



A new shoulder model with a biologically inspired glenohumeral joint



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ABSTRACT

Kinematically unconstrained biomechanical models of the glenohumeral (GH) joint are needed to study the GH joint function, especially the mechanisms of joint stability. The purpose of this study is to develop a large-scale multibody model of the upper limb that simulates the 6 degrees of freedom (DOF) of the GH joint and to propose a novel inverse dynamics procedure that allows the evaluation of not only the muscle and joint reaction forces of the upper limb but also the GH joint translations. The biomechanical model developed is composed of 7 rigid bodies, constrained by 6 anatomical joints, and acted upon by 21 muscles. The GH joint is described as a spherical joint with clearance. Assuming that the GH joint translates according to the muscle load distribution, the redundant muscle load sharing problem is formulated considering as design variables the 3 translational coordinates associated with the GH joint translations, the joint reaction forces associated with the remaining kinematic constraints, and the muscle activations. For the abduction motion in the frontal plane analysed, the muscle and joint reaction forces estimated by the new biomechanical model proposed are similar to those estimated by a model in which the GH joint is modeled as an ideal spherical joint. Even though this result supports the assumption of an ideal GH joint to study the muscle load sharing problem, only a 6 DOF model of the GH joint, as the one proposed here, provides information regarding the joint translations. In this study, the biomechanical model developed predicts an initial upward and posterior migration of the humeral head, followed by an inferior and anterior movement, which is in good agreement with the literature.

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1. Introduction

Knowledge of muscle and joint reaction forces can enhance clinical decision making in neurological and orthopaedic problems [1–3]. Recently, instrumented prostheses have been developed to estimate in-vivo joint reaction forces [4,5], but the estimation of individual muscle forces is still an open issue [3]. Therefore, detailed biomechanical models provide, so far, the only feasible method to estimate both muscle and joint reaction forces [1,2].

Several complex musculoskeletal models of the upper limb have been developed to study the glenohumeral (GH) joint [6–9]. The GH joint, also known as shoulder joint, is the most mobile joint in the human body, at the cost of intrinsic stability, which is primarily ensured by the coordinated action of the rotator cuff muscles [10]. Considering that, on average, the articular surfaces of the GH joint are almost spherical and congruent [11,12], most biomechanical models assume the GH joint as an ideal spherical joint, with

no relative translation. The GH translations are generally neglected because the GH joint position is very difficult to measure in-vivo with conventional motion measurement systems [3].

Cadaver and in-vivo studies validate the assumption of an ideal spherical joint, given the limited translation ranges of the GH joint reported [13–16], but individual variability can and do affect the joint behavior [17]. Note that many shoulder joint pathologies are assumed to be associated with inadequate control of the joint translations [14]. The natural translations of the humeral head are therefore a key factor in the study of the GH joint function, especially of the joint stability [18–20], and their relevance becomes even more crucial in the analysis of less conforming articular prostheses, designed for the replacement of the GH joint, for which joint instability represents a serious complication [21,22].

Terrier et al. [19,20], Favre et al. [10], and Sins et al. [22] are the only researchers proposing musculoskeletal models that simulate the humeral translations of the GH joint. Both Terrier et al. [19] and Favre et al. [10] developed 3D finite element models with 6 degrees of freedom (DOF) for the GH joint. However, because their models are limited to the GH joint only, they do not take into account the effect of adjacent musculoskeletal structures. Furthermore, none of the models proposed consider the dynamic

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effects of motion. The finite element model developed by Terrier et al. [19,20] has been applied to study not only the native GH joint, but also the prosthetic GH joint resulting from an anatomical total shoulder arthroplasty (aTSA) [23]. Considering the large-scale musculoskeletal model of the AnyBody Modeling System, Sins et al. [22] introduced the simulation of the GH translations into the model using the force-dependent kinematics approach, proposed by Andersen et al. [24], to study the joint in an aTSA. Despite the model proposed by Sins et al. [22] not being limited to the GH joint, as the models of Terrier et al. [19,20] and Favre et al. [10], the GH joint is only modelled as a 5 DOF joint, which may impair the computation of contact between the articular surfaces.

The purpose of this study is to develop a large-scale multibody model of the upper limb with a 6 DOF GH joint and to propose a novel inverse dynamics procedure able to compute the muscle and joint reaction forces of the upper limb as well as the GH joint translations. The biomechanical model developed here is based on that of Quental et al. [9,25], but the contact between the humeral head and the glenoid cavity is described by a mathematical model of a spherical joint with clearance [26,27]. The customization of the features of the spherical joint with clearance allows the simulation of different geometries of the GH joint, including those after an aTSA. The proposed model is used to compute the muscle and joint reaction forces, and the position of the humeral head during an abduction motion in the frontal plane, acquired at the Lisbon Biomechanics Laboratory (LBL). The GH translations obtained here are compared to those reported in the literature, and the muscle and joint reaction forces are compared to those estimated by the original model of Quental et al. [9,25], which considers the GH joint as an ideal spherical joint.

2. Methods

2.1. Upper limb model with a biologically inspired glenohumeral joint

The biomechanical model of the upper limb developed here is based on the multibody model presented by Quental et al. [9,25]. The skeletal system is composed of the thorax, rib cage, clavicle, scapula, humerus, ulna, and radius. The thorax and rib cage are considered to be static. The clavicle and scapula are constrained by the sternoclavicular and acromioclavicular joints, which are modelled as 3 DOF spherical joints, and by two holonomic constraints that force the scapula to glide over the thorax. The ulna and radius are constrained by 1 DOF hinge joints at the humeroulnar and radioulnar joints, respectively. The GH joint, which is originally described by a 3 DOF spherical joint [9], is modeled here as a 6 DOF spherical joint with clearance [26,27]. Regardless of the fact that ovoids may reproduce better the humeral head geometry [28], the shape of the humeral articular surface is described by a sphere with a curvature radius of 25 mm, located at the native GH joint centre, based on Garner and Pandy [29]. The shape of the scapular articular surface is reproduced by fitting a sphere to the 3D geometry of the glenoid cavity, generated from the visible human male dataset [30]. Because the curvature radius of the glenoid is particularly sensitive to the thickness of its articular cartilage [12], and because its accurate segmentation from the visible human male dataset is complex, especially toward the periphery, a radial clearance of 1.7 mm is assumed [17].

Instead of enforcing kinematic constraints between the humerus and scapula, the mathematical formulation of the spherical joint with clearance penalizes the relative displacement between these by contact forces. In this work, the elastic force developed in the contact between the humeral head and the glenoid cavity is described by a Hertz contact force model written

as:

$$\begin{cases} F_N = 0, & \delta < 0 \\ F_N = K\delta^n, & \delta > 0 \end{cases} \quad (1)$$

where K is the generalized stiffness constant and δ is the relative normal deformation between the articular surfaces. The stiffness K and the exponent n are set to 500 N/mm^{3/2} and 1.5, respectively [31]. Considering c the radial clearance, and \mathbf{r}_H and \mathbf{r}_S the global coordinates of the centres of the humeral and scapular articular surfaces, respectively, as illustrated in Fig. 1, the relative normal deformation δ is given by:

$$\delta = \sqrt{(\mathbf{r}_H - \mathbf{r}_S)^T (\mathbf{r}_H - \mathbf{r}_S)} - c. \quad (2)$$

A more detailed description of the spherical joint with clearance is presented in Flores and Lankarani [27].

The skeletal model is supported by 21 muscles, described by 69 muscle bundles [25], which are outlined in Fig. 2. The muscle paths are described as a concatenation of straight- and curved-line segments using via points and 3D geometric shapes such as spheres and cylinders [9]. A Hill-type muscle model consisting of a contractile element (CE) and a passive elastic element (PE) is considered to simulate the dynamics of muscle contraction [32]. The force produced by a muscle m is expressed as:

$$\begin{cases} F^m = F_{CE}^m(L^m, \dot{L}^m, a^m) + F_{PE}^m(L^m) \\ F_{CE}^m = \frac{F_L(L^m)F_{\dot{L}}(\dot{L}^m)}{F_0^m} a^m \end{cases} \quad (3)$$

where L^m and \dot{L}^m represent the length and rate of length change, respectively, F_0^m represents the maximum isometric force, and a^m represents the muscle activation of muscle m . The force-length relationship F_L and force-velocity relationship $F_{\dot{L}}$ are taken from Silva and Ambrósio [32]. Considering the physiological data for the muscle to be known, and obtaining all kinematic quantities, i.e., muscle length and rate of length change, directly from the kinematic data, the only unknown in Eq. (3) is the muscle activation a^m .

2.2. Inverse dynamics optimization

The recommendations from the International Society of Biomechanics [33] were used to acquire an unloaded motion of abduction in the frontal plane, from 13° to 109°, for a male subject (25 years, 179 cm, 75 kg). At the LBL, the subject was instructed to start with the arm at the side, and to reach the maximum arm elevation without moving the trunk. The methodology proposed by Senk and Chèze [34] was used to dynamically track the scapula. On the basis of the data of the *Art. Acromioclaviculare* and *Angulus Acromialis* landmarks of the scapula, and of an additional surface marker placed onto the scapular spine, an optimization procedure was applied to recalculate the positions of the *Angulus Inferior* and *Trigonum Spinae* landmarks. For the definition of the humerus orientation, the GH joint centre was estimated using the algorithm of Gamage and Lasenby [35]. Note that, as a first step, the position, velocity, and acceleration vectors of the upper limb bodies were computed assuming an ideal spherical GH joint. The axial orientation of the clavicle was estimated by minimizing the AC joint rotations [36].

Considering that the kinematic data is known, the only unknowns in a biomechanical model composed of ideal joints are the internal forces, i.e., the muscle and joint reaction forces, which are typically defined as design variables in the context of an optimal problem. In addition to these, the unknowns of the biomechanical model presented here also comprise the translations of the GH joint that result from its more realistic model. Note that the GH joint translations cannot be measured experimentally because

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