities for estimating un-measurable metrics or future outcomes. DTs of human bodies can be used to track and predict outcomes of health, performance, and/or injury risk (Delp et al., 2007; Erol et al., 2020; Lloyd et al., 2023). Previously we presented a software called Ergomechanic (Cohen and Harrison 2021) which has been used to develop human digital twins (HDTs) (Harrison and Cohen 2021). Ergomechanic uses markerless motion capture (MMC) (Harrison et al. 2023) to non-invasively measure body size, pose and movement using cameras, computer vision and biomechanical modelling, but requiring no wearable items placed on the body (active or passive). The full non-invasiveness of this method enables its use in places such as the workplaces, the home, the sports field, or the hospital without affecting the participants' movement in any manner. One of the features of a HDT model is the calculation of model parameters that can be compared to population data. Joint angles are a common choice for pose related (or kinematic) metrics as they have been shown to be consistent across a range of body sizes and shapes. The calculation of joint angles in a real time application of Ergomechanic is the focus of this work.

Not all features of Ergomechanic are currently available in the real-time use case as their processing requirements are too high. One such feature is called Inverse Kinematics (IK), which is the fitting of joint angles, in the framework of a 3D biomechanical model of the body, to a live stream of body pose data. IK requires the development of recursive equations that relate the position of each joint to its parent by its length and its current joint angles. The solution of IK equations is done by a least squares optimisation approach. Whilst this can be done in about one second per frame, it is too expensive to be done in a real-time pipeline aimed at running multiple frames per second. Even with a 10x increase in efficiency it would be unsuitable for a pipeline already strained by processing multiple camera streams through deep learning pose models and producing 3D visualisations of system results.

Here we present a simplified and faster method for calculating approximate IK results from the outputs of MMC, which we call FastIK. It is not expected to be as accurate as the full IK method (which we call SlowIK), but if its accuracy is tolerable in certain situations, then it could enable better interpretations of MMC data in real-time applications. We describe the FastIK method and its assumptions and then test its use for sequence of simple movements.

2. METHODS

2.1. Markerless camera-based motion capture

Human bodies and objects are identified in each video frame, from each camera, using machine learning approaches. Body pose can be characterised by the position of each major joint (e.g., shoulder, elbow, knee etc). Here we use deep learning libraries such as OpenPose (Cao et al., 2018) or Detectron2 (Wu et al., 2019) to identify the joints in each image.

2.2. Human participant recordings

Recordings of movement were made using the Ergomechanic software and three Logitech Brio webcams. Video was captured at 30 frames per second. All protocols were approved by the CSIRO Health and Medical Human Research Ethics board.

2.3. “Slow”, accurate inverse kinematics (“SlowIK”)

Previously we described the method for inverse kinematics, which we label here “SlowIK”, using the following method:

A musculoskeletal model can be fit to the skeleton joint data using an inverse kinematics approach. We use operations in the Bio-Mechanic plugin (Harrison and Cohen, 2019), implemented in the Workspace workflow environment (Cleary et al. 2019). Each joint i in the human structural model has between 0 and 6 degrees of freedom (DoF). The total number of DoF for the whole body is N . The value of each DoF at any time instance is stored in a single vector, \mathbf{q} , for the whole body.

These DoF are either rotational or translational, and the direction of the movement is determined by an axis and an origin that are defined in the local frame of the body segment. For instance, the knees and elbows are often treated as a one DoF joint in which the DoF is the flexion angle. The shoulders and hips are treated as three DoF joints that can rotate about all three axes. The root joint can rotate and translate relative to the origin and so this interaction is treated as a six DoF joint.

The position and orientation of the i th body segment relative to its parent body (k th body segment) in the i th coordinate frame is expressed as a 4x4 matrix, $\mathbf{T}_{i,k(j)}$, which is dependent only on the degrees of freedom:

$$\mathbf{T}_{i,k(j)} = \begin{bmatrix} \mathbf{R}(\mathbf{q}) & \mathbf{u}(\mathbf{q}) \\ 0 & 1 \end{bmatrix} \quad (1)$$

The position of the i th body segment in WC (0th frame) can be calculated recursively using the relative transforms from each body segment from the root joint to the i th segment:

$$\mathbf{T}_{i,0(0)} = \prod_{j=1}^i \begin{bmatrix} \mathbf{R}_j & \mathbf{u}_j \\ 0 & 1 \end{bmatrix} \quad (2)$$

For each time increment of the video data, the centre of the joints (specified by the data in $\mathbf{T}_{i,0(0)}$) can be compared to the project 3D data from the MMC process. An optimisation procedure is used to find the set of DoF, \mathbf{q} , that produce the smallest error in joint centre position. The Dlib library is used currently to perform this optimisation (King, 2009). Typically, each of the DoF are temporally smoothed once the inverse kinematics process is complete. Here we use a top hat filter with two passes and a half-width of one datapoint.

2.4. Fast, approximate inverse kinematics (“FastIK”)

In our proposed approach, the joint angles are estimated simply from the approximate joint centre locations, which are calculated from the current set of video images (see Section 2.1). For instance, for the knee and elbow joints, which can be considered a 1 DoF joint, the joint angle, θ , is simply:

$$\cos(\theta) = \frac{\mathbf{a} \cdot \mathbf{b}}{|\mathbf{a}| |\mathbf{b}|} \quad (3)$$

where \mathbf{a} and \mathbf{b} are the vectors from the knee or elbow joint to their parent and child joints (hip and ankle or shoulder and wrist, respectively).

Other joints such as the hips and shoulders have 3 DoFs, and such a simple method is not viable. However, during many activities, such as walking, only 1 DoF is used predominantly. In this case Equation (3) may be viable. If this is not suitable then improper adduction and flexion angles can be estimated by projecting the limb into the sagittal plane. The internal-external rotation angle can be estimated by projecting a non-rotated version of the same limb into the adducted and flexed position and calculating the angle between the middle joint (elbow for the arm, and knee for the leg).

Once the joint angles are calculated using this FastIK method the system outputs are more useful for evaluating injury risk and performance, as joint angles are better correlated to these outcomes than joint position.

3. SYSTEM APPLICATION TO SIMPLE MOVEMENTS

We apply the system to two simple movements: walking and a simple workout.

Walking is a movement in which the major joints, including the ankles, knees, hips, shoulders, and elbows, rotate predominantly in the sagittal (side) plane. This means that it is suitable for an easy first evaluation of the FastIK algorithm. Images from one of three video recordings of the walking trial used are shown in Figure 1a.

A more complex sequence of movements including shadow boxing and jogging is also used to evaluate the model. Images of the sequence are shown in Figure 1b. In this case there are rotations of the hip and shoulder joints about each of the three axes.

Table 1 shows a comparison of computer wall-clock time required to complete the fast and slow IK methods for the two movement recordings. The FastIK method is 145 times faster than the SlowIK method for the walking activity and 348 times faster than the SlowIK method for the workout activity. This difference in results between the activities is likely to come from the more complicated movements in the workout activity compared to the walking activity, which requires more optimisation calculations in the SlowIK approach. The extremely large improvement in speed suggests that the FastIK method could be used in a real-time application of the HDT model.

Calculated joint angles for two movement patterns are shown in Figures 2 and 3. RMS differences in the results are shown in Table 2. The knee joint angle is very similar for SlowIK and FastIK methods. The root mean square (RMS) error is less than 5 degrees for each case, and this is suitable for most biomechanics applications. The elbow joint angle results follow a similar trajectory between the two methods, but an offset is present for the left elbow of the walking trial. Additionally, the orientation of the arm switches in the latter part of the workout trial (due to internal rotation of the shoulder joint) and the sign of the elbow angle calculated is then

incorrect, leading to a large RMS error in this case. These results suggest that the FastIK method could produce acceptable results for a range of applications, with some refinement for orientation of parent joints.

Table 1. RMS error in calculating joint angles using FastIK, when compared to results from the SlowIK method, normalised to the range of motion of the joint

	Walking	Work out
Number of frames	75	51
MMC time (s)	16	12
SlowIK time (s)	96	73
FastIK time (s)	0.66	0.21
Speed up (SlowIK / FastIK)	145x	348x

Table 2. RMS error in calculating joint angles using FastIK, when compared to results from the SlowIK method, normalised to the range of motion of the joint

	RMS error [degrees] (Angle range [degrees])	
	Walking	Work out
Left knee	3.7 (54)	5.7 (55)
Right knee	4.8 (62)	3.9 (46)
Left elbow	4.2 (14)	11 (114)
Right elbow	11 (26)	19 (104)

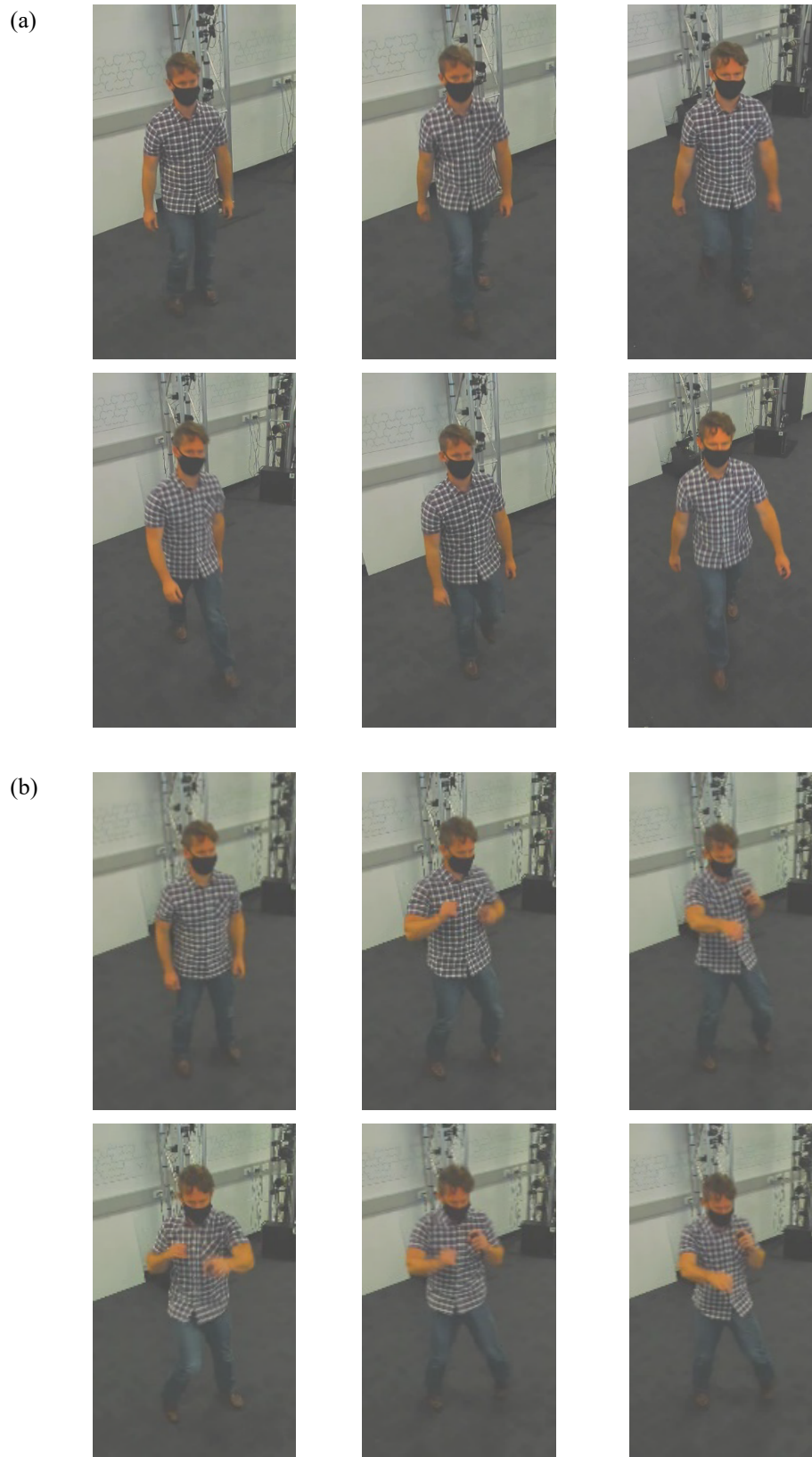


Figure 1. Images of the movements used to evaluate the FastIK algorithm for (a) the walking activity and (b) a workout activity that includes shadow boxing and jogging movements

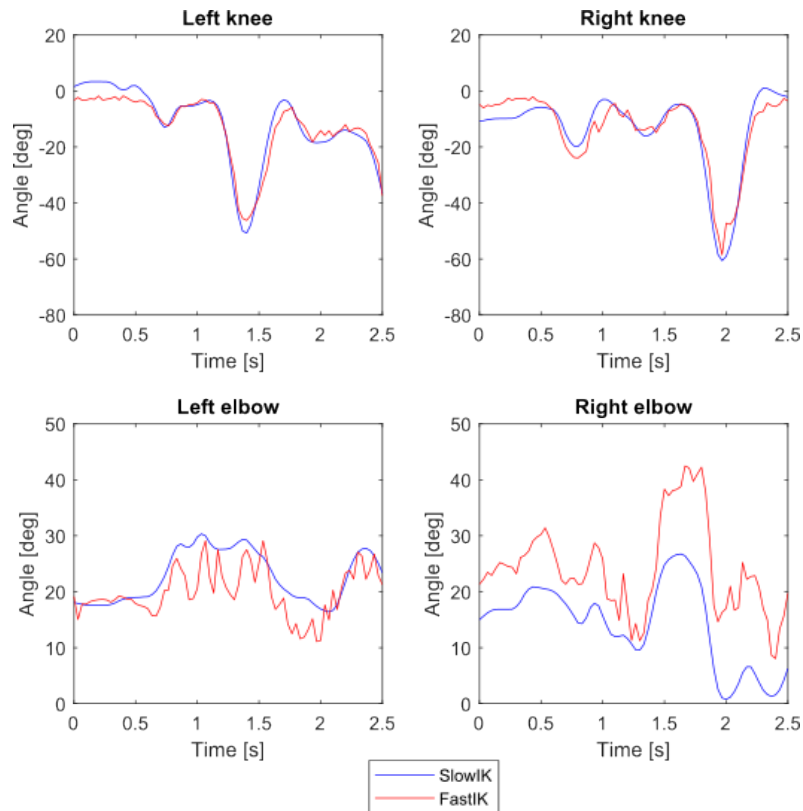


Figure 2. Comparison of knee and elbow flexion angles for the walking activity using the SlowIK (blue line) and FastIK (red line) approaches

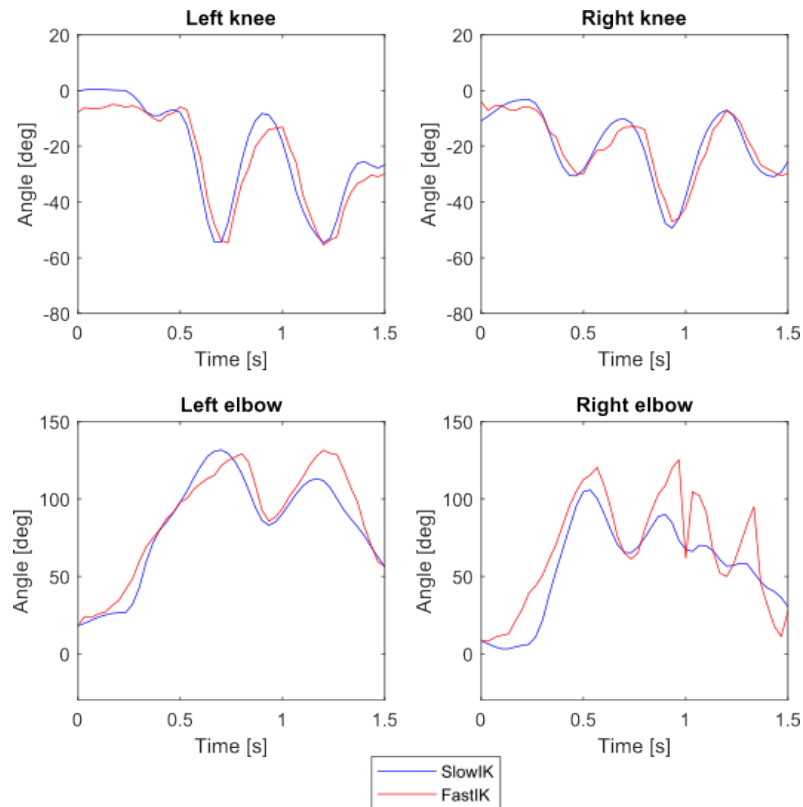


Figure 3. Comparison of knee and elbow flexion angles for the work out activity using the SlowIK (blue line) and FastIK (red line) approaches

4. CONCLUSIONS

We have presented a fast approximation to the inverse kinematics (IK) problem that is solved when calculating joint angles for human body motion. This method is implemented in a Human Digital Twin (HDT) modelling system called Ergomechanic. By forming an explicit approximation to the IK system of equations, we show that the new method, called “FastIK”, is more than 100x faster than our implementation of the full solution (which we call “SlowIK”) for two test activities. The method is tested in application to human walking, which is almost planar in movement, and a workout activity that involves all degrees of freedom of the upper and lower limb joints. Knee angles are shown to be well reproduced by the FastIK method in comparison to the SlowIK solution. Elbow angles are typically well reproduced, but we found one case with a small systematic bias and another in which the sign of the angle was incorrect. These results will be used to develop a more robust version of the FastIK algorithm. The FastIK algorithm was shown to be sufficiently accurate for many biomechanics applications and to be fast enough for real-time HDT applications.

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