ADVANCES IN UPPER LIMB MODELLING: IMPLICATIONS FOR TESTING CRICKET BOWLING ACTIONS

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This study investigates the effect of glenohumeral joint centre (GHJ) mislocation on elbow flexion-extension kinematics and outlines the development and validation of functionally based 2DoF upper-limb model that is proposed to more accurately measure elbow flexion-extension angles. The findings suggest that a new regression equation be adopted to calculate the GHJ centre used in the definition of the upper arm anatomical coordinate system. The research also proposes that a 2DoF mean finite helical axis model (HAM) be used to describe upper limb motion as it more accurately measures flexion-extension angles when compared with traditional anatomically based models as validated against a mechanical arm moving through known ranges and angles. The HAM model also eliminated cross-talk on elbow flexion-extension kinematics.

KEY WORDS: glenohumeral joint location, elbow angle, cricket bowling.

INTRODUCTION:

The calculation of an elbow joint angle requires anatomical coordinate systems (ACS) to be established at the forearm and humerus. This commonly involves a tester accurately identifying relevant anatomical landmarks (AL's) assumed to represent joint centres and axes of rotation. However, it is well documented that the imprecise location of ALs can lead to mislocation of the ACS, propagating to downstream errors in joint kinematics (Della Croce et al., 1999). In addition, recent authors (King & Yeadon, 2006; Gurney & Kersting, 2006) have questioned current methods of calculating elbow angles in cricket bowlers suggesting that alternative modelling methods should be investigated if false positives or negatives are to be avoided.

The purpose of this study was twofold. First, to determine the three dimensional (3D) accuracy of four methods in calculating the centre of the glenohumeral joint (GHJ) compared to the known location determined via magnetic resonance imaging (MRI). As this landmark is crucial in the definition of the humeral ACS, the effect of any 3D error in determining its location on the elbow flexion-extension angle during bowling was examined. The second purpose of this paper was to develop and validate a functionally based 2 DoF upper-limb model (HAM) to measure rotations of the forearm and to compare this model to one that is anatomically based (ANAT)following Cardan ZXY angle decomposition methods. It was hypothesised that the upper limb model that employed a mean finite helical axis method to define the flexion extension axis of the forearm, combined with a 2 degree of freedom (2DoF) upper limb segment that shared a common flexion axis between the humerus and forearm would eliminate kinematic cross-talk commonly observed in traditional elbow joint modelling methods. In vivo comparisons of the modelling methods were also obtained from cricket bowling actions.

METHODS:

Two individual data sets were collected and processed to answer the research questions outlined above.

Study A - Locating the GHJ: Twenty healthy males were recruited and underwent a MRI scan directly followed by 3D motion analysis on the same day. A custom marker set; with the markers covered in retro reflective tape and filled with oil to permit visibility in both imaging systems was affixed to the participant's dominant shoulder. All subjects lay supine with their upper arm secured to their torso, level with their midline in both imaging systems, so that the GHJ centre relative to skin based markers could be reconstructed in the MRI and the motion

capture trial. The location of the markers and the GHJ in each MRI were determined using medical imaging software, Mimics (Materialise Software Inc.). The digitising process included manual segmentation of the humeral head and all the markers in each transverse plane slice in which these appeared (Figure 1a). The border of each object was then defined using B-spline polynomial contour lines, which were subsequently used to create 3D spheres representing the humeral head and each marker (Figure 1b). Using a custom Matlab program (Mathsworks Inc.), the 3D locations of the GHJ and markers enabled the transformation of the MRI GHJ into a coordinate system created using a rigid triad of markers affixed to the acromion. A twelve camera Vicon MX motion analysis system operating at 250Hz was used to collect the 3D motion analysis data.



Figure 1: (a) Transverse plane slice of a subject MRI, including a portion of the segmented humeral head, and the anterior shoulder & clavicle markers; (b) Processed MRI demonstrating 3D reconstruction of the humeral head and marker representative spheres.

The accuracy of four methods used to calculate the GHJ location from external markers were examined. Two calculations methods were adopted from the literature (Schmidt et al., 1999; Lloyd et al., 2000); the third method was Vicon's generic calculation method (Plug-In-Gait) and lastly a customised regression equation for calculating the GHJ centre location from the MRI data was developed and assessed. For the regression method, the GHJ location was determined from the MRI images of 15 participants and used in a stepwise linear regression analysis (SPSS) to create three regression models to estimate the *x*, *y* and *z* coordinates of the GHJ. Five possible independent variables were employed: 1) subject height, 2) subject mass, 3) the 3D distance between the sternal notch and the 7th cervical vertebrae (SN-C7) 4) the 3D distance between the SN and C7 markers and (ACRLR-CN) and 5) the 3D distance between a marker placed on the anterior aspect of the shoulder and one placed on the posterior aspect of the shoulder.

First, the difference in the MRI digitised GHJ locations and those predicted by the new predictive regression model and the three established methods was calculated using the data from the 20 participants. In this, the root mean square errors (RMSE), average x, y, and z coordinate errors, and the euclidean distances from each method were calculated. The data from a subset of 15 subjects was then used to create a new predictive regression equation to determine the centre of the GHJ. The data from all 20 subjects was then used to test the predictions from the new regression model and previously published predictive methods. The applied relevance of GHJ centre mislocation was further examined by moving the reconstructed GHJ position by the error offsets recorded for each method and then determining its effect on the modelled and output elbow flexion-extension angle.

Study B – Elbow Angle Determination: The second study validated and compared kinematic data obtained from two models (ANAT & HAM) that differed in both ACS definition and joint angle decomposition methods. A mechanical linkage was constructed that represented an upper arm and in addition ten male cricketers were recruited to perform bowling tasks. The mechanical arm comprised an elbow allowing the forearm 3 DoFs;

flexion-extension (F-E), pronation-supination (P-S) and adduction-abduction (AB-AD). These three axes had known locations and orientation, bisecting each other at a known location, and could be fixed in certain postures. The forearm could be flexed through a range of 135°, depending on amount of set abduction. Two methods of forearm abduction (imposed joint configurations) were employed; 1) abduct the forearm such that the F-E axis of the elbow remained in the same orientation, and 2) allow the F-E axis to be completely abducted by 10° or 20°, thus giving the F-E axis an abduction (frontal plane) tilt (see Table 2). The same marker set was used for both the mechanical arm and human trials. Functional calibration trials were performed to establish the elbow F-E axis, whereby the forearm was moved through the full F-E range of motion five times. For the mechanical arm, motion data was collected to establish the effect of constant static joint configurations on recorded joint kinematics (i.e an imposed forearm abduction angle). In these, the mechanical elbow was fixed in varying amounts of abduction while a series of different F-E tasks were performed. For the human trials, 5 grade (community) level male cricketers aged between 8-27yrs were recruited. Each bowled 6 trials in an indoor laboratory that allowed a full run up and pitch length. All mechanical arm and human trials were recorded at 250Hz using a 12 camera Vicon MX motion analysis system. All marker movement data were smoothed using a quintic spline (Woltring, 1986), with a MSE of 15 applied to the mechanical arm data and 20 MSE for the human data. For both mechanical arm and human HAM models the elbow F-E axis was determined from the F-E functional movement calibration trials. A custom MATLAB program calculated the F-E FHA's for every change in angle of 25° based on the protocols established by Besier et al. (2003).

RESULTS & DISCUSSION:

Study A - Locating the GHJ: Three final predictive regression equations were established from using the known MRI established GHJ location from 15 of the 20 subjects:

- $x = 96.2 0.302 \times (SN-C7) 0.364 \times height + 0.385 \times mass$
- $y = -66.32 + 0.309 \times (SN-C7) 0.432 \times mass$
- z = 66.468 0.531 × (AcrLR-CN) + 0.571 × mass

These regressions were then cross validated on the remaining 5 subjects. The three dimensional *x*, *y*, *z* error of four calculation methods compared to the known centre of the GHJ as determined by MRI are presented in Table 1. Schmidt's and colleagues method of dropping 7cm vertical offset from the acromio-clavicular (AC) joint to estimate GHJ location resulted in the largest errors across the three planes of 11, 23 and 38mm respectively. This was closely followed by the Plug-In-Gait method of using half the 2D shoulder width measured at the level of the GHJ as a vertical scale from the AC joint to the GHJ position recorded errors of 11, 14 and 38mm. Lloyd and colleagues (2000) method of calculating the GHJ location as the intersection of a vector between markers positioned on the anterior and posterior surface of the shoulder (in line with the visually estimated level of the GHJ) and a perpendicular vector dropped from the centre of the acromial lateral ridge resulted in slightly lower errors of 14, 7 and 10mm. Compared to the vertical drop methods, the developed regression equation had significantly smaller errors of 4, 4 and 6mm. In addition the vertical drop methods consistently estimated the GHJ more medial (24mm ±8) and anterior (11mm ±5) than the known MRI GHJ location.

GHJ location Method	Absolute Error (<i>mm</i>)			
n=20	X(AP)	Y(SP-INF)	z(ML)	
Plug-in-Gait	11	14	38	
Schmidt et al. (1999)	11	23	38	
Lloyd et al. (2000)	14	7	10	
UWA Regression (n=5)	4	4	6	

 Table 1: Average absolute error in GHJ location from known MRI position

The effect of applying the GHJ location errors (from the known GHJ location), on the resulting elbow F-E angle using the same model, during cricket bowling (n=5) is presented in Figure 2. As can be seen in the graph, the GHJ location errors recorded for the UWA regression and Lloyd et al. (2000) methods resulted in a small non-significant standardised offset shift in the elbow flexion extension angle. The result of significantly larger errors in GHJ location of the Plug-In-Gait and Schmidt. et al. (1999) methods on elbow flexion-extension were significantly greater and resulted in a change in the polarity of the flexion-extension angle prior to ball release.

Study B – Elbow Angle Determination:

The degree of correlation (cross talk) between the F-E and AB-AD angle, for 8 different elbow joint configurations, when applying the ANAT or HAM models are shown in Table 2. As hypothesised the ANAT model displayed high levels of cross talk (0.67±0.51) in all joint configuration conditions. Interestingly, this finding was especially evident in all joint configuration conditions where the F-E Axis angle was tilted yet no corresponding tilt in the actual forearm abduction angle was observed (r=0.99). As expected when using the 2 DoF HAM model negligible levels of F-E and AB-AD angle cross talk was observed (0.00±0.02).





	Tested	Forearm Abd	F-E Axis	ANAT Model	HAM Model
	Motion	ion Angle (°) Abd Angle (°)		F-E & Ad-Ab cross talk (r)	
nical	Flx-Ext	0	0	0.90	-0.02
	Flx-Ext	10	0	0.81	0.00
har Arm	Flx-Ext	20	0	-0.49	-0.01
Mec	Flx-Ext	0	10	0.99	0.00
	Flx-Ext	0	20	0.99	0.00
			Mean (SD)	0.67 (0.51)	0.00 (0.02)

Table 2: Cross talk measured by the ANAT and HAM models for the various mechanical arm trials.

The effect of applying the HAM model in a cricket setting can be seen in Table 3 where three different models were applied to the same bowling data and elbow F-E angles derived. Surprisingly, the Plug-In-Gait model, produced the most repeatable data as determined by lower standard deviations. However, Plug-In-Gait shows the bowler in 19.3° of flexion at upper arm horizontal (UAH) and 18.5° at ball release suggesting that while repeatable, data may not be accurate. Conversely, the ANAT and HAM models record the bowler in hyperextension at the same time points. Given that the cricket law does not include hyperextension in the total elbow joint excursion range this finding is significant. An adjusted extension range, removing hyperextension from the data shows lower ranges of extension levels than initially recorded.

CONCLUSION:

The research shows that the developed GHJ regression equation is a more accurate method of locating the GHJ centre than traditional methods and that the HAM model is capable of accurately measuring F-E when validated with a mechanical arm of known ranges and angles. Furthermore, the HAM model eliminated cross-talk by sharing a common flexion axis

between the humerus and forearm. The improved accuracy of these methods suggests both should be considered for use in the testing of illegal bowling actions in cricket where minimising error is paramount.

	Model			
Elbow Angle (*)	Plug-In-Gait	ANAT	HAM	
Upper Arm Horizontal	19.3 (±3.2)*	1.1 <i>(</i> ±8 <i>.4</i>)	-4.5 (±8.0)	
BR	18.5 (±1.8)*	-1.1 (±8.9)	-6.6 (±8.2)	
Max Ext to BR	18.5 (±1.8)*	-1.1 (±8.9)	-6.6 (±8.2)	
Ext Range	0.8 (±1.7)	2.1 (±2.7)	2.1 (±2.8)	
Adjusted Ext Range	0.8 (±1.7)	0.7 (±0.9)	0.1 (±0.1)	

Table 3: Elbow F-E angle variables across 3 modelling methods.

* sig dif to ANAT and HAM models (p<0.01)

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