

Stability analysis of nonlinear muscle dynamics using contraction theory

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Abstract— Biological motor control systems have a distributed, rather than centralized, architecture. Instabilities in movement, such as tremor, can in part arise from the interactions between different physiological feedback mechanisms. Contraction theory provides tools for analyzing the stability of nonlinear distributed control systems. Here we use contraction theory to investigate the stability provided by the mechanical feedback of muscle dynamics, finding that these dynamics are exponentially stable. This theoretical result complements previous computational and experimental findings regarding the efficacy of viscoelastic properties of muscle in compensating for disturbances.

Keywords— stability, muscle, distributed control

I. INTRODUCTION

The control of movement occurs through the coordinated action of many feedback loops, accessing a variety of different circuits within the central nervous system. The feedback loops may be viewed to have a hierarchical organization based on latency of response and level of access to the nervous system. At the bottom of this hierarchy is the mechanical feedback provided by the intrinsic viscoelasticity of the musculoskeletal system [8]. This non-neural feedback loop, or preflex [1], can result in nearly instantaneous correction of errors between the actual mechanical state, i.e. position and velocity, and the centrally-specified equilibrium state. Further up the hierarchy are spinal reflexes and supraspinal reflexes, which use time-delayed somatosensory feedback and exert basic restoring actions following a perturbation using a minimum of neural computation. At the top of the hierarchy are feedback loops that use not only somatosensory feedback, but visual feedback, internal models of the peripheral dynamics, and possibly high level task goals to more skillfully and efficiently track desired movements

and attenuate disturbances.

In addition to the hierarchical structure, there is also a parallel organization to the feedback loops, as evident anatomically in the parallel proprioceptive feedback pathways to the spinal cord. Additionally, in many vertebrate systems there is evidence for independent functional modules of control embedded in the spinal cord, many of which utilize state feedback, that act in parallel to produce basic movements [11]. There may also exist multiple internal model-based feedback controllers in the human cerebellum that act in parallel for skilled limb movements [4]. Furthermore, feedback loops at different levels of the hierarchy described above may functionally act in parallel (i.e. act independently of lower levels), although possibly with different response latencies.

From an engineering perspective, a central issue for any system under feedback control is the system stability. One challenge to movement stability based on the physiology discussed above is the relatively long transmission delays in sensorimotor loops. Recognition of this potentially destabilizing mechanism has led to several theories on how biological feedback controllers may operate. In particular, higher levels of the feedback control hierarchy may circumvent the time delays of sensory feedback by using estimates of the current state provided by composite signals carried on afferent fibers or by internal forward models. A second challenge to movement stability is the distributed feedback control architecture itself. Instabilities can arise from interconnected feedback loops, even if each loop on its own ensures stable closed-loop dynamics [5]. However, little theoretical work has been devoted to this mechanism, particularly for nonlinear models of the motor system. Indeed, mathematical models of biological movement control almost exclusively use a centralized feedback control law, disregarding the distributed architecture altogether.

Recently, advances in stability theory have provided useful tools for analyzing distributed feedback control systems [6] [9] [10]. Here we use these tools to analyze the stability provided by the bottom feedback loop of the hierarchy, the intrinsic muscle viscoelasticity.

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II. CONTRACTION THEORY

In this section, we summarize the basic result of contraction theory, as originally described in [6], as well as discuss a recent extension of this result, known as higher-order contraction theory [7], both of which we will use to analyze the stability properties of muscle dynamics. We consider the general nonlinear, deterministic system dynamics of the form

$$\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}, t) \quad (1)$$

where \mathbf{x} is the state vector. The result from [6] is stated in the following theorem.

Theorem 1. *All trajectories of (1) converge exponentially to a single trajectory if and only if there exists a uniformly positive definite metric $\mathbf{M}(\mathbf{x}, t) = \Theta^T \Theta$ such that the associated generalized Jacobian, $\mathbf{F} = (\dot{\Theta} + \Theta \frac{\partial \mathbf{f}}{\partial \mathbf{x}}) \Theta^{-1}$, is uniformly negative definite.*

Systems that satisfy this condition are said to be contracting and the Euclidean distance between any two system trajectories exponentially goes to zero at a rate greater than or equal to the largest eigenvalue of the symmetric part of \mathbf{F} . If \mathbf{F} is only negative definite in a finite region of state space, then only system trajectories starting in the largest ball, with respect to the metric \mathbf{M} , contained in that region are guaranteed to exponentially converge. Furthermore, if \mathbf{F} is only negative semi-definite, then system trajectories may converge only asymptotically to a single trajectory and the system is said to be semi-contracting.

An important feature of this theory, which in part motivates the present work, is that contracting systems can be combined in a variety of ways, including hierarchical, parallel, and feedback combinations, while preserving the overall system stability. Theorem 1, therefore, provides a simple condition which, if satisfied by each sensorimotor feedback mechanism, would ensure stability of movement derived from their coordinated action.

The challenge of this study is to apply this theory to the complicated dynamics of the neuromusculoskeletal system, which will generally require a computational rather than analytical analysis. One approach is to solve a nonlinear partial differential equation, specified in [6], to find a metric that satisfies the condition in Theorem 1. A more tractable approach, and the one taken here, is to satisfy a modified condition, derived from higher-order contraction theory [7], which only requires one to find the solutions to a nonlinear algebraic inequality. For the second-order systems discussed in this paper of the form $\ddot{x} = g(x, \dot{x})$, this inequality is,

$$\sqrt{\left| -\frac{\partial g}{\partial x} + \frac{1}{4} \left(\frac{\partial g}{\partial \dot{x}} \right)^2 - \frac{1}{2} \frac{d}{dt} \left(\frac{\partial g}{\partial \dot{x}} \right) \right|} - \frac{1}{2} \frac{\partial g}{\partial \dot{x}} \leq 0. \quad (2)$$

If this inequality can be satisfied over a suitable range of x and \dot{x} , then the system is contracting on this range

with a convergence rate equal to the left-hand side of (2). The tradeoff for using this simpler computational approach is that, unlike the condition in Theorem 1, the higher-order contraction condition is only sufficient and thus not necessary for a system to be exponentially convergent. However, it is a more inclusive sufficient condition than merely requiring the system Jacobian, $\frac{\partial \mathbf{f}}{\partial \mathbf{x}}$, to be negative definite (which corresponds to using an identity metric in Theorem 1 and which is also Krasovskii's Theorem in the time-invariant case).

III. ANALYSIS OF MUSCLE DYNAMICS

As discussed in the Introduction, at the bottom of the hierarchy of feedback loops controlling movement is the mechanical feedback provided by intrinsic muscle viscoelasticity. In this section, we examine whether these muscle dynamics are contracting and therefore exponentially convergent. For simplicity, we first consider an atendous, tetanic, nonlinear Hill-type muscle dynamics with linear viscoelastic properties:

$$\ddot{x} + c_p^v \dot{x} + c_p^e(x - x_{eq}) + c_a^{ve} \dot{x} = F(t) \quad (3)$$

where c_p^v is the passive viscosity/muscle mass, c_p^e is the passive elasticity/muscle mass, c_a^{ve} is the active viscoelasticity/muscle mass, x_{eq} is the equilibrium length of the muscle, and F is the muscle force.

A. Analytical analysis of basic nonlinear Hill-model

First, we first analyzed these dynamics using the contraction condition given in Theorem 1. The system Jacobian of (3) in companion form is,

$$\frac{\partial \mathbf{f}}{\partial \mathbf{x}} = \begin{bmatrix} 0 & 1 \\ -c_a^{ve} \dot{x} - c_p^e & -c_a^{ve} x - c_p^v \end{bmatrix}. \quad (4)$$

If we choose the metric, $\mathbf{M}(\mathbf{x}) = \Theta^T \Theta$,

$$\Theta = \begin{bmatrix} \sqrt{c_p^e} & 0 \\ c_a^{ve} x + c_p^v & 1 \end{bmatrix} \quad (5)$$

then the generalized Jacobian is,

$$\mathbf{F} = \begin{bmatrix} -(c_a^{ve} x + c_p^v) & \sqrt{c_p^e} \\ -\sqrt{c_p^e} & 0 \end{bmatrix}. \quad (6)$$

Since $x > 0, \forall t$ (i.e. muscle lengths cannot be negative), the generalized Jacobian is uniformly negative semi-definite and therefore (3) is semi-contracting. In other words, all trajectories of (3) converge asymptotically to $\mathbf{x} = [x_{eq} \ 0]^T$. Note that the metric in (5) was found analytically, but it may not provide the best estimate of the system convergence properties. Metrics used to prove a system is contracting are, in general, not unique and some metrics will give more conservative estimates of the system stability than others. Moreover, with the metric in (5), we are able to prove only asymptotic stability. However, as we demonstrate below, using the computational analysis we can in fact prove (3) is exponentially stable for certain values of c_p^v , c_p^e , and c_a^{ve} .

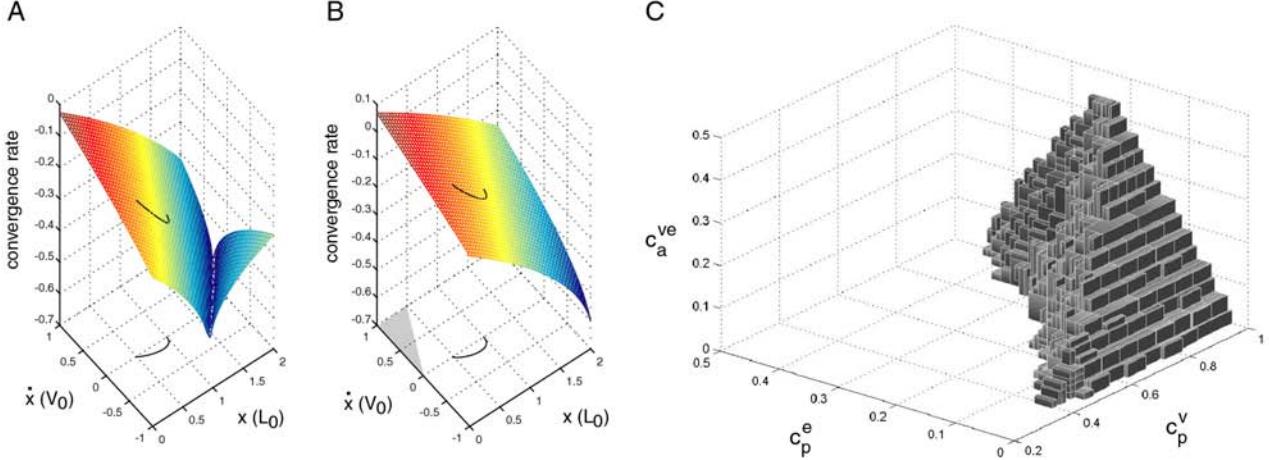


Figure 1: Computational contraction analysis of the dynamics given in (3). A: The state-dependent convergence rate, as computed from (2), for the muscle dynamics when $c_p^v = 1.0$, $c_p^e = 0.4$, and $c_a^{ve} = 0.15$. A sample system trajectory, with initial conditions $x = L_0$ and $\dot{x} = 0$ is plotted in the phase plane and projected onto the convergence rate plane. B: The convergence rate for the muscle dynamics when $c_p^v = 1.0$, $c_p^e = 0.5$, and $c_a^{ve} = 0.15$. The gray region on the phase plane indicates the states for which the convergence rate is greater than zero, thus not satisfying the contraction condition given in (2). C: The values of c_p^v , c_p^e , and c_a^{ve} that make the muscle dynamics contracting over the whole range of states, $0 \leq x/L_0 \leq 2$ and $-1 \leq \dot{x}/V_0 \leq 1$, as determined by the Bernstein branch-and-bound algorithm.

B. Computational analysis of basic nonlinear Hill-model

For the computational analysis of (3), we let $x_{eq} = 0.5L_0$, where L_0 is the optimal muscle length, and considered the dynamics over the domain, $0 \leq x \leq 2L_0$ and $-V_0 \leq \dot{x} \leq V_0$, where V_0 is the maximum shortening velocity. Over this range of states, we computed the convergence rate, as given by the left-hand side of (2), for two different sets of parameter values: (i) $c_p^v = 1.0$, $c_p^e = 0.4$, and $c_a^{ve} = 0.15$ and (ii) $c_p^v = 1.0$, $c_p^e = 0.5$, and $c_a^{ve} = 0.15$. The state-dependent convergence rates for the muscle dynamics with parameters (i) and (ii) are shown in Fig. 1A and Fig. 1B, respectively. For the first set of parameters, the convergence rate is negative for all states (Fig. 1A), and therefore, by the condition given in (2), the dynamics are contracting on this region. For the second set of parameters, the convergence rate is negative for most states, but positive at short muscle lengths and lengthening (positive) velocities (Fig. 1B). The states corresponding to positive convergence rates are indicated by the gray region in Fig. 1B. In both Fig. 1A and Fig. 1B, a sample system trajectory, starting at $x = L_0$ and $\dot{x} = 0$, is shown projected onto the phase plane and convergence rate plane. This computational analysis, therefore, indicates that our analytical stability result for the dynamics in (3) was indeed conservative. For some values of c_p^v , c_p^e , and c_a^{ve} , these dynamics are actually contracting, rather than just semi-contracting.

Next, we were interested in finding all sets of parameters that make the dynamics in (3) contracting over $0 \leq x \leq 2L_0$ and $-V_0 \leq \dot{x} \leq V_0$, as in Fig. 1A. In other words, we would like to know how robust this stability property is to changes in the system parameters. This

type of problem can be solved using many methods, including symbolic quantifier elimination and algorithms using interval arithmetic. Since the dynamics are only polynomial in the state, we can use the simple Bernstein branch-and-bound algorithm [3]. This algorithm involves converting a multivariate polynomial from the power basis to the Bernstein basis, the coefficients of which can then bound the polynomial over a given domain. With this method, we found the sets of parameters indicated by the gray boxes in Fig. 1C, all of which make (3) contracting over the whole range of states, as in Fig. 1A.

C. Computational analysis of experimentally-derived model

Finally, we extended our analysis of muscle dynamics to a model that had more realistic, nonlinear viscoelastic properties. In particular, we chose to analyze empirically-determined muscle dynamics from the work of Loeb and colleagues [2]. As in the muscle model analyzed above, we do not consider activation dynamics and simply set the activation to 1 (tetanic activity). Due to the complexity of the dynamics specified in [2], an analytical contraction analysis was not possible. Therefore we used the computational approach. Using the parameters for slow twitch muscle from [2], we computed the convergence rate over a range of muscle lengths and velocities. Since in this case the convergence rate was also dependent on muscle acceleration (\ddot{x}), due to the time-derivative term in (2), the convergence rates were actually computed over a three-dimensional state-space. In

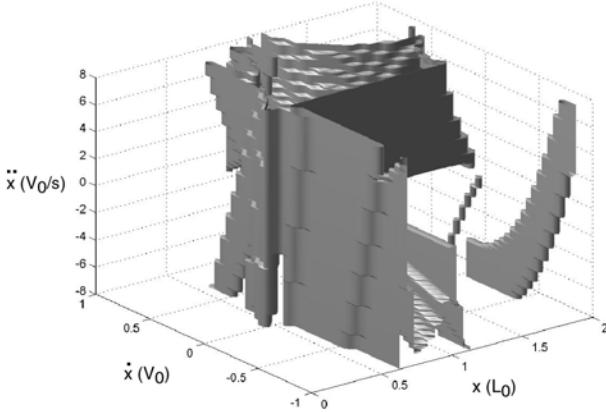


Figure 2: Computational contraction analysis of the muscle dynamics specified in [2]. The gray volume indicates the particular muscle lengths (x), velocities (\dot{x}), and accelerations (\ddot{x}) at which the convergence rate is less than or equal to zero, and thus where the dynamics are contracting.

Fig. 2, the gray volume indicates the muscle lengths, velocities, and accelerations at which the convergence rate was less than or equal to zero, thus satisfying the contraction condition in (2). As one can see, this contraction region occupied a large portion of the relevant muscle states indicating a large region of exponential stability for these muscle dynamics. However, there are also regions, particularly at shortening (negative) velocities, of positive convergence rate and thus non-contracting behavior. The muscle dynamics may in fact be exponentially stable in these regions, but we could not prove such stability using our sufficient, but not necessary, contracting condition given in (2). Future work will examine how changes in the parameters of these dynamics impact the contraction region, as done for the previous muscle model with the Bernstein branch-and-bound method, only using a method that can handle non-polynomial dependencies on the state.

IV. CONCLUSION

In this paper, we analyzed the stability of nonlinear muscle dynamics using contraction theory. The dynamics were, for the most part, found to be exponentially stable. This analysis provides formal theoretical results to complement both computational [1] and experimental [8] findings regarding the efficacy of viscoelastic properties of muscle in compensating for disturbances. The advantage of using contraction theory for this analysis is that these results can be expanded upon, in a modular fashion, to investigate the stability properties of movement produced by the full distributed neuromuscular controller. Specifically, future work will analyze muscle activation dynamics and parallel proprioceptive feedback pathways [5] to better understand the mech-

anisms governing stability and instability in biological movement.

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