

A global optimization method for prediction of muscle forces of human musculoskeletal system

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Abstract

Inverse dynamic optimization is a popular method for predicting muscle and joint reaction forces within human musculoskeletal joints. However, the traditional formulation of the optimization method does not include the joint reaction moment in the moment equilibrium equation, potentially violating the equilibrium conditions of the joint. Consequently, the predicted muscle and joint reaction forces are coordinate system-dependent. This paper presents an improved optimization method for the prediction of muscle forces and joint reaction forces. In this method, the location of the rotation center of the joint is used as an optimization variable, and the moment equilibrium equation is formulated with respect to the joint rotation center to represent an accurate moment constraint condition. The predicted muscle and joint reaction forces are independent of the joint coordinate system. The new optimization method was used to predict muscle forces of an elbow joint. The results demonstrated that the joint rotation center location varied with applied loading conditions. The predicted muscle and joint reaction forces were different from those predicted by using the traditional optimization method. The results further demonstrated that the improved optimization method converged to a minimum for the objective function that is smaller than that reached by using the traditional optimization method. Therefore, the joint rotation center location should be involved as a variable in an inverse dynamic optimization method for predicting muscle and joint reaction forces within human musculoskeletal joints.

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1. Introduction

Quantitative data of *in vivo* muscle forces, joint reaction forces and moments have been pursued for decades (Pedotti et al., 1978; An et al., 1981, 1984; Crowninshield and Brand, 1981; Kaufman et al., 1991; Happee, 1994; Glitsch and Baumann, 1997; Li et al., 1999; Chadwick and Nicol, 2000). A human musculoskeletal joint is an indeterminate biomechanical system, where the number of unknown forces and moments generated by the muscles as well as the joint reaction

forces and moments outnumber the equilibrium equations of the joint system. A unique solution for these unknowns cannot be obtained. An inverse dynamic optimization procedure has been widely used to predict the unknown individual muscle forces and joint reaction forces.

Recently, it has been demonstrated that the forces predicted using a traditional inverse dynamic optimization method are coordinate system-dependent (Pierce and Li, 2004). The predicted muscle forces and joint reaction forces vary with the location of the origin of the joint coordinate system. Furthermore, it was shown that the objective function usually did not reach an actual minimum through the optimization procedure. This was attributed to not maintaining the joint moment

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equilibrium. In general, the joint reaction moment was set to zero in the moment constraint condition in traditional optimization methods (Raikova, 1996; Glitsch and Baumann, 1997; Li et al., 1998, 1999; Chadwick and Nicol, 2000). Such treatment of joint reaction moments is similar to modeling the joint as a frictionless pure rotation joint with its center located at the origin of the coordinate system (Li et al., 1999; Pierce and Li, 2004). This simplification of the joint presents an additional constraint to the optimization procedure, i.e. $\bar{M}^{\text{Joint}} = 0$. However, none of the optimization methods considered the effect of this constraint on the optimization procedure. Therefore, if the origin of the coordinate system is not the true rotation center, the actual joint reaction moment may not be zero, and the moment equilibrium of the joint is thus violated. An inaccurate selection of the joint center, where the joint reaction moment is actually not zero, may not result in an actual minimum for the objective function and may lead to unrealistic muscle force predictions using the optimization procedure (Pierce and Li, 2004).

The objective of this study was to develop a global optimization procedure that determines the rotation center of the joint and constructs a moment equilibrium equation with respect to the rotation center. A human elbow joint was used as a joint model in this study. A three-dimensional (3D) static optimization procedure, utilizing a cubic muscle stress criterion, was formulated to estimate forearm muscle forces and joint reaction forces in the elbow joint during an isometric flexion activity. The rotation center location was used as an optimization variable in the optimization procedure.

2. Methods

2.1. Traditional optimization method for prediction of muscle forces

A 3D anatomic model has been developed previously using a cadaveric human forearm specimen (female, 62 years old) (Pierce and Li, 2004). The model included bony geometry, insertion and origin areas of major muscles, and the action lines of the muscles (Fig. 1). The bony model of the elbow joint consisted of the humerus, the radius and ulna. The humerus was fixed in space. The radius and ulna were treated as one rigid body in quasi-static equilibrium. A joint coordinate system was created to describe the position and orientation of the muscles in the forearm system (Fig. 1). The geometric center of the trochlea was chosen as the elbow joint center (Morrey and Chao, 1976; An et al., 1981) and was used as the origin of the coordinate system. The elbow flexion–extension axis (the y -axis) was found by passing a line through the center of three concentric circles fit to

the bottoms of the trochlear sulcus, capitulum, and medial facet of the trochlea (London, 1981; Bottlang et al., 2000; Murray et al., 2002). The z -axis was defined as being perpendicular to the y -axis, passing proximally along the longitudinal axis of the humerus. The x -axis was determined by the cross-product of the y - and z -axes.

Six muscles were simulated in the forearm model: the biceps brachii (BIC), brachialis (BRA), brachioradialis (BRD), pronator teres (PRT), anconeus (ANC), and triceps brachii (TRI) (An et al., 1981; Raikova, 1996; Bernstein et al., 2000). The joint model was used to simulate the equilibrium state of the elbow at 90° of flexion in the neutral forearm position under the muscle and external loads (Fig. 1). Muscle forces were applied to the bones at their respective points of insertion and along the action lines of the muscles. The action lines of the BRD, PRT, and ANC muscles were represented as vectors along the straight line connecting their respective origin and insertion points. The remaining muscles were represented by digitized lines of action, which were obtained by digitizing, or tracing, a line about 5 cm in length along the direction of the muscle orientation in the cadaver specimen (Pierce and Li, 2004).

Under equilibrium conditions, the external force system (including applied moments and forces and the weight of the forearm and hand) was balanced by the internal force system (including muscle forces, joint reaction forces, and moments). The joint reaction force, composed of the joint articular contact (humeroradial and humeroulnar) and ligamentous (medial and lateral collateral ligaments) forces, acted at the chosen joint center with a reaction moment (Fig. 1b). A free-body analysis of the elbow joint yielded the following equilibrium equations (Pierce and Li, 2004),

$$\begin{aligned} \text{(a)} \quad & \sum_{i=1}^6 f_i^M \bar{e}_i + \bar{F}^{\text{Joint}} = \bar{F}^{\text{int}}, \\ \text{(b)} \quad & \sum_{i=1}^6 f_i^M (\bar{r}_i \times \bar{e}_i) + \bar{M}^{\text{Joint}} = \bar{M}^{\text{int}}, \end{aligned} \quad (1)$$

where f_i^M represents the magnitude and \bar{e}_i represents the unit directional vector of the i th muscle force; \bar{r}_i is the vector pointing from the origin of the coordinate system to the insertion centroid of i th muscle; \bar{F}^{Joint} and \bar{M}^{Joint} are the joint reaction forces and moments; and \bar{F}^{int} and \bar{M}^{int} are the intersegmental forces and moments calculated from the external loads. The equilibrium equations shown above have 12 unknowns: 6 muscle force magnitudes, 3 components of the joint reaction force, and 3 components of the joint reaction moment, thereby representing a statically indeterminate biomechanical system. It should be noted that the above equilibrium equations are coordinate system independent. Location

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