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► **To cite this version:**

François Bailly. Polynomial regressions on muscle parameters can approximate the muscle/tendon equilibrium. 47th congress of the Society of Biomechanics, Oct 2022, Monastir, Tunisia. pp.S14-S16, 10.1080/10255842.2022.2116885 . hal-04213855

**HAL Id: hal-04213855**

**<https://inria.hal.science/hal-04213855>**

Submitted on 21 Sep 2023

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# Polynomial regressions on muscle parameters can approximate the muscle/tendon equilibrium

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## 1. Introduction

Fast and accurate knowledge of muscle forces is paramount in biomechanics, as it would enrich clinician's diagnoses, enhance interactive biofeedback during rehabilitation and refine motion prediction studies based on numerical simulations. Given the impossibility to directly measure muscle forces, several methods have been proposed to compute them numerically, relying on musculoskeletal models of the human body. Among them, static optimization is the most widely used, even if it presents several drawbacks (Ackerman et al. 2009). Forward approaches relying on numerical optimal control have shown promising results in recent years (Bailly et al. 2021). Hybrid approaches are also available (Pizzolato et al. 2015) even if they retain some drawbacks of static optimization. One of the limits of forward approaches lies in their computational cost which, until recently, had disqualified them for real-time applications. Even if recent works have drastically improved this aspect, they are often restricted to models using rigid tendons. This assumption significantly simplifies the problem as the muscle/tendon equilibrium does not need to be solved, reducing the numbers of variables and ordinary differential equations (ODEs) involved in the optimization problem. However, this assumption is not always justified, especially in humans, where many muscles have long tendons, which stretch significantly under load conditions. In the present work, we provide a modeling analysis of the muscle length at equilibrium which shows that using root-finding algorithms or solving initial value problems might not be always necessary to account for elastic tendons. By interpolating analytical relationships between muscle length at equilibrium and simulation parameters, this preliminary work paves the way for including contractile dynamics in forward approaches to estimate or predict muscle forces without over-complexifying the underlying optimization problems, and thus without compromising real-time applications.

## 2. Methods

### 2.1 Equations of Hill's muscle model

Hill's muscle model is the most used in human biomechanics. It is a massless model, made of an

active force-producing unit in parallel with a passive resistive one, both in series with a passive unit representing the tendon. During forward dynamic simulations, the length and velocity of the muscle-tendon unit ( $l^{mt}$ ,  $v^{mt}$ ) are inputs of the problem determined by the skeletal kinematics. The muscle tendon equilibrium is given by:

$$[a * f_{act}(l^m) f_v(\dot{l}_m) + f_{pas}(l^m)] \cos(\alpha) = f_t(l^t), \quad (1)$$

where  $a$  is the muscle activation and  $f_{act}$  is the active part of the muscle force, depending on  $l^m$ , the muscle length.  $f_v$  is the force/velocity relationship depending on the muscle velocity  $\dot{l}_m$  and  $f_{pas}$  is the passive part of the muscle force.  $\alpha$  is the pennation angle of the muscle and  $f_t$  is the tendon force, depending on the tendon length,  $l^t$ . To be consistent with (Delp et al. 2007) implementation of (Thelen et al. 2003), Eq. (1) is solved for the muscle length ( $l^m$ ), acting as the state variable while the muscle activation is the control (other choices can be made, e.g.: choosing the muscle forces as state variables). In these conditions, the differential equation governing the contractile dynamics is as follows:

$$\dot{l}_m = f_v^{-1} \left\{ \frac{f_t(l^t) / \cos(\alpha) - f_{pas}(l^m)}{a * f_{act}(l^m)} \right\}, \quad (2)$$

where analytical expressions for  $f_v$ ,  $f_{act}$ ,  $f_{pas}$  and  $f_t$  are taken from (De Groot et al. 2016). It should be noted that, in general, there is no closed-form solution to Eq. (2). Then, compared to skeletal modeling, in which the state vector is composed of joint positions and velocities and the system of ODEs is governing the multibody system dynamics, for any simulation including the contractile dynamics, the state vector and system of ODEs must respectively be augmented with muscle lengths and Eq. (2), for each muscle/tendon unit. Given the high number of muscles present in the body, this modeling dramatically increases the size and thus the complexity of the problem to be solved.

### 2.2 Simulating the contractile dynamics

The contractile dynamics of the Hill muscle was simulated for several muscle types, with muscle/tendon length (MTL) ratios ranging from 0.08 to 1.8, levels of muscle activation ranging from 0.1 to 1 and tendon slack lengths ( $l_{s1}^t$ ) ranging from 0.1 to 0.4m. For every set of parameters, Eq. (2) was solved for several initial values, and every time, the steady state of the solution (i.e.: the muscle length at equilibrium,  $l_{eq, s.t.}^m = 0$ ) was kept for analyzing how it depends on the parameters.

## 3. Results and discussion

The convergence of the solutions of Eq. (2) towards their steady state is fast ( $< 50ms$ , often much faster), supporting the idea that the transient of the contractile dynamics can be approximated by the steady state value, without compromising the accuracy of the resulting simulation. This approximation is all the more relevant when simulating a trajectory, since the initial values of the problem (solution at  $t_{i-1}$ ) should be much closer to the steady state (at  $t_i$ ) than the ones purposefully used in this study. In Fig. 1,  $l_{eq}^m$  is represented for several MTL ratios and for several values of  $l_{sl}^t$  for a given muscle stretch ( $l^{mt} = l_{sl}^t + \cos(\alpha_0)l_0^m$ , similar results were obtained for other values of muscle stretch), where  $\alpha_0$  is the pennation angle at optimal muscle length,  $l_0^m$ . This set of parameters spans every muscle type from small  $l_{sl}^t$  with low MTL ratios corresponding to short muscles with short tendons, to large  $l_{sl}^t$  with high MTL ratios corresponding to long muscle with long tendons. Linear regressions on the relationships between  $l_{eq}^m$  and MTL ratios for each  $l_{sl}^t$  give really good fits ( $R^2 > 0.99$ ). In Fig. 2,  $l_{eq}^m$  is represented for several values of normalized muscle stretch ( $\widehat{l}^{mt} = l^{mt}/l_{sl}^t$ ) and for several values of  $l_{sl}^t$  for a given MTL ratio of 0.1 (similar results were obtained for other values of MTL). Second-order polynomial regressions on the relationships between  $l_{eq}^m$  and  $\widehat{l}^{mt}$  for each  $l_{sl}^t$  give really good fits ( $R^2 > 0.99$ ).

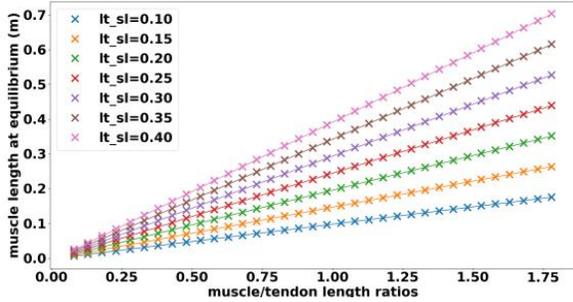


Figure 1. Linear regressions on  $l_{eq}^m$  for varying MTL ratios and  $l_{sl}^t$ .

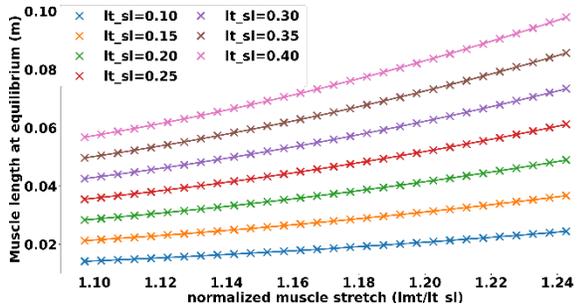


Figure 2. Second-order polynomial regressions on  $l_{eq}^m$  for varying  $\widehat{l}^{mt}$  and  $l_{sl}^t$ .

## 4. Conclusions

Approximating the transient of contractile dynamics by the muscle length at equilibrium is a promising solution for including muscle/tendon equilibrium in musculoskeletal simulations. This can be done by exhibiting analytical relationships between simulation parameters and the steady state of the contractile dynamics. The present work paves the way in that direction. In a future work, the whole surfaces ( $l_{eq}^m$ (MTL ratio,  $\widehat{l}^{mt}$ ), for each  $l_{sl}^t$ ) must be interpolated, so that their extrapolated analytical expressions can be used to solve the muscle tendon equilibrium for any set of simulation parameter. In order to corroborate the approximation of the contractile dynamics' transient by its steady state value, thorough simulations should be conducted to evaluate the error resulting from this assumption.

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**Keywords:** biomechanics, musculoskeletal modeling, contractile dynamics

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