Predicting Forearm Rotation Using a 4-Bar Linkage

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Summary

The biomechanics of the forearm is complex, especially its rotation axis, which shifts depending on the supination angle. However, more kinematics models define as a fixed axis rotation. One technique to solve these problems is using a statistical shape model with a 4-bar kinematics chain to accurately model the shape and supination-pronation. Using this model, the model average fitting error was 1.92 mm (± 0.27). More interestingly, the pose error reduced from 6.35° (±8.60°) to 3.69° (±5.08°). These results suggest that the 4-bar kinematics and the shape model improved the forearm's representation. This could be useful in understanding forearm biomechanics and deformities.

Introduction

Biomechanical models of the forearm can be useful to understand forearm deformities and guide complex osteotomies. However, to restore function, we need to accurately model supination-pronation, which is challenging as the rotation axis shifts throughout the range of motion [1]. Furthermore, like all kinematic modelling, estimates of forearm rotation are influenced by model scaling. We propose a solution to these challenges by using an articulated shape model to predict the coupled morphology of the humerus, radius and ulna and using a 4-bar linkage to define forearm supination-pronation.

Methods

The articulated shape model was created using 45 segmented CT scans of the upper limb (28 females, 35 ± 11 years, 1.66 ± 0.07 m, and 64.4 ± 15.4 kg; VIFM Ref: 2023-Choisne-1143-2385/3). The model included the humerus, radius and ulna, with two degrees-of-freedom (elbow flexion and forearm supination). A 4–bar kinematic chain of the forearm was created using the radial head articular disk, the centre of the radius-carpal and ulna-carpal articulated surfaces, and the humeral trochlea (Figure 1 inset). Supination-pronation rotations were defined using a vector describing the radius-carpal and ulna-carpal articular surface relative to the epicondyles of the humerus. The articulated shape model was fit to five additional segmented CT scans (three females, 47 ± 5 years, 1.60 ± 0.08 m, and 60.2 ± 10.9 kg) by adjusting the principal components and kinematic degrees of freedom. The fitting error (RMSE) and pose difference (degrees) determined how well the model could predict the morphology and orientation of different bones in new configurations, respectively. We also fit an existing OpenSim upper limb model [2] to the experimental CT data as a comparison.

Results and Discussion

The articulated shape model captured the segmented training data set with a mean RMS error of 1.92 mm ± 0.27, with the largest error occurring at the distal articulating surface. An example of this is shown in dataset 5 (Figure 1). This indicated the shape model's poor ability to predict this individual's bone length. A larger training dataset is currently being included, and a cross-validation analysis will be performed on the final model to evaluate model performance. The mean pose error to the unseen dataset was 3.7° ± 5.0° (Table 1). Compared to the pose of the linear scaled OpenSim model [2], the articulated shape model had lower errors, which could be attributed to the combination of morphological variation and differences in calculating the supination-pronation. Further analysis will reveal these independent differences.

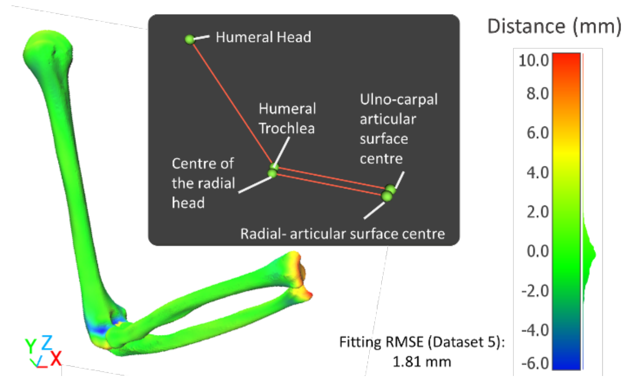

Figure 1: Distance (mm) between the CT segmented mesh and fitted shape model for Dataset 5. Inset shows 4-bar kinematic chain.

Table 1: Absolute pose fitting error (in degrees) between the New Model and OpenSim model [2] compared to segmented CT data.

Dataset	1	2	3	4	5	Mean (SD)
New Model	0.52	2.01	3.40	0.04	12.5	3.69 (±5.08)
OpenSim [2]	13.7	4.73	2.43	24.2	10.0	6.35 (±8.60)

Conclusions

We have developed an articulated shape model of the humerus, radius and ulna, using a 4-bar linkage to represent forearm supination-pronation. This model removes the need to describe the rotation axis of the forearm and enables accurate prediction of bone morphology and position. Increasing the training dataset will enable predictions of a larger cohort of individuals, including those with pathology.

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References

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