

BIOMECHANICAL MODELLING OF HUMAN MOVEMENTS: EFFECTS OF JOINT CONSTRAINTS AND MODEL COMPLEXITY

^{1*}Lei Ren, ¹Amaraporn Boonpratotong, ²Ruth E Mayagoitia

¹School of Physical Sciences and Engineering, King's College London, London, WC2R 2LS, U.K.

Division of Applied Biomedical Research, King's College London, London, SE1 1UL, U.K.

*email: lei.ren@kcl.ac.uk

INTRODUCTION

Mathematical models of the human musculoskeletal system are of great value in biomechanics, which provide valuable tools to investigate joint kinetics, muscle loadings and neuromotor control strategies involved in various motor activities. However, as with any mathematical model of a complex biophysical system, the major barriers in the routine use of these models are their consistency and biofidelity to the real biophysical system [1]. Most previous studies have been mainly focused on the sensitivity of the dynamic models to various model parameters [4, 5]. Few studies have been conducted to investigate the biofidelity of the biomechanical human models.

The objective of this study is to use a three-dimensional (3D) whole-body model to investigate how modelling methods and model complexity would affect the model biofidelity. Experimental measurements were conducted to support and validate the modelling work using a specially designed infrared marker system. The model biofidelity was quantified by measuring the difference between the inverse dynamics prediction of the ground reaction forces and moments with the simultaneously recorded force transducer data. Further analysis was conducted to investigate the effects of joint constraints and system topology on the model prediction accuracy.

METHODS

A 3D whole-body model with 18 segments and 37 degrees of freedom was constructed by simplifying all the major joints as ideal hinge or ball-and-socket joints [2] (Figure 1). Experimental measurements were conducted to support and validate the modelling. Three subjects were instructed to walk barefoot along a walkway to perform walking, running, maximum vertical and long jumping motions. An eight-camera motion analysis system (Qualisys, Sweden; 150 Hz) was used to capture the 3D motion data. A six-force-plate array (Kistler, Switzerland; 1000 Hz) were used to record simultaneous ground reaction data.

A specially designed infrared marker cluster system was used to capture the whole body motions [3] (Figure 1). The torso was considered as a four-segment system according to the different functional spinal regions. All the anatomical joint positions and orientations were determined using in-vivo functional methods, and were then imposed into the whole-body model as joint constraints. Three different methods were used to reconstruct the segmental motions of the human body: an anatomically based calibration method CAST [6] without joint constraints, using markers on anatomical landmarks with joint constraints and using plate marker clusters with joint constraints. The joint kinematics was derived using a least squares optimisation process

similar to [2, 4]. The model biofidelity was derived by calculating the RMS errors between predicted ground reactions with recorded force plate data. The effects of modelling methods and model complexity were investigated by applying different kinematic methods and varying system topology from simple to complex configuration.

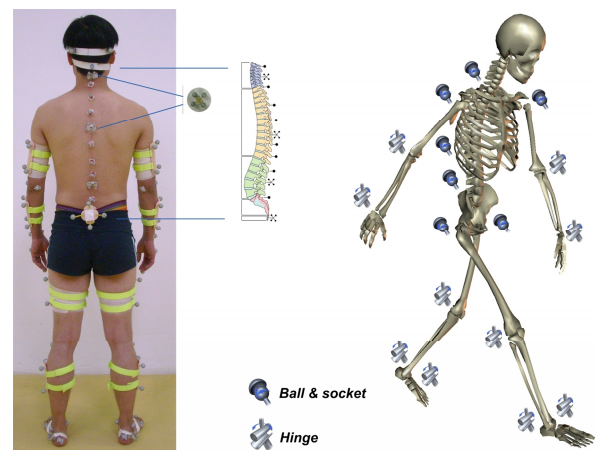


Figure 1: The infrared marker system to capture whole body motion and the constructed whole-body model with 18 segments and 37 degrees of freedom

RESULTS AND DISCUSSION

Our preliminary results show that the ground reaction prediction is slightly improved by imposing joint constraints especially for out-of-plane components. When combined with joint constraints, the plate markers outperform the markers on anatomical landmarks for most of the cases. The changes on the upper body complexity in the model have moderate effects on prediction results. However, too simple upper body model results in poor predictions especially the anterior-posterior ground reaction force.

A thoroughly validated whole-body human model can be used in a wide range of fields to investigate musculoskeletal system performance using both inverse and forward dynamics. This becomes of greater interest because of the availability of inertial measurement units capable of estimating segment motions outside the laboratory [3].

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