Pergamon

J. Biomechanics, Vol. 28, No. 8, pp. 999–1005, 1995

0021–9290/95 $9.50 + .00

0021–9290(94)00145-6

TECHNICAL NOTE

A COMPUTATIONALLY EFFICIENT METHOD FOR SOLVING THE REDUNDANT PROBLEM IN BIOMECHANICS

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Abstract—Determining the optimal set of musculotendon forces with which to produce a forward dynamic simulation of movement typically involves a huge investment of time and computational resources. A new, computationally efficient method is proposed that simultaneously achieves the desired trajectory and the dynamically optimized set of muscle stresses, and hence forces, according to the maximal endurance criterion function of Crowninshield and Brand (1981). Muscle-induced accelerations of the system resulting from unit stress contractions of individual muscles are superposed via the new pseudoinverse method to yield the desired motion trajectory. The method is tested on a control problem involving a five degree-of-freedom (DOF), 30 muscle, upper extremity model, which incorporates a dual rigid-body forearm to represent pronation and supination more adequately. The pseudoinverse method delivered the desired motion to within 0.25° for each DOF during a three-second simulation. It is anticipated that the methodology can be easily and accurately applied to other highly redundant optimal control problems in biomechanics.

Keywords: Optimization; Gait; Muscle forces.

INTRODUCTION

Mathematical optimization has been utilized as an important tool with which to noninvasively determine the muscular forces involved in creating coordinated multijoint movements. Historically, this problem has been termed 'the redundant problem in biomechanics' (Chao and An, 1978), because apparently many more muscles exist than are needed to actuate movements having many degrees of freedom (DOF). Because of the muscle redundancy, inherent is the presumption that the organism must somehow distribute the forces among muscle set so as to create and control its movement optimally. Both quasistatic optimizations involving inverse dynamic analyses of movement (Chao and Rim, 1973; Hardt, 1978; Olney and Winter, 1985; Patriarco *et al.*, 1981; Pierrynowski and Morrison, 1985; Pedotti *et al.*, 1978; Seireg and Arvikar, 1975; White and Winter, 1993) and dynamic optimizations involving forward dynamic simulations of movement (Bobbert and van Ingen Schenau, 1988; Davy and Audu, 1987; Hatze, 1981; Khang and Zajac, 1989a, b; Pandy and Zajac, 1991; Pandy *et al.*, 1992; Thunissen, 1993; Veltink *et al.*, 1992; Yamaguchi and Zajac, 1990; Yoshihuku and Herzog, 1990) have been performed on a number of movement tasks. The general motivation was to explore mechanical issues pertinent to the redundant problem: the effects of muscle moment arm, strength and the viability of the criterion or cost function used to measure the performance of the particular force distribution.

Several authors have acknowledged the limitations of the inverse dynamic quasistatic methods (Hardt, 1978; Herzog, 1987; Patriarco *et al.*, 1981). One such limitation is the inherent presumption that any muscle considered individually is not unique in its mechanical action, and that a muscle can only act locally as a source of joint torque. Dynamic optimization methods can overcome these limitations, but involve significant investments of time, computational resources, and effort to obtain viable solutions for all but the simplest (few DOF and/or few muscles) forward dynamic simulations of movement (Hatze, 1981; Yamaguchi and Zajac, 1990).

We have developed a new, computationally efficient method of performing dynamic optimizations of movement that is well suited to a subclass of problems involving (i) complex forward dynamic musculoskeletal models, (ii) well-defined desired movement trajectories, and (iii) muscle stress-related cost functions for which the costs are expressible in terms of vector lengths. The *pseudoinverse method* described herein takes advantage of a recently proposed forward dynamic interpretation of muscle function, namely that each muscle has a unique line of action and therefore generates a unique *global* pattern of segmental angular accelerations (Kuo, 1994; Meglan *et al.*, 1991; Yamaguchi and Zajac, 1990; Zajac and Gordon, 1989).

METHODS

The method is illustrated using a musculoskeletal model of the upper extremity (Fig. 1) and the criterion (cost) function C of Crowninshield and Brand (1981),

$$C = \sqrt[p]{\sum_{j=1}^{m}\left(\frac{f_j}{\mathrm{PCSA}_j}\right)^p}, \qquad (1)$$

Received in final form 28 *September* 1994.

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which empirically relates the sum of muscle stresses raised to the pth power to the endurance time of a task. In the equation, f_j represents the force in a particular musculotendon actuator, PCSA_j is the physiological cross-sectional area of the muscle j, and m is the number of muscles.

The m muscles, of course, must exert only tensile forces at their endpoints on the skeletal system having n ($n < m$) DOF. The n equations governing the resulting motions at any instant of time t can be written in matrix–vector form as:

$$M\ddot{\boldsymbol{\theta}} = \mathbf{T} + \mathbf{V} + \mathbf{G} + \mathbf{E}, \tag{2}$$

where M is the $(n \times n)$ mass matrix describing the mass distribution of the system at time t, $\ddot{\boldsymbol{\theta}}$ $(n \times 1)$ contains the second time derivatives of the n segment or joint angles, $\mathbf{T}$ is the $(n \times 1)$ vector of segmental torques, and $\mathbf{V}$, $\mathbf{G}$, and $\mathbf{E}$ are $(n \times 1)$ vectors describing the moment contributions of the inertial, gravitational, and external forces, respectively. The angular accelerations of the system can be predicted as:

$$\ddot{\boldsymbol{\theta}} = \ddot{\boldsymbol{\theta}}_t + \ddot{\boldsymbol{\theta}}_{\mathrm{vge}}, \tag{3}$$

where the active muscular contributions to the segmental accelerations and the other contributions to $\ddot{\boldsymbol{\theta}}$ may be computed as

$$\ddot{\boldsymbol{\theta}}_t = M^{-1}\mathbf{T}, \tag{4}$$

$$\ddot{\boldsymbol{\theta}}_{\mathrm{vge}} = M^{-1}[\mathbf{V} + \mathbf{G} + \mathbf{E}]. \tag{5}$$

Zajac and Gordon (1989) refer to $\ddot{\boldsymbol{\theta}}_t$ as 'muscle-induced accelerations' because they predict the accelerations that would result from the instantaneous body configuration at time t created by the muscle forces alone.

Assuming that it is possible for the musculature to produce the required segmental accelerations, it is reasonable to assume that muscle-induced accelerations can be superposed to produce a desired trajectory. Given the nature of the redundant problem, there is an infinite number of solutions with which equation (2) can be solved for $\ddot{\boldsymbol{\theta}}$. The effort here is to determine an optimal solution by superposing the accelerations created by known individual muscle contractions without employing computationally intensive gradient searches.

A unit level of stress (i.e. $1.0\ \mathrm{N\,cm^{-2}}$ distributed over the PCSA) is used to compute muscle-induced accelerations for reasons described below. In turn, each of the m muscles is assigned a unit stress, with the other muscles given a stress value of zero. The inverse mass matrix defines a transformation, then, for the vector of segmental accelerations produced by a unit stress in muscle j:

$$\ddot{\boldsymbol{\theta}}_j = M^{-1}\mathbf{t}_j \quad (j = 1, \ldots, m). \tag{6}$$

Vector $\mathbf{t}_j$ $(n \times 1)$ contains the segmental moments created by muscle j. $\mathbf{t}_j$ is necessarily sparse (i.e. mostly zero) in systems with many DOF, because muscle j can only create nonzero moments in segments to which the muscle directly attaches to or spans. Transformation by the nonsparse, configuration-dependent matrix M^{-1}, however, yields the vector $\ddot{\boldsymbol{\theta}}_j$, which except by coincidence, will have n non-negligible, nonzero terms (Yamaguchi and Zajac, 1990). Thus, *system-wide* accelerations are produced by singular muscle contractions.

Assembling the m column vectors $\ddot{\boldsymbol{\theta}}_j (n \times 1)$ into a rectangular matrix A $(n \times m)$ defines a rectangular system of linear equations

$$A\mathbf{x} = \mathbf{b}, \tag{7}$$

where

$$A = \left[[\ddot{\boldsymbol{\theta}}_1]\ [\ddot{\boldsymbol{\theta}}_2]\ [\ddot{\boldsymbol{\theta}}_3] \ldots [\ddot{\boldsymbol{\theta}}_m] \right], \tag{8}$$

$\mathbf{x}$ is the vector of unknown multipliers with which the columns of A are to be superimposed, and $\mathbf{b}$ is the vector of segmental accelerations desired from the muscles at time t to obtain the segmental accelerations $\ddot{\boldsymbol{\theta}}$:

$$\mathbf{b} = \ddot{\boldsymbol{\theta}}_{\mathrm{mus}} = \ddot{\boldsymbol{\theta}} - \ddot{\boldsymbol{\theta}}_{\mathrm{vge}}. \tag{9}$$

The solution $\mathbf{x}$ is achieved through the right pseudoinverse A^+ of matrix A,

$$A\mathbf{x} = (AA^+)\mathbf{b} = \mathbf{b}, \tag{10}$$

$$\mathbf{x} = A^+\mathbf{b}. \tag{11}$$

For row-independent matrices A of rank n the pseudoinverse can be easily found:

$$A^+ = A^{\mathrm{T}}(AA^{\mathrm{T}})^{-1}. \tag{12}$$

Note, that because matrix A is $(n \times m)$ and $n < m$, the inversion $(AA^{\mathrm{T}})^{-1}$ is performed efficiently for a relatively small $(n \times n)$ matrix. Thus, the major computational costs include only an $(n \times n)$ matrix inversion and matrix multiplication.

Via the pseudoinverse technique, the solution $\mathbf{x}$ delivered yields the optimal solution having minimum error $e = |\boldsymbol{\varepsilon}| = |A\mathbf{x} - \mathbf{b}|$, and minimum vector length (Strang, 1976). That is, the solution

$$\mathbf{x} = [\sigma_1 \quad \sigma_2 \quad \sigma_3 \quad \ldots \quad \sigma_m]^{\mathrm{T}} \tag{13}$$

will have minimum magnitude

$$|\mathbf{x}| = \sqrt{\sigma_1^2 + \sigma_2^2 + \sigma_3^2 + \cdots + \sigma_m^2}. \tag{14}$$

Because the elements σ_j ($j = 1,\ldots,m$) represent the multipliers which superpose the acceleration vectors $\ddot{\boldsymbol{\theta}}_j$ created by *unit* muscle stresses, the elements of the vector $\mathbf{x}$ *can be interpreted to be the muscle stresses themselves*. Therefore, $\mathbf{x}$ contains the set of muscle stresses that simultaneously achieves the trajectory and minimizes the sum of the squared muscle stresses. With the criterion function of equation (1) ($p = 2$), $\mathbf{x}$ contains the optimal set of muscle stresses

$$\sigma_j = \left(\frac{f_j}{\mathrm{PCSA}_j}\right) \quad (j = 1, \ldots, m). \tag{15}$$

Because muscles can only exert tensile forces (i.e. positive stresses), the pseudoinverse optimal control method, as applied to biomechanical problems, requires each of the elements of the muscle stress vector $|\mathbf{x}|$ to be positive. But because lower cost solutions are delivered when negative muscular stresses are employed, some iteration is required to guarantee that the solutions are physically realistic. The elements in $\mathbf{x}$ are searched at each time instant to find those which had values less than a negligible negative value ξ (e.g. $\xi = -0.01$). The muscle k having the largest negative stress is identified, and its corresponding column (i.e. column k) in the A matrix is then divided by a large positive number Z (e.g. $Z = 1000$) in order to essentially eliminate that muscle from consideration without reducing the rank of A. For the algorithm to utilize that 'pushing' muscle thereafter would require it to assign an unreasonably large stress (e.g. Z times its former value), which would adversely affect the value of the criterion function. The pseudoinverse algorithm is then repeated and rechecked until all the negative stresses in $\mathbf{x}$ are serially eliminated. A similar iterative algorithm is used to eliminate solutions requiring greater strength (stress) than a given muscle can deliver at a particular contraction velocity.

Given the $2n$ desired trajectories ($\boldsymbol{\theta}$, $\dot{\boldsymbol{\theta}}$) as a function of time, the pseudoinverse algorithm (with iterative postprocessing) allows the m optimal muscle stresses to be obtained in a single multi-input, multi-output (MIMO) operation. If the muscle activations are desired, it is relatively simple to determine the activations by including the known musculotendon force, length, and velocity histories on a muscle-by-muscle (single-input, single-output or SISO) basis.

The above approach was used to calculate the muscle stresses in a dynamic three-dimensional simulation of upper

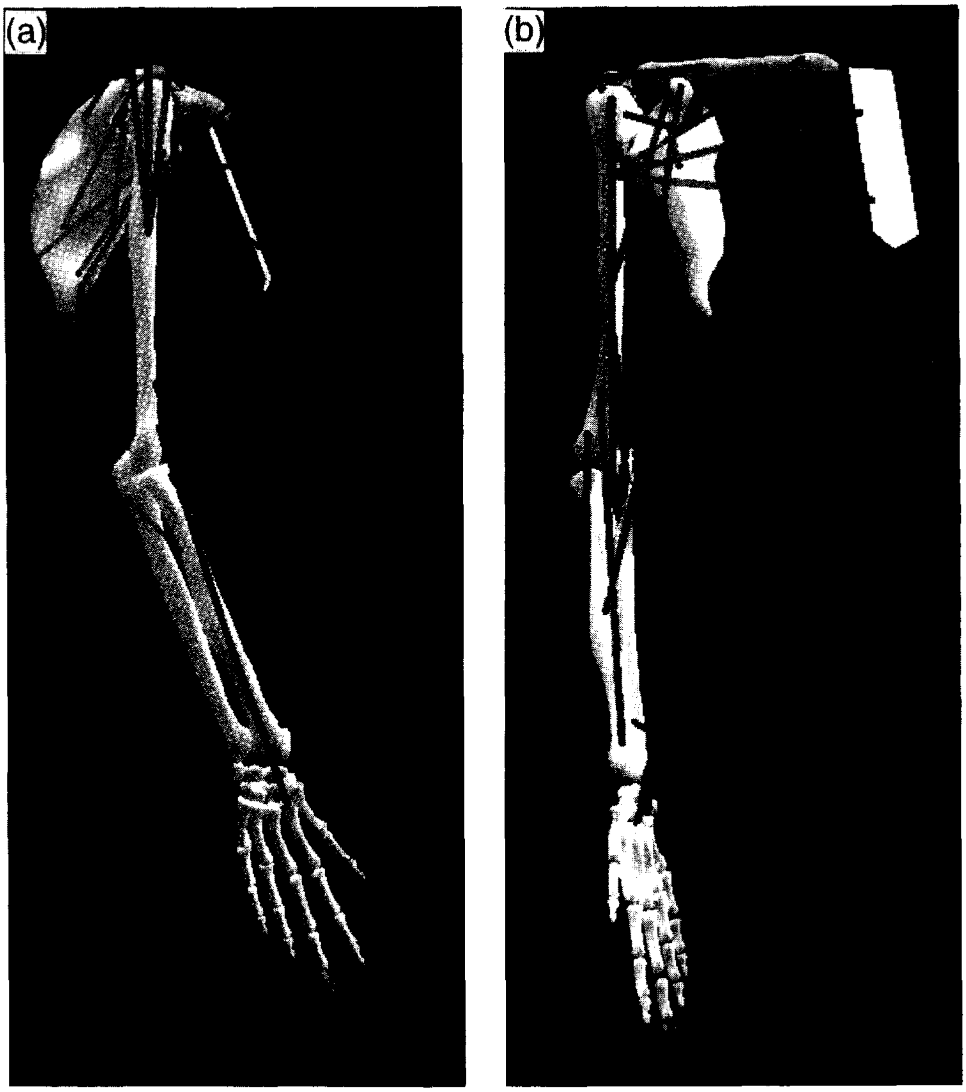

Fig. 1. The 5-DOF dynamic upper extremity model used to verify the pseudoinverse optimal control method. (a) Sagittal view. (b) Frontal view with the forearm slightly supinated. Three DOF are represented at the shoulder, and one DOF is used to represent the humeral-ulnar joint. A separate rigid body for the radius and an additional DOF is used to create actual pronation–supination, with the radius revolving about an axis passing through the centroid of the proximal radius and the midpoint of the wrist. Via points are depicted as dots along the 30 muscle-tendon pathways.

extremity movement on a Silicon Graphics Personal IRIS workstation (4D/35GT). A 5-DOF (Fig. 1) musculoskeletal model of a human arm was developed to compute musculotendon force solutions for the 30 major upper extremity muscles listed. Bony geometries for the humerus, ulna, radius, and hand were scaled from original data defined by Stredney (1989). Muscle origins, insertions, and PCSAs of the 30 upper extremity muscles used to control the model were taken from the literature (Yamaguchi *et al.*, 1990) and augmented with 'via' (wrapping) points as needed to prevent muscle-tendon pathways from passing through bone. The software package SIMM (MusculoGraphics, Inc., Evanston, IL) was used to define the via points as well as to verify the skeletal kinematics.

Dynamic equations of motion for the model were derived via Kane's method (Kane and Levinson, 1985). The model represents the bones of the forearm as two separate rigid bodies for the radius and ulna, which allows pronation and supination to be adequately represented. Thus, the model consists of a 3-DOF shoulder joint, a 1-DOF ulnar-humeral joint to achieve elbow flexion-extension, and a 1-DOF radial-ulnar joint to allow pronation-supination.

Smooth, desired trajectories were prescribed for a 'saluting' motion that involved all five DOF (Fig. 2). Our implementation of the above theory initialized the dynamic model with the initial states and calculated the muscle-induced accelerations by a forward integration algorithm instead of the instantaneous computation given in equations (4) and (5). These accelerations were calculated by projecting the angular velocities forward in time, taking the finite difference, and then dividing by the time difference (5 ms). Though this was slower than the instantaneous computation, it was more accurate as it allowed accumulated trajectory errors to be compensated for (Fig. 3), and also allowed the optimization to be performed over a series of time intervals rather than quasistatically at discrete instants in time. This was advantageous because an optimal decision sequence that brings the system state from one time interval to the next (and then to the next, and so forth) via optimal subpaths thus determines the optimal way to bring the system from its initial state to its final state by Bellman's principle of optimality (Kirk, 1970). Therefore, utilizing interval computations yielded a solution that was dynamically optimized over the entire simulation.

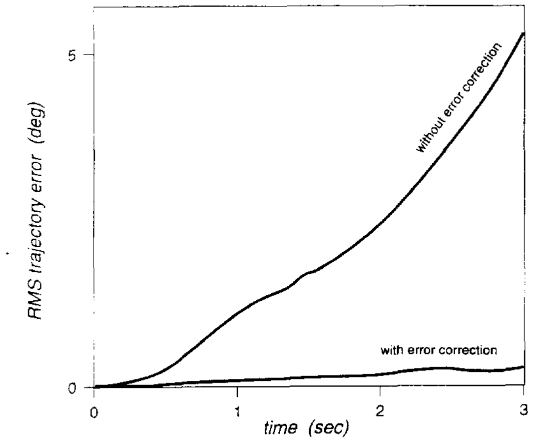

Fig. 3. RMS segmental trajectory errors computed for the 5-DOF simulation. Without real-time error correction, the errors grow to about five degrees after three seconds. With on-line error correction the RMS trajectory errors are minimized to less than 0.25°.

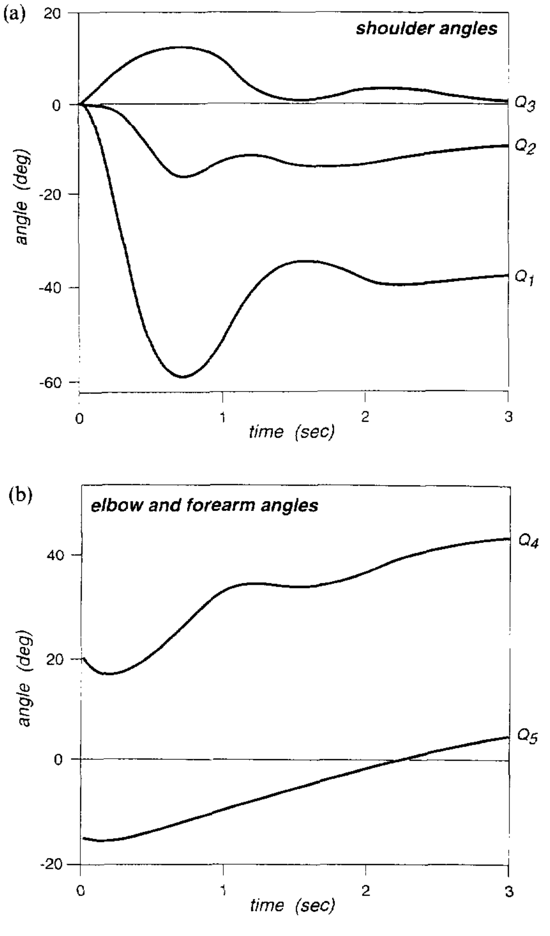

Fig. 2. Segmental trajectories for the (a) shoulder, and (b) elbow and forearm obtained using the pseudoinverse control algorithm. The desired angular trajectories are not shown, because the trajectories obtained have miniscule angular deviation from the desired trajectories (see Fig. 3), and thus are essentially the same curves as those shown.

RESULTS

Using the pseudoinverse algorithm, desired segmental trajectories were matched to within 0.25° RMS throughout the simulation (Fig. 3), and optimal musculotendon stresses were obtained as shown in Fig. 4. Typically, $m/3$ of the muscles needed to have negative stresses iteratively eliminated, and no muscles were found to saturate. Both the optimization and the forward-dynamic simulation of movement were completed in a minimum of CPU time (3 1/2 h).

DISCUSSION

The pseudoinverse algorithm was developed in response to the need for a computationally efficient method of dynamically solving the redundant problem in biomechanics. Solving the redundant problem has traditionally been a two-stage process, first solving for the joint torques quasistatically, and then distributing forces amongst the musculature to deliver these 'torques'. This has lead to an interpretation of muscle function as 'local generators of joint torque'. The traditional approach also tends to disregard mass configurational issues, in that the configuration of the system is only

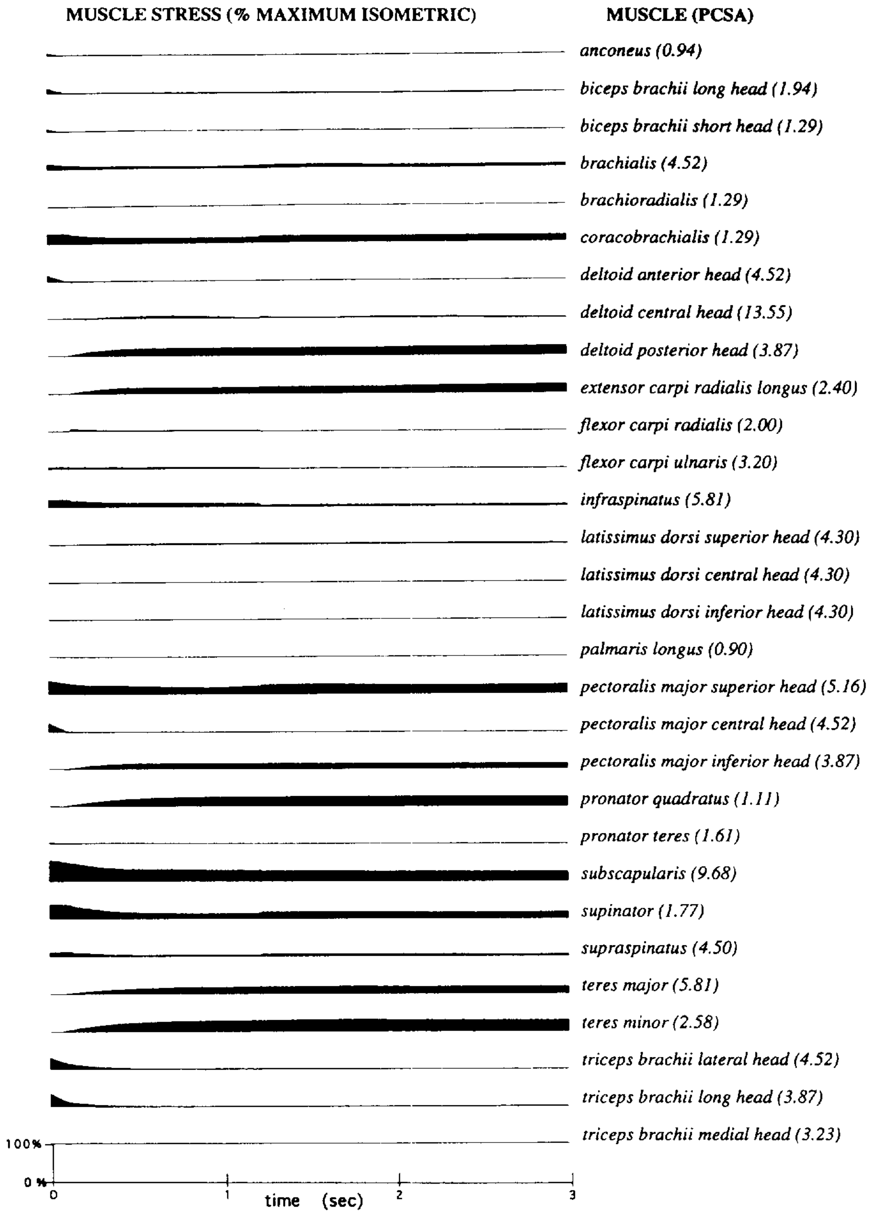

Fig. 4. Musculotendon stresses computed by the pseudoinverse algorithm as a function of time. All negative stresses have been eliminated via the serial post-processing algorithm. Muscle stresses are normalized to a maximum isometric (100%) stress level of 31.39 N cm^{-2} (3.2 kg cm^{-2}), which is consistent with the range of specific muscle forces reported in the literature (Zajac, 1989). Muscle PCSAs (cm^2) are listed in parentheses.

included computationally via the muscle moment arms, which are dependent only upon joint angles.

In contrast, the pseudoinverse algorithm delivers the muscle stresses (forces) in a single forward dynamic operation. Moreover, it is based on a dynamic interpretation of muscle function that considers the systemwide effects of singular muscle contractions. This is an especially important consideration with the trend toward increasingly complex musculoskeletal models. With models composed of multi-DOF joints, even small changes in muscle-tendon path geometries can produce noticeable differences in the muscle-induced accelerations. The pseudoinverse algorithm provides the ability to utilize and differentiate between these muscle-induced accelerations, even when they are produced by functionally similar muscles. The proposed methodology thus is founded on the philosophy that each and every muscle has a specific purpose and acts with global implications.

Although the approach is computationally attractive, there are limitations. The pseudoinverse delivers the minimum vector length for stress vectors having *m* terms. Therefore, the algorithm is only adaptable to optimization criteria involving the sums of *m squared* terms. It would have been preferable to sum muscle stresses raised to the third (or another) power, as it was reported by Crowninshield and Brand (1981) to be representative of the consensus of values reported in the literature. However, Crowninshield and Brand found no difference in the number of active muscles predicted by their optimization when using values of p between 2.0 and 4.0, and only slight changes in the predicted values of muscle forces. We therefore expect that the pseudoinverse algorithm will predict the correct numbers of active muscles and that the muscle stress values will be only slightly in error if indeed p is not equal to two for the particular muscles involved in the current task. Certainly this awaits experimental validation.

Another limitation is that the pseudoinverse algorithm only solves the MIMO problem for the muscle-tendon stresses as discussed in the Methods section. It is well known that muscles cannot be instantaneously activated or deactivated, but there is no provision for preventing this numerically in the algorithm. Although this was not observed in the upper-extremity trial, such an occurrence might be expected in the event that a rapidly changing external load was applied to the system. The algorithm used to constrain the stresses to physiological values could then be used.

In summary, the redundant problem in biomechanics can be formulated using forward dynamic equations and solved via the pseudoinverse algorithm, provided the task is amenable to a quadratic cost function relating to muscle endurance. Even for complex musculoskeletal models, the method efficiently and accurately solves for the optimal muscle stresses.

Acknowledgements—This work has been supported in part by grants from The Whitaker Foundation, the National Institutes of Health (2R01 NS26375-05) and the National Science Foundation (BCS 9257395 and BCS 9110658). The authors also thank Kathy Stott for providing her editing skills.

REFERENCES

Bobbert, M. F. and van Ingen Schenau, G. (1988) Coordination in vertical jumping. *J. Biomechanics* **21,** 249–262.

Chao, E. Y. and An, K. N. (1978) Graphical interpretation of the solution to the redundant problem in biomechanics. *J. biomech. Engng* **100,** 159–167.

Chao, E. Y. and Rim, K. (1973) Application of optimization principles in determining the applied moments in human leg joints during gait. *J. Biomechanics* **6,** 497–510.

Crowninshield, R. D. and Brand, R. A. (1981) A physiologically based criterion of muscle force prediction in locomotion. *J. Biomechanics* **14,** 793–801.

Davy, D. T. and Audu, M. L. (1987) A dynamic optimization technique for predicting muscle forces in the swing phase of gait. *J. Biomechanics* **20,** 187–201.

Hardt, D. E. (1978) Determining muscle forces in the leg during normal human walking—an application and evaluation of optimization methods. *J. biomech. Engng* **100,** 72–78.

Hatze, H. (1981) A comprehensive model for human motion simulation and its application to the take-off phase of the long jump. *J. Biomechanics* **14,** 135–142.

Herzog, W. (1987) Individual muscle force estimations using a non-linear optimal design. *J. Neurosci. Meth.* **21,** 167–179.

Kane, T. R. and Levinson, D. A. (1985) *Dynamics: Theory and Applications.* McGraw-Hill, New York.

Khang, G. and Zajac, F. E. (1989a) Paraplegic standing controlled by functional neuromuscular stimulation: Part I—Computer model and control system design. *IEEE Trans. biomed. Engng* **36,** 873–884.

Khang, G. and Zajac, F. E. (1989b) Paraplegic standing controlled by functional neuromuscular stimulation: Part II–Computer simulation studies. *IEEE Trans. biomed. Engng* **36,** 885–894.

Kirk, D. E. (1970) *Optimal Control Theory. An Introduction.* Prentice-Hall, Englewood Cliffs, NJ.

Kuo, A. D. (1994) A mechanical analysis of force distribution between redundant, multiple degree-of-freedom actuators in the human: implications for the central nervous system. *Human Movement Science* (in press).

Meglan, D., Berme, N. and Sheldon, R. S. (1991) Evaluation of coupled dynamics in observed locomotion. *Proc. Am. Soc. Biomechanics* **15,** 36–37.

Olney, S. J. and Winter, D. A. (1985) Predictions of knee and ankle moments of force in walking from EMG and kinematic data. *J. Biomechanics* **18,** 9–20.

Pandy, M. G., Anderson, F. C. and Hull, D. G. (1992) A parameter optimization approach for the optimal control of large-scale musculoskeletal systems. *J. biomech. Engng* **114**(4), 450–460.

Pandy, M. G. and Zajac, F. E. (1991) Optimal muscular coordination strategies for jumping. *J. Biomechanics* **24,** 1–10.

Pandy, M. G., Zajac, F. E., Sim, E. and Levine, W. S. (1990) An optimal control model for maximum-height human jumping. *J. Biomechanics* **23,** 1185–1198.

Patriarco, A. G., Mann, R. W., Simon, S. R. and Mansour, J. M. (1981) An evaluation of the approaches of optimization of models in the prediction of muscle forces during human gait. *J. Biomechanics.* **14,** 513–525.

Pedotti, A., Krishnan, V. V. and Stark, L. (1978) Optimization of muscle-force sequencing in human locomotion. *Math. Biosci.* **38,** 57–76.

Pierrynowski, M. R. and Morrison, J. B. (1985) Estimating the muscle forces generated in the human lower extremity when walking: a physiological solution. *Math. Biosci.* **75,** 43–68.

Seireg, A. and Arvikar, R. J. (1975) The prediction of muscular load sharing and joint forces in the lower extremities during walking. *J. Biomechanics* **8,** 89–102.

Strang, G. (1976) *Linear Algebra and its Applications.* Academic Press, New York.

Thunnissen, J. (1993) Muscle force prediction during human gait. Ph.D. dissertation, University of Twente.

Veltink, P. H., Franken, H. M., Van-Alste, J. A. and Boom, H. B. (1992) Modelling the optimal control of cyclical leg movements induced by functional electrical stimulation. *Int. J. Artificial Organs* **15**(12), 746–755.

White, S. C. and Winter, D. A. (1993) Predicting muscle forces in gait from EMG signals and musculotendon kinematics. *J. Electromyography and Kinesiology* **2**(4), 217–231.

Yamaguchi, G. T., Sawa, A. G.-U., Moran, D. W., Fessler, M. J. and Winters, J. M. (1990) *Appendix: A Survey of Human Musculotendon Actuator Parameters. Multiple Muscle Systems: Biomechanics and Movement Organization* (Issue) (Edited by J. M. Winters and S. L.-Y. Woo). Springer, New York, pp. 717–773.

Yamaguchi, G. T. and Zajac, F. E. (1990) Restoring unassisted natural gait to paraplegics with functional neuromuscular stimulation: a computer simulation study. *IEEE Trans. biomed. Engng* **37**(9), 886–902.

Yoshihuku, Y. and Herzog, W. (1990) Optimal design parameters of the bicycle-rider system for maximal muscle power output. *J. Biomechanics* **23,** 1069–1079.

Zajac, F. E. (1989) Muscle and tendon: properties, models, scaling, and application to biomechanics and motor control. *CRC Crit. Rev. biomed. Engng* **17**(4), 359–411.

Zajac, F. E. and Gordon, M. E. (1989) Determining muscle's force and action in multi-articular movement. *Exercise and Sport Sci. Rev.* **17,** 187–230.