

A Distribution-Moment Approximation for Kinetic Theories of Muscular Contraction

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ABSTRACT

A rational mathematical procedure is proposed for approximating solutions to the partial differential equations of cross-bridge kinetics in theories of muscular contraction of the type first proposed by A. F. Huxley. The essence of the procedure is to approximate the exact bond-distribution functions by distributions of prescribed form, and this leads to a set of first-order ordinary differential equations on the low-order moments of the approximate distributions. Thus the procedure effectively results in a lumped-parameter model of muscle approaching the structural simplicity of the classic two-element model, but one which exhibits more realistic behavior. The approximation is worked out in detail for Huxley's original (1957) two-state model (modified slightly to produce a more realistic stretch response), compared with exact solutions of the model, and used to predict muscle behavior under various conditions. It is anticipated that this approximation, with its attendant conceptual and computational simplifications, will make recent theoretical advances in molecular contraction mechanics more accessible for applications in macroscopic muscle dynamics. Generalizations of the procedure to the case of length-dependent behavior are discussed.

INTRODUCTION

Since its introduction by A. V. Hill [1] in 1938, the classic two-element model of muscle has proven to be a very useful concept in muscle physiology. Despite its attractive simplicity, the model explained qualitatively, and to some extent quantitatively, several of the mechanical phenomena exhibited by muscle, including the response on isotonic release, the rise of isometric tension, and the redevelopment of tension after quick release. It has been used to make quantitative predictions of mechanical behavior both in isolated skeletal muscle preparations [2, 3] and *in vivo* [4, 5]. Further, it has seen wide applications in cardiac muscle mechanics. This model, which is illustrated in Fig. 1(a), asserted that from an operational point of view muscle may be regarded as a series combination of a series elastic element (SE) and

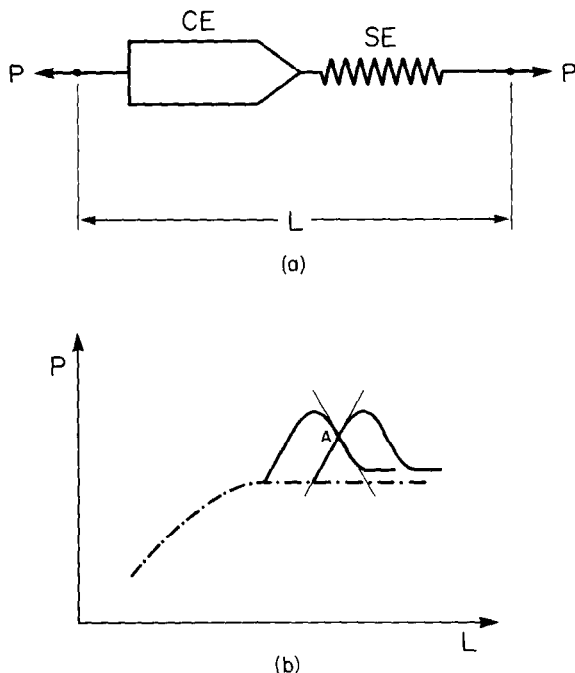


FIG. 1. (a) The two-element model of muscle. (b) Schematic force-length trajectories for muscle stretched at constant velocity when subjected to constant electrical stimulation, starting from an isometric state. The interrupted line represents an isometric tension-length curve. After [6].

an active force-generating contractile element (CE). It was assumed that at a constant level of activation the stretch of the SE and the stretch rate of the CE were uniquely determined by the instantaneous muscle force. The mathematical statement of the model is

$$\dot{L} = C\dot{P} - V(P, P_0), \quad (1)$$

where L denotes the overall muscle length, P the muscle force, and the superposed dot indicates differentiation with respect to time. The level of activation is measured by the isometric force P_0 , the compliance (reciprocal stiffness) of the SE is denoted by C , and V is the velocity of shortening of the CE. The compliance C , as well as V , depends in general on the muscle force P and the activation P_0 .

Although several complications were recognized (part of the "series" elasticity resides in the contractile tissue, P_0 and V vary with length at constant stimulation, etc.) the model has been remarkably useful in cases

which involve no substantial lengthening of actively contracting muscle. It is clear, however, that this model is inadequate to represent the observed response of skeletal muscle during stretch. This is illustrated in Fig. 1(b), which shows schematically the constant-velocity stretch response of isolated cat soleus observed by Joyce et al. [6]. Even at low velocities, and at all but the highest stimulation rates, when a muscle is stretched at constant velocity the force at first rises sharply and then drops, often to levels below the isometric force at the current length. This means that force-length trajectories starting at neighboring points will intersect. On the other hand, for a series of stretches at a constant stimulation rate and velocity, P_0 and \dot{L} are constant and $\dot{P} = (dP/dL)\dot{L}$, so that Eq. (1) may be written as

$$\frac{dP}{dL} = C^{-1}(P, P_0) \left[1 + (\dot{L})^{-1} V(P, P_0) \right], \quad (2)$$

which requires that the (L, P) trajectories have a well-defined slope at each point. This contradicts the experimental observation illustrated in Fig. 1(b) that trajectories passing through a given point like *A* may have different slopes. (The inclusion of length dependence in C and V does not alter this conclusion.) Thus it appears that the traditional two-element model should be abandoned in seeking even approximate quantitative models for muscle undergoing both shortening and lengthening.

Beginning with A. F. Huxley's [7] mathematical formulation of the sliding-filament theory in 1957, a series of increasingly sophisticated kinetic models have appeared which attempt to predict the mechanics and energetics of muscle on the basis of chemical interactions between actin and myosin at the cross-bridge level [8–12]. In particular, T. L. Hill and his associates [13] have developed a self-consistent thermodynamic formalism for models of this type. These models have the advantage of being based directly on current physiological knowledge of the microscopic structure of muscle and the molecular mechanisms of contraction, and they are capable of reproducing realistically various aspects of muscle behavior if appropriate assumptions are made about the nature of the actin-myosin interactions. Mathematically these models are expressed as sets of coupled first-order partial differential equations on distribution functions representing the populations of the various biochemical states as functions of bond length and time.

Unfortunately these kinetic models are too complex to be used directly for macroscopic descriptions of whole muscle. They require a large computational effort to simulate even simple experiments [12]. Such elaborate computations are justified for the purpose of interpreting precise experiments on isolated muscle fibers in order to test hypotheses concerning molecular contraction mechanisms, but they would be unwarranted and prohibitive for studies of limb motion where several muscles, length-dependent behavior,

and time-varying stimulation, as well as passive viscoelastic properties, play a role. The kinetic models simultaneously require and give too much information from a macroscopic point of view. They require too much because fine details of the molecular interactions, such as the precise variation of the rate parameters as functions of bond length and the free energies of the various biochemical states, must be specified, and these are not directly measureable by experiments. They give too much information because a solution of the relevant equations yields the complete distribution functions, whereas one is usually interested only in the low-order moments of these functions, which represent physically measurable quantities such as force, stiffness, and rate of heat generation.

The object of this paper is to propose a mathematical procedure for obtaining approximations to the required low-order moments directly without first solving the partial differential equations of the kinetic theories. This is a compromise which attempts to retain some of the realistic behavior of the kinetic models and their intimate connection with the underlying molecular phenomena while eliminating much of the mathematical complexity. In this paper the consequences of the procedure will be developed in detail only for a slightly modified version of the original Huxley two-state model, but the procedure itself can be applied to more complicated models in a straightforward manner. The result is that a muscle is represented by a set of three first-order ordinary differential equations, as compared to one first-order ordinary differential equation for the classic two-element model and one first-order partial differential equation for the Huxley two-state model. This result is sufficiently simple that it could be useful in studies of limb dynamics, even if further elaborations are required to account for length dependence and time-varying activation, and it retains a connection between macroscopic muscle behavior and microscopic contraction mechanisms.

KINETIC MODELS OF CONTRACTION

In his classic 1957 paper [7] A. F. Huxley proposed a mathematical theory to unify the then existing knowledge about muscle structure, mechanics, and energetics. A number of assumptions underlie models of this type. These have been reviewed by T. L. Hill [11] and include (1) the assumption that cross bridges are independent force generators, and (2) the assumption that at any instant of time each cross-bridge has accessible to it with significant probability only one actin binding site. Huxley's original theory assumed that a cross-bridge could exist in two biochemical states—an attached state and a detached state—and that in the former state it generated a force proportional to its displacement x from a neutral equilibrium position. The mathematical consequences of these assumptions may be summarized as follows. Let $n(x, t)$ be a distribution function representing the fraction of

attached cross-bridges with displacement (bond length) x at time t . Then assuming first-order kinetics for the actin-myosin bonding reaction, n satisfies the equation

$$\left(\frac{\partial n}{\partial t}\right)_x - v(t)\left(\frac{\partial n}{\partial x}\right)_t = f(x) - [f(x) + g(x)]n. \quad (3)$$

In the above f represents the forward (bonding) rate parameter, g represents the backward (unbonding) rate parameter, and $v(t)$ represents the speed of shortening of a half sarcomere. A critical assumption of the theory is that both of these parameters are functions of x , the distance from the equilibrium position of a cross-bridge. Once $n(x, t)$ has been determined, various macroscopic variables of interest can be computed as moments of this distribution. Thus assuming that the force-displacement characteristics of a cross-bridge are linear with a spring constant k , the force per unit area (the Eulerian stress) is

$$S(t) = \frac{P}{A} = \alpha C_1 \int_{-\infty}^{\infty} x n(x, t) dx, \quad (4)$$

where C_1 is a constant depending on the microstructural characteristics of the contractile tissue and α is a parameter indicating the level of activation. Specifically

$$C_1 = \frac{msk}{2l}, \quad (5)$$

where m is the number of cross-bridges per unit volume, s is the sarcomere length, l is the distance between successive actin binding sites, and k is the cross-bridge spring constant. If the muscle length and cross-sectional area do not vary too much, then the right-hand side of Eq. (4) can be assumed proportional to the muscle force. The activation parameter α can be interpreted as the fraction of actin binding sites which are available for interaction with the myosin cross bridges, or alternately αm can be regarded as the number of "participating" cross-bridges per unit volume. Both α and the rate parameters may be assumed to depend on the time course of stimulation, although the quantitative nature of this dependence is not well understood at present; if the stimulation remains constant for a sufficiently long time, then these parameters can be assumed constant, provided that the changes in muscle length are not too large.

Other macroscopic variables may be computed from $n(x, t)$ in a manner similar to the force. Thus while the force is proportional to the first-order moment of the bond distribution, the instantaneous stiffness k of the contractile tissue—that is, the force change per unit length change in a quick

stretch or release, not including tendon compliance—is proportional to the zero-order moment

$$k(t) = \alpha C_1 \int_{-\infty}^{\infty} n(x, t) dx \quad (6)$$

Equation (6) assumes linearly elastic cross-bridges and rigid myofilaments. In the original theory the total rate of energy liberation, \dot{E} , was computed for shortening muscle on the assumption that one ATP molecule was hydrolysed to ADP for each complete cycle of cross-bridge attachment and detachment. Thus

$$\dot{E}(t) = \alpha C_2 \int_{-\infty}^{\infty} g(x) n(x, t) dx \quad (7)$$

where

$$C_2 = \frac{m\varepsilon}{l}$$

and ε represents the hydrolysis energy of one ATP molecule. By assuming simple specific forms for the rate functions f and g , Huxley was able to secure excellent agreement between the predictions of this theory and the mechanical and heat measurements of A. V. Hill on shortening, tetanized frog muscle.

Since it was originally proposed, this theory has been developed and reviewed critically by its author and other workers [13–15]: while the general framework of the theory is still considered valid by most muscle physiologists, more precise experimental data on isolated muscle fibers have indicated the need for some revisions in its details. The major modification in the more recent models is that the cross-bridges are assumed to cycle between several biochemical states rather than just two. A thermodynamic formalism has been developed by T. L. Hill and his associates for constructing and analyzing models of this type. In place of a single equation like Eq. (3) for a two-state system, this formalism leads to a set of $N-1$ coupled first-order partial differential equations in a model where N distinct biochemical states are assumed for the cross-bridge [13],

$$\left(\frac{\partial p_i}{\partial t} \right)_x - v(t) \left(\frac{\partial p_i}{\partial x} \right)_t = \sum_{\substack{j=1 \\ j \neq i}}^N f_{ji}(x) p_j - p_i \sum_{\substack{j=1 \\ j \neq i}}^N f_{ij}(x), \quad i=1, 2, \dots, N-1, \quad (8)$$

with

$$\sum_{i=1}^N p_i = 1.$$

In these equations p_i represents the population probability of the i th biochemical state and f_{ij} represents the rate parameter for transitions from state i to state j . Further, the rate parameters are not independent, but are related to each other and to the displacement of the cross-bridge by equations of the form

$$f_{ij}/f_{ji} = e^{-(A_i - A_j)/\kappa T}, \quad (9)$$

where κ is Boltzmann's constant, T is the absolute temperature, and A_i is the free energy of state i (which includes the elastic energy of the cross-bridge if i is an attached state).

In the simplest case of a two-state model [one attached state (1) and one detached state (0)] such as that contemplated in Huxley's original version, the Hill formalism postulates two separate reaction paths between these states and results in a single equation on the distribution function $n(x, t)$ for the attached state [11],

$$\left(\frac{\partial n}{\partial t} \right)_x - v(t) \left(\frac{\partial n}{\partial x} \right)_t = [f(x) + g'(x)][1 - n(x, t)] - [f'(x) + g(x)]n(x, t), \quad (10)$$

where f and f' are respectively the rate parameters for attachment and detachment along the first reaction path, and g and g' are respectively the rate parameters for detachment and attachment along the second reaction path. These four functions can not be chosen arbitrarily but must satisfy the relations (9), i.e.

$$f/f' = e^{-(A_1 - A_0)/\kappa T} \quad \text{and} \quad g/g' = e^{-(A_0 - A_1 - \epsilon)/\kappa T}, \quad (11)$$

where A_0 and A_1 represent respectively the free energies of the detached and attached states. At constant temperature A_0 may be considered constant, while A_1 should be assumed quadratic in x ,

$$A_1(x) = A_1^0 + \frac{1}{2} kx^2, \quad (12)$$

if the cross-bridges are assumed linearly elastic. From a mathematical point of view Huxley's original theory (3) and Hill's refinement (10) have an identical form. Further, the force and stiffness are still computed by Eqs. (4) and (5) in the latter theory. But the rate of energy liberation becomes [11]

$$\dot{E} = \alpha C_2 \int_{-\infty}^{\infty} \{g(x)n(x, t) - g'(x)[1 - n(x, t)]\} dx, \quad (13)$$

which coincides with Eq. (7) only if $g \gg g'$; this condition will certainly be satisfied for large stretches, since then A_1 must become large due to the increase in elastic energy, and the detachment rate parameters f' and g must dominate according to Eq. (11).

EXACT SOLUTIONS OF THE HUXLEY MODEL

In the original presentation of his model [7] Huxley discussed only the steady-state solutions, but the general solution to Eq. (3) can easily be constructed by the method of characteristics. If we define

$$\xi(x, t) = x + \delta(t), \quad \text{where} \quad \delta(t) = \int_0^t v(\tau) d\tau, \quad (14)$$

and

$$H(x) = f(x) + g(x),$$

then Eq. (1) becomes

$$\left(\frac{\partial n}{\partial t} \right)_\xi = f\{\xi - \delta(t)\} - H\{\xi - \delta(t)\} n(\xi, t), \quad (15)$$

which may be integrated to give

$$\begin{aligned} n(\xi, t) = n_0(\xi) \exp \left[- \int_0^t H\{\xi - \delta(\tau)\} d\tau \right] \\ + \int_0^t f\{\xi - \delta(\tau)\} \exp \left[- \int_\tau^t H\{\xi - \delta(\beta)\} d\beta \right] d\tau, \end{aligned} \quad (16)$$

where $n_0(x)$ is the distribution at $t=0$. If $v(t)$ is specified, Eq. (16) can be used to compute n and therefore $S(t)$, $k(t)$, and other macroscopic quantities of interest. The first term on the right-hand side of Eq. (16) is a transient representing the influence of initial conditions, and decays with time for reasonable functions $H(x)$. If v is constant, then it is easy to show that as $t \rightarrow \infty$ the second term on the right-hand side of Eq. (16) yields the steady-state (time-independent) solution

$$n(x) = - \frac{1}{v} \int_{\pm\infty}^x f(\eta) \exp \left[- \frac{1}{v} \int_x^\eta H(\beta) d\beta \right] d\eta, \quad (17)$$

where the plus sign on the lower limit of the outer integration applies if $v > 0$ and the minus sign applies if $v < 0$.

The character of these solutions is exhibited in Fig. 2, which shows the time evolution of the bond distribution in a constant-velocity release from an

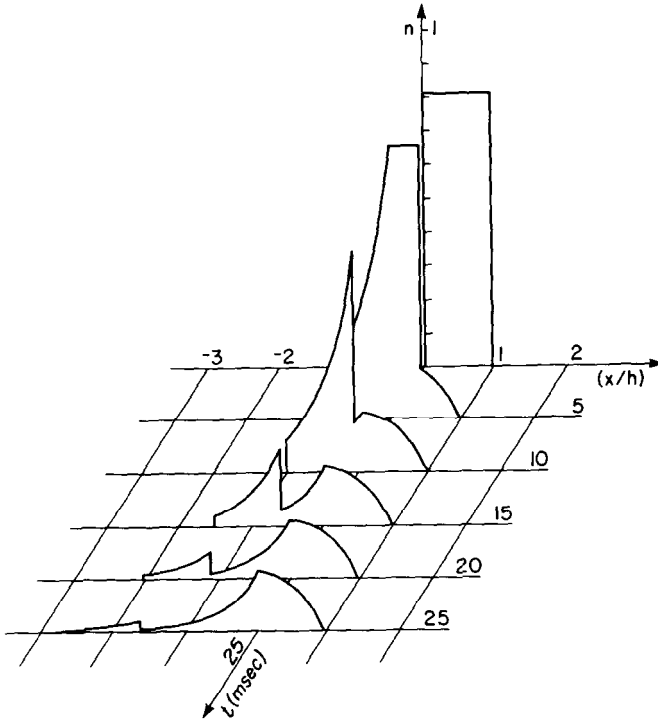


FIG. 2. Time evolution of the bond-distribution function $n(x, t)$ during a constant-velocity release starting from an isometric state. Huxley model, Eq. (3), with $f_1 = 43.3 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 209 \text{ sec}^{-1}$, and $v/h = 110 \text{ sec}^{-1}$.

isometric state. In this example, the specific rate functions used by Huxley in his 1957 paper are used for purposes of illustration, namely

$$f(x) = \begin{cases} 0, & -\infty < x < 0, \\ f_1 \left(\frac{x}{h} \right), & 0 < x < h, \\ 0, & h < x < \infty, \end{cases} \quad (18a)$$

and

$$g(x) = \begin{cases} g_2, & -\infty < x < 0, \\ g_1 \left(\frac{x}{h} \right), & 0 < x < \infty. \end{cases} \quad (18b)$$

Figure 2 shows that the distribution settles down quickly to its steady-state form, and the hyperbolic character of the governing differential equation is

apparent in the propagation of discontinuities of the initial data along the characteristics $\xi = \text{const}$. As noted previously, for linearly elastic cross-bridges the force is proportional to the first moment of the distribution, and the fact that the centroid of the steady-state distribution is close to $x=0$ indicates that the release velocity is close to the maximum velocity of unloaded shortening in this example.

The forms of the rate functions (18) were chosen by Huxley for mathematical simplicity and convenience, and the values $f_1 = 43.3 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, and $g_2 = 209 \text{ sec}^{-1}$ were chosen to provide the best fit of the steady-state response to the mechanical and heat data obtained by A. V. Hill for tetanized isotonically shortening frog muscle. The consequence of these assumptions was that while the model predictions corresponded very well with the experimental observations for shortening muscle, they were greatly in error for lengthening muscle. In particular, under the stated assumptions, (1) the model does not exhibit "yielding" on stretch, and (2) for large stretch velocities the force approaches 5.33 times the isometric force, a value much larger than observed in experiments. These results are essentially consequences of the assumption that the detachment rate parameter g remains small for large values of the cross-bridge stretch x . But both physical intuition and Eq. (11) indicate that this is unlikely to be the case: for large values of bond stretch the elastic energy of the attached state becomes large and detachment should dominate. Therefore for purposes of this paper a minimal modification of the rate functions will be introduced which leaves the behavior of the model in shortening unaffected, but produces a more realistic response in stretch by making the detachment rates high for large bond stretch. Thus the modified form of $g(x)$ is taken as

$$g(x) = \begin{cases} g_2, & -\infty < x < 0, \\ g_1 \left(\frac{x}{h} \right), & 0 < x < h, \\ g_1 \left(\frac{x}{h} \right) + g_3 \left(\frac{x}{h} - 1 \right), & h < x < \infty, \end{cases} \quad (19)$$

which introduces only one additional rate parameter g_3 ; if g_3 is set equal to zero one recovers the original Huxley rate parameters. This modified model retains the simplicity of Huxley's original and is adequate to illustrate the approximation procedure presented in the next section. The effect of the modified $g(x)$ on the model response is illustrated in Fig. 3: as noted, the shortening response is unaffected, while the stretch response becomes more realistic, exhibiting some yielding and a decrease in the steady-state force.

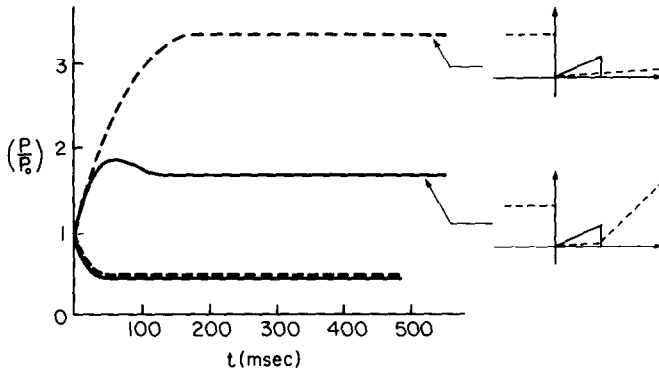


FIG. 3. Effect of modifying the unbonding rate function $g(x)$ on the performance of the Huxley model. Parameter values: $f_1 = 43.3 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 209 \text{ sec}^{-1}$, $v/h = \pm 20 \text{ sec}^{-1}$. Dashed lines correspond to $g_3 = 0$ (unmodified Huxley model), and solid lines correspond to $g_3 = 50 \text{ sec}^{-1}$ (modified Huxley model).

THE APPROXIMATION

The following mathematical approximation scheme was motivated by the fact that while Huxley's and similar kinetic theories of contraction require a solution for the bond distribution function(s), only certain moments of these functions are needed to describe macroscopic muscle behavior. Thus the scheme aims at a direct approximation of these moments, avoiding the solution of the partial differential equations governing the bond distributions. For Huxley's equation the scheme is implemented as follows: multiply both sides of Eq. (3) by x^λ ($\lambda = 0, 1, 2, \dots$) and integrate over the domain of x :

$$\int_{-\infty}^{\infty} x^\lambda \left\{ \frac{\partial n}{\partial t} - v(t) \frac{\partial n}{\partial x} \right\} dx = \int_{-\infty}^{\infty} x^\lambda \{ f(x) - [f(x) + g(x)]n \} dx.$$

This gives

$$\begin{aligned} \frac{d}{dt} \int_{-\infty}^{\infty} x^\lambda n dx - v(t) \int_{-\infty}^{\infty} x^\lambda \frac{\partial n}{\partial x} dx \\ = \int_{-\infty}^{\infty} x^\lambda f(x) dx - \int_{-\infty}^{\infty} x^\lambda [f(x) + g(x)]n dx. \end{aligned} \quad (20)$$

But

$$\int_{-\infty}^{\infty} x^\lambda \frac{\partial n}{\partial x} dx = [x^\lambda n]_{-\infty}^{\infty} - \lambda \int_{-\infty}^{\infty} x^{\lambda-1} n dx = -\lambda \int_{-\infty}^{\infty} x^{\lambda-1} n dx,$$

as it may be assumed that $x^\lambda n$ vanishes for large absolute x . Further define $M_\lambda(t)$ as

$$M_\lambda(t) = \int_{-\infty}^{\infty} x^\lambda n(x, t) dx, \quad (21)$$

the λ th moment of the bond-distribution function, and b_λ as

$$b_\lambda = \int_{-\infty}^{\infty} x^\lambda f(x) dx, \quad (22)$$

the λ th moment of the bonding rate function. Then Eq. (20) can be written as

$$\begin{aligned} \frac{dM_\lambda}{dt} + \lambda v(t) M_{\lambda-1} &= b_\lambda - \int_{-\infty}^{\infty} x^\lambda [f(x) + g(x)] n(x, t) dx, \\ \lambda &= 0, 1, 2, \dots \end{aligned} \quad (23)$$

If n is regarded as known, then the equations (23) are an infinite set of coupled linear first-order ordinary differential equations on the moments of the bond distribution: these equations are completely equivalent to Eq. (3), as the complete set of moments of a function determines the function. There has been no approximation up to this point, but neither can the moments be determined from Eq. (23), because $n(x, t)$ is not known unless Eq. (3) is solved subject to appropriate initial conditions.

If, however, a reasonable functional form can be postulated *a priori* for n , then the equations (21) become explicit differential equations for the moments $M_\lambda(t)$; further, this remains true if the approximating function is assumed to depend explicitly on the moments. Of course the accuracy of the moments determined by integrating these equations depends on the accuracy with which the postulated distribution models the exact solution to the original partial differential equation. A compromise must be struck between a desire for accuracy and for simplicity. It is proposed here to approximate n by a Gaussian distribution

$$n(x, t) \doteq \frac{M_0(t)}{\sqrt{2\pi}\sigma(t)} e^{-[x - \mu(t)]^2 / 2\sigma^2(t)}, \quad (24)$$

where

$$\mu(t) = \frac{M_1(t)}{M_0(t)} \quad \text{and} \quad \sigma(t) = \left\{ \frac{M_2(t)}{M_0(t)} - \left[\frac{M_1(t)}{M_0(t)} \right]^2 \right\}^{1/2}. \quad (25)$$

Thus $n(x, t)$ is approximately characterized by its first three moments $M_0(t)$, $M_1(t)$, and $M_2(t)$ —or equivalently by the area under the distribution, the

centroid of the distribution, and its standard deviation. If Eq. (24) is inserted into the equations (23) and the first three of the latter are retained, one obtains

$$\begin{aligned}\frac{dM_0}{dt} &= b_0 - F_0(M_0, M_1, M_2), \\ \frac{dM_1}{dt} &= b_1 - F_1(M_0, M_1, M_2) - v(t)M_0, \\ \frac{dM_2}{dt} &= b_2 - F_2(M_0, M_1, M_2) - 2v(t)M_1.\end{aligned}\tag{26}$$

The equations (26) are the final result of applying the proposed approximation scheme to a two-state model governed by equations like (3) or (10), and will be referred to as the distribution-moment (DM) Model. The original partial differential equation is replaced by three ordinary differential equations on the first three moments. The exact forms of the functions F_1 , F_2 , and F_3 depend on the assumed form of the rate functions as well as on the approximate form of $n(x, t)$: these functions are calculated explicitly in Appendix A for the Gaussian approximation to n , Eq. (24), and the (modified) Huxley rate functions, Eqs. (18a) and (19); these specific forms were used in the illustrative examples presented in the remainder of this paper. The equations (26) were integrated numerically with a straightforward Cauchy-Euler algorithm.

For constant velocity the equations (26) become an autonomous system, and steady-state solutions are given by the singular points corresponding to solutions of the system of simultaneous equations obtained by setting the left sides of (26) equal to zero. For the particular case $v=0$ the steady-state solution corresponds to an isometric state and provides initial conditions on M_0 , M_1 , and M_2 in the simulations presented below.

An inspection of Fig. 2 indicates that the assumed Gaussian distribution may be a rather crude model for the detailed variation of $n(x, t)$ with x . Nevertheless this assumption appears to be adequate for a description of the macroscopic parameters such as force, stiffness, and energy which depend on integrals of the distribution and not on its detailed variation. This point is illustrated in Figs. 4 and 5, which compare the performance of the DM model with the unmodified Huxley model using exactly the same values of the rate parameters in both cases. Figure 4 exhibits the tension response in constant-velocity stretches and releases as function of time. Figure 5 shows the force and the rate of energy liberation [Eqs. (4) and (7)] as functions of velocity in steady-state shortening. While the correspondence is not perfect, it is reasonably good, and could be expected to be even better if the parameters of the DM model were left adjustable rather than being fixed at the same values as those of the Huxley model.

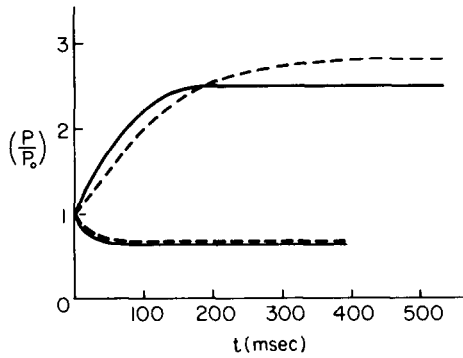


FIG. 4. Comparison of the transient constant-velocity stretch and release responses of the (unmodified) Huxley model and the DM approximation. Parameters: $f_1 = 43.3 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 209 \text{ sec}^{-1}$, $g_3 = 0$, $v/h = \pm 10 \text{ sec}^{-1}$. Solid lines correspond to the Huxley model, and dashed lines correspond to the DM approximation.

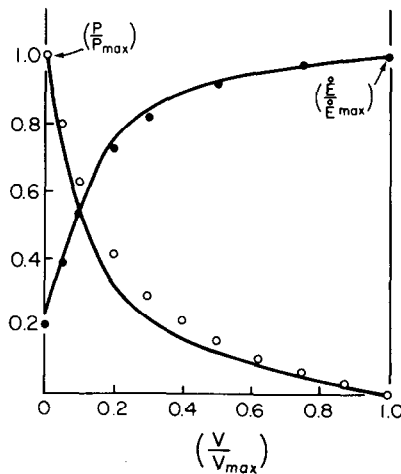


FIG. 5. Comparison of the steady-state response of the (unmodified) Huxley model and the DM approximation for shortening at constant velocity. Parameters: $f_1 = 43.3 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 209 \text{ sec}^{-1}$, $g_3 = 0$. For both the DM approximation and the parent Huxley model the velocities have been normalized with respect to the maximum velocity of unloaded shortening, the forces have been normalized with respect to the isometric force, and the energy rates have been normalized with respect to the rate at maximum velocity.

Having established that the performance of the DM model is substantially equivalent to that of its parent Huxley model, the predictions of the former will be exhibited in some cases of experimental interest. The modified $g(x)$, Eq. (19), will be used throughout. Up to this point the rate parameters f_1 , g_1 , g_2 , and g_3 have been regarded as constants, an assumption which is appropriate if the muscle is subjected to constant stimulation (and the length does not vary too much). In order to gauge the possible effects of different levels of constant stimulation, one could vary the magnitudes of the rate parameters. Figure 6 shows the tension response of the DM model to a constant-velocity release or stretch lasting 400 milliseconds starting from an isometric state. The muscle is held isometrically after the release or stretch. The bonding rate constant f_1 is varied to simulate variations in stimulation intensity. On release the force drops rapidly to its steady-state value, al-

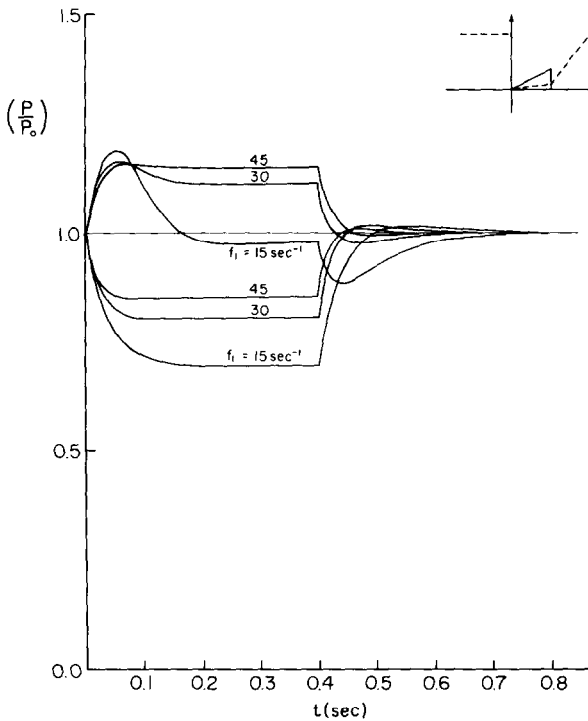


FIG. 6. Force response of the DM approximation to the modified Huxley model during a ramp-and-hold change in length. The speed during the ramp is $v/h = 5 \text{ sec}^{-1}$, for both stretch and release. The ramp starts at $t = 0 \text{ sec}$ and terminates at $t = 0.4 \text{ sec}$. Parameters $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 210 \text{ sec}^{-1}$, $g_3 = 100 \text{ sec}^{-1}$, and the values of f_1 are indicated on their associated response curves.

though the drop is slower at low values of f_1 . At the end of the ramp release the force rapidly recovers its isometric value, but again the recovery is slower at the lower values of f_1 . Also there is a slight overshoot in the force before it returns to the isometric value. More dramatic efforts are evident on stretch. At the highest f_1 the stretch response is qualitatively a mirror image of the corresponding release response. But at lower values of the bonding rate the muscle "yields"—that is, the force decreases abruptly after the initial sharp increase: the magnitude of the yielding increases as f_1 decreases. At sufficiently low f_1 the force during stretch drops to a steady-state value lower than the initial isometric force. Further, on recovery at the end of the stretch the force undershoots its final isometric value, and this undershoot can be considerable at low values of f_1 .

Figure 7 shows some force responses of the DM model to sinusoidal stretch. For each trace the muscle stretch as a function of time is of the form

$$v(t) = v_0 \sin(2\pi t/T), \quad (27)$$

with v_0 held constant and the period of oscillation T varied. The bonding rate

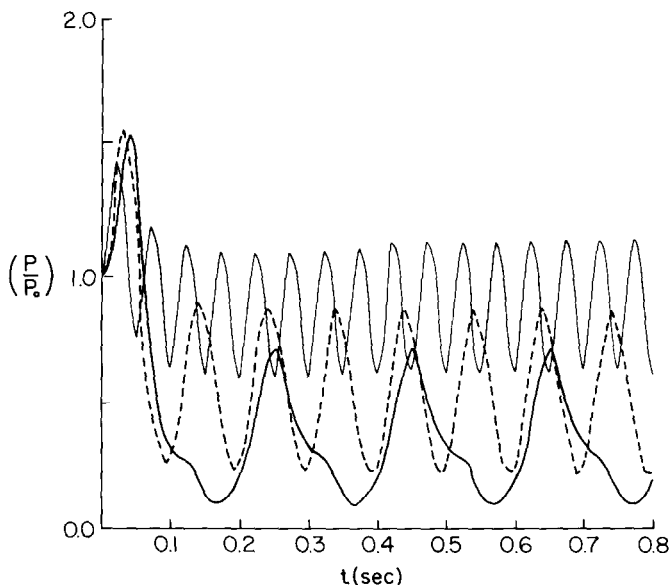


FIG. 7. Force response of the DM approximation to the modified Huxley model during a stretch starting from an isometric state at $t=0$ sec and varying sinusoidally with time. The velocity is of the form $v(t) = v_0 \sin(2\pi t/T)$ for $t > 0$. Parameters: $f_1 = 1 \text{ sec}^{-1}$, $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 210 \text{ sec}^{-1}$, $g_3 = 100 \text{ sec}^{-1}$, $v_0/h = -25 \text{ sec}^{-1}$. Upper solid curve: $T = 0.05 \text{ sec}^{-1}$; dashed curve: $T = 0.10 \text{ sec}^{-1}$; lower solid curve: $T = 0.20 \text{ sec}^{-1}$.

parameter has been set equal to a low value for all three traces. It is seen that in all cases the mean force during oscillatory stretching drops below the isometric force: the (relative) drop is slight for high-frequency, low-amplitude oscillations and becomes large at low frequencies and large amplitudes. Further, the harmonic distortion of the force response increases progressively as the mean force decreases.

Various features of the model response described in the last two paragraphs correspond at least qualitatively to actual observed behavior of isolated muscle under constant controlled stimulation. These features include pronounced yielding at low to moderate stimulation rates and less or no yielding at high stimulation rates (for a given velocity), the possibility of forces during stretch which fall below the isometric force, the drop in the mean force below the isometric level during oscillatory stretch, and the harmonic distortion of the force waveform with oscillatory stretches of increasing amplitude. One effect not considered so far is the possibility that the rate parameters vary with muscle length, but it is necessary to admit this possibility if the model is to reproduce the marked length dependence of muscle behavior [6]. For purposes of illustrating the potential of the model Fig. 8 has been included; the specific assumptions and parameter values underlying the construction of this figure are listed in Appendix B. In this calculation the detachment rate parameters g_1 , g_2 , and g_3 have been held constant, while the activation parameter α has been allowed to vary with muscle length, and the attachment rate parameter f_1 has been allowed to vary with both length and stimulation. The assumed variations of these parameters are shown in the inset to Fig. 8. It is emphasized that no claim is made that these parameters actually vary in the way shown; this is a question that will require a detailed examination of the model in the light of more extensive quantitative data than are currently available to the author. But if the parameters are assumed to vary as indicated, then the force-length trajectories shown in Fig. 8 follow from (26). Comparison of the stretch trajectories, say, at $\dot{L} = 13$ mm/sec with Fig. 3 of [6] shows that the model response is indeed realistic. Features of the model response which correspond to actual observed response include (1) pronounced yielding at low and intermediate stimulation and little yielding at high stimulation (unless the velocity becomes high), (2) a decrease in the force to levels below the isometric force at the current length, (3) a "scaling down" of the stretch response at a given stimulus rate with decreasing initial muscle length. Further, an interesting aspect of the model behavior is that it exhibits "asymptotic" responses in the following sense: starting at any initial isometric state, the force first changes in a transient manner and then approaches a trajectory

$$P = \phi(L; \dot{L}, \nu) \quad (28)$$

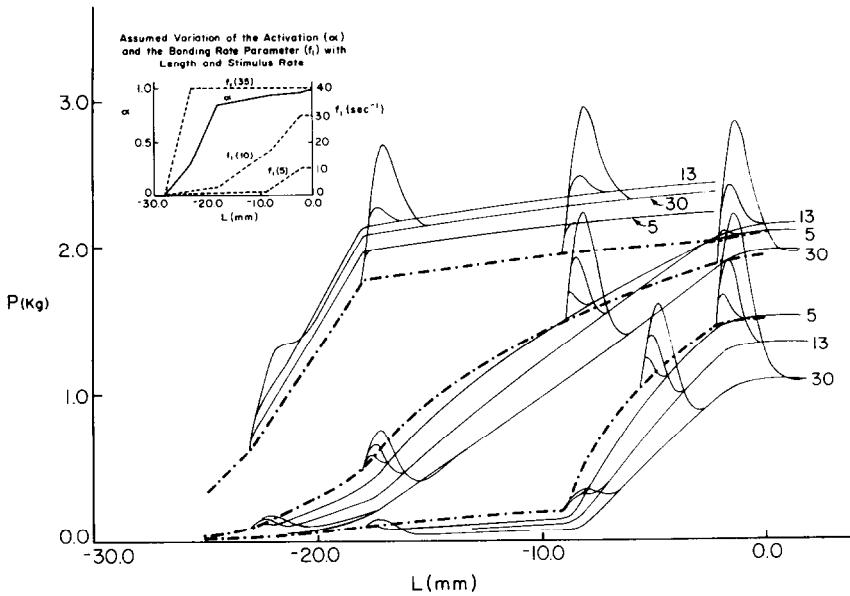


FIG. 8. Tension-length trajectories for a muscle subjected to constant-velocity stretches starting from isometric states corresponding to various initial lengths and stimulus rates, according to the DM approximation for the modified Huxley model. The inset shows the assumed variations of the activation parameter and the bonding rate parameter with muscle length and stimulus rate, and three heavy interrupted curves in the main diagram are the resulting isometric length-tension curves for stimulus rates of 5, 10, and 35 impulses/sec. The thin curves in the main diagram are the stretch responses and are labeled with the stretch velocity in mm/sec. Details of this calculation, and numerical values of all relevant parameters (the choice of which was motivated by the cat soleus data of Joyce et al. [6]) are given in Appendix B.

depending on the muscle length L , the velocity \dot{L} , and the stimulation ν . Equation (28) will be termed the “asymptotic response trajectory” corresponding to a given velocity and stimulation rate, because the force $P(L)$ approaches this curve (after a brief transient) regardless of initial conditions. An examination of Joyce et al.’s data (Fig. 3, [6]) strongly suggests that real muscle exhibits such asymptotic responses, although the stretches applied in those experiments were not long enough to define the trajectories clearly. Figure 8 displays a number of asymptotic trajectories for various stimulation rates and stretch velocities. Note that these trajectories may intersect other trajectories or the isometric curves (the zero-velocity trajectories). Similar calculations for constant-velocity releases show that the transient shortening trajectories do not intersect and that they too approach asymptotic limit

curves (although if the imposed shortening speed is too high, the force will drop to zero before the asymptotic trajectory is attained).

DISCUSSION

The result of the mathematical approximation scheme proposed in this paper is to reduce a comparatively complicated mathematical model of muscle contraction, embodied in partial differential equations such as (3) or (10), to a comparatively simple model embodied in the three ordinary differential equations (26). The second equation of (26) resembles the classic two-element model (1), because in view of Eqs. (4) and (6) it can be written as

$$\dot{L} = C\dot{P} - \left[M_0^{-1} \{ b_1 - F_1(M_0, M_1, M_2) \} \right], \quad (29)$$

but the resemblance is superficial, because the last term in this equation is not determined by muscle length, velocity, and stimulation rate. Equation (29) must be integrated with the other two equations of (26) to determine simultaneously M_0 , M_1 , and M_2 , and it is this fact that leads to the richer repertoire of responses of the DM model.

The DM approximation is, of course, no substitute for the full partial differential equations in cases where detailed and precise calculations of the complete kinetic model response are necessary. The DM model yields, after all, only an approximation to the solutions of the kinetic equations. It has, however, several features which make it attractive as a mathematical representation of macroscopic, whole-muscle behavior. (One must not lose sight of the fact that the kinetic theories concentrate on the actin-myosin interaction in contractile tissue and usually ignore complicating factors such as tendon stiffness, the distribution of passive elasticity, and tissue-fluid viscosity, which are difficult to evaluate quantitatively but may assume some importance for whole muscle *in vivo*). The virtues of the DM model may be summarized as follows:

- (1) It is simple in structure (approaching the simplicity of the classic SE/CE model) and easily tractable analytically and computationally.
- (2) It permits a direct computation of the low-order moments, representing quantities of physical interest such as the force or the contractile-tissue stiffness, without the necessity of first determining the bond distribution functions.
- (3) Even when based on the simplest two-state kinetic theory, it is capable of realistically approximating, at least qualitatively, the complicated experimental behavior of skeletal muscle in stretch, shortening, and oscillation.

(4) It provides a direct mathematical connection between the microscopic parameters of contraction contained in the kinetic theories and the macroscopic parameters of a whole-muscle model.

(5) Because the basic model (26) is comparatively simple, it remains tractable when elaborations are introduced to account for the effects of muscle length and varying stimulation.

Despite these encouraging attributes, a number of important questions remain to be resolved. A minor and easily remedied deficiency of the model as presented in this paper is the lack of a genuine "series" elasticity to represent the tendonacious component of muscle; as it stands, the only stiffness included in the model is that of the contractile tissue. A more formidable problem is the determination of how the activation and rate parameters vary with muscle length and stimulation level. Presumably this question should be approached via detailed quantitative comparisons of the model predictions with extensive mechanical and thermodynamic measurements to find the parameter variations which produce an optimum correspondence between model and experiment; this process should be guided qualitatively by available biophysical and biochemical information. Probably the most difficult question which must be settled before the DM model can serve as a useful quantitative description of whole-muscle behavior is the connection between time-varying electrical stimulation, the activation parameter α , and the rate parameters: at present there seems to be a very sparse experimental basis for addressing this problem.

While the equations (26) have been referred to as *the* DM model, it is clear that the suggested approximation procedure embodied in (23) is capable of generating models of varying degrees of sophistication and complexity, depending on the parent kinetic theory and the functional forms chosen to represent the distribution functions. Thus one could try to represent $n(x, t)$ by an N -parameter functional form retaining the first N equations of (23); in the limit an infinite series expansion could be assumed for $n(x, t)$, and (23) used to determine the parameters of the series as functions of time. While such elaborations are possible, they would quickly reduce the simplicity of the approximate model to the point where it would have no advantage over the full kinetic theory. The third-order system of equations (26), based on a two-state kinetic theory and a Gaussian representation of the bond distribution, appears to be the simplest model of this type capable of showing physically realistic behavior. The extent to which the predictions of this simplest model can be correlated quantitatively with experimental measurements remains for future work to determine.

A final comment can be made regarding the "asymptotic" trajectories predicted by the model and displayed in Figure 8. Houk et al. [16] have

observed strikingly similar behavior in the relation between the firing rates of cat soleus spindle afferents and muscle length during constant-velocity stretches. In these experiments it was observed that after a brief transient the firing rate settled down to an asymptotic response curve independent of initial conditions, but in contrast to the trajectories for muscle, the asymptotic firing-rate-length trajectories for spindles were straight lines. These observations suggest that such asymptotic responses are inherent characteristics of the mechanical behavior of contractile tissue and that they may determine the firing rate of spindles, but the precise nature of this connection is unclear at present.

CONCLUSIONS

A mathematical procedure, termed the distribution-moment (DM) approximation, has been proposed for approximating solutions to the partial differential equations of cross-bridge kinetics. The procedure permits direct computation of estimates for the low-order moments of the bond-distribution functions (and therefore approximations for macroscopic variables of interest such as the stiffness, force, and energy liberation rate) without the necessity of solving the relevant partial differential equations. This represents a considerable conceptual and computational simplification, and results effectively in a lumped parameter model for muscle which approaches the simplicity of the classic two-element model. However, in contrast to the latter model, the DM approximation has the virtues, among others, that (1) it is capable of predicting realistic mechanical responses in both stretch and shortening, and (2) it retains a direct (albeit approximate) connection between macroscopic muscle behavior and molecular contraction mechanisms. Detailed calculations have been presented for the original Huxley two-state model and a modification thereof, and it has been shown that the behavior of the resulting DM model is essentially equivalent, so far as macroscopic parameters are concerned, to the parent kinetic model. Further it has been shown that length dependences of the activation and rate parameters can be postulated which produce experimentally realistic behavior of the DM model in constant-velocity stretches and releases, although these postulated dependences must be regarded as speculative at this point. The DM approximation has the potential of yielding a reasonably simple and accurate mathematical model of muscle which could be useful in studies of limb dynamics, reflex function, and related areas, but the details of the optimal model (choice of parent kinetic theory, approximating functions for the bond distributions, length dependences of the activation and rate parameters) remain for future analysis and experimentation to resolve.

APPENDIX A—THE FUNCTIONS F_0 , F_1 , AND F_2 FOR THE (MODIFIED) HUXLEY MODEL

In this appendix the functions $F_0(M_0, M_1, M_2)$, $F_1(M_0, M_1, M_2)$, and $F_3(M_0, M_1, M_2)$ entering Eqs. (26) are constructed explicitly. Define

$$\xi = \frac{x}{h}, \quad Q_\lambda = \frac{M_\lambda}{h^{\lambda+1}}, \quad \beta_\lambda = \frac{b_\lambda}{h^{\lambda+1}}, \quad u = \frac{v}{h},$$

$$p = \frac{\mu}{h}, \quad q = \frac{\sigma}{h}, \quad \phi_\lambda = \frac{F_\lambda}{h^{\lambda+1}} = \int_{-\infty}^{\infty} \xi^\lambda [f(\xi) + g(\xi)] n(\xi, t) d\xi, \quad (\text{A-1})$$

where

$$n(\xi, t) = \frac{Q_0}{\sqrt{2\pi}q} e^{-(\xi-p)^2/2q^2}, \quad (\text{A-2})$$

$$p(Q_0, Q_1) = \frac{Q_1}{Q_0} \quad \text{and} \quad q(Q_0, Q_1, Q_2) = \sqrt{\frac{Q_2}{Q_0} - \left(\frac{Q_1}{Q_0}\right)^2}. \quad (\text{A-3})$$

The function n is implicitly a function of time through Q_0 , Q_1 , and Q_2 . With these definitions the equations (26) can be written as

$$\frac{dQ_\lambda}{dt} = \beta_\lambda - \phi_\lambda(Q_0, Q_1, Q_2) - \lambda u Q_{\lambda-1}, \quad \lambda = 1, 2, 3. \quad (\text{A-4})$$

For the modified Huxley model we take

$$f(\xi) = \begin{cases} 0, & \xi < 0, \\ f_1\xi, & 0 < \xi < 1, \\ 0, & 1 < \xi \end{cases} \quad \text{and} \quad g(\xi) = \begin{cases} g_2, & \xi < 0, \\ g_1\xi, & 0 < \xi < 1, \\ g_1\xi + g_3(\xi - 1), & 1 < \xi. \end{cases} \quad (\text{A-5})$$

Thus for rate functions of this specific form

$$\begin{aligned} \phi_\lambda = & g_2 Q_0 \int_{-\infty}^0 \frac{1}{\sqrt{2\pi}q} \xi^\lambda e^{-(\xi-p)^2/2q^2} d\xi \\ & + (f_1 + g_1) Q_0 \int_0^1 \frac{1}{\sqrt{2\pi}q} \xi^{\lambda+1} e^{-(\xi-p)^2/2q^2} d\xi \\ & + (g_1 + g_3) Q_0 \int_1^\infty \frac{1}{\sqrt{2\pi}q} \xi^{\lambda+1} e^{-(\xi-p)^2/2q^2} d\xi \\ & - g_3 Q_0 \int_1^\infty \frac{1}{\sqrt{2\pi}q} \xi^\lambda e^{-(\xi-p)^2/2q^2} d\xi. \end{aligned} \quad (\text{A-6})$$

Consider an integral of the form

$$J_k(\eta) = \frac{1}{\sqrt{2\pi}q} \int_{-\infty}^{\eta} \xi^k e^{-(\xi-p)^2/2q^2} d\xi. \quad (\text{A-7})$$

If $\zeta = (\xi - p)/q$ and $\tau = (\eta - p)/q$, we may write

$$J_k(\tau) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\tau} (p + q\zeta)^k e^{-\zeta^2/2} d\zeta. \quad (\text{A-8})$$

If the integrand of Eq. (A-8) is expanded there result a series of integrals of the form

$$I_k(\tau) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\tau} \zeta^k e^{-\zeta^2/2} d\zeta \quad (\text{A-9})$$

Integration of Eq. (A-9) by parts leads to the recurrence formula

$$kI_{k-1} = \frac{\tau^k e^{-\tau^2/2}}{\sqrt{2\pi}} + I_{k+1} \quad (\text{A-10})$$

with $I_0(\tau) = \Phi(\tau) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\tau} e^{-\zeta^2/2} d\zeta$, the error function, and

$$I_1(\tau) = -\frac{e^{-\tau^2/2}}{\sqrt{2\pi}}.$$

In view of Eq. (A-10), the equations (A-8) become

$$J_0(\tau) = \Phi(\tau)$$

$$J_1(\tau) = p\Phi(\tau) - q \frac{e^{-\tau^2/2}}{\sqrt{2\pi}}$$

$$J_2(\tau) = p^2\Phi(\tau) - 2pq \frac{e^{-\tau^2/2}}{\sqrt{2\pi}} + q^2 \left\{ \Phi(\tau) - \frac{\tau e^{-\tau^2/2}}{\sqrt{2\pi}} \right\} \quad (\text{A-11})$$

$$J_3(\tau) = p^3\Phi(\tau) - 3p^2q \frac{e^{-\tau^2/2}}{\sqrt{2\pi}} + 3pq^2 \left\{ \Phi(\tau) - \frac{\tau e^{-\tau^2/2}}{\sqrt{2\pi}} \right\} - q^3(2 + \tau^2) \frac{e^{-\tau^2/2}}{\sqrt{2\pi}}$$

Inserting (A-11) into (A-6), we obtain

$$\begin{aligned}
 \frac{\phi_0}{Q_0} &= g_2 J_0\left(-\frac{p}{q}\right) + (f_1 + g_1) \left[J_1\left(\frac{1-p}{q}\right) - J_1\left(-\frac{p}{q}\right) \right] \\
 &\quad + g_1 \left[p - J_1\left(\frac{1-p}{q}\right) \right] + g_3 \left[p - J_1\left(\frac{1-p}{q}\right) - 1 + J_0\left(\frac{1-p}{q}\right) \right], \\
 \frac{\phi_1}{Q_0} &= g_2 J_1\left(-\frac{p}{q}\right) + (f_1 + g_1) \left[J_2\left(\frac{1-p}{q}\right) - J_2\left(-\frac{p}{q}\right) \right] \\
 &\quad + g_1 \left[p^2 + q^2 - J_2\left(\frac{1-p}{q}\right) \right] + g_3 \left[p^2 + q^2 - J_2\left(\frac{1-p}{q}\right) - p + J_1\left(\frac{1-p}{q}\right) \right], \\
 \frac{\phi_2}{Q_0} &= g_2 J_2\left(-\frac{p}{q}\right) + (f_1 + g_1) \left[J_3\left(\frac{1-p}{q}\right) - J_3\left(-\frac{p}{q}\right) \right] \\
 &\quad + g_1 \left[p^3 + 3pq^2 - J_3\left(\frac{1-p}{q}\right) \right] \\
 &\quad + g_3 \left[p^3 + 3pq^2 - J_3\left(\frac{1-p}{q}\right) - (p^2 + q^2) + J_2\left(\frac{1-p}{q}\right) \right].
 \end{aligned} \tag{A-12}$$

The above equations together with (A-11), (A-3), and the scaling relations (A-1) define F_0 , F_1 , and F_2 as explicit functions of M_0 , M_1 , and M_2 , and these F_i were inserted into the right-hand sides of the equations (26) to compute numerically the DM model responses exhibited in this paper.

APPENDIX B—CALCULATION OF THE DM MODEL RESPONSE WITH LENGTH-DEPENDENT PARAMETERS

In the construction of Fig. 8 it was necessary to consider variations of activation and rate parameters with muscle length, and to allow for large changes in length. The assumptions underlying this calculation are described below.

First, the muscle is assumed to be homogeneous cylinder of incompressible contractile tissue, and the compliance of the tendons is ignored. Next, it must be recognized that Eq. (4) gives the Eulerian stress $S(t)$ rather than the muscle force $P(t)$. If length and area changes are small S and P are approximately proportional, but if large length changes are contemplated, as in this calculation, the difference between stress and force must be accounted for. The parameters k and l can be considered constant for a given muscle, and so can the parameter m if the muscle is assumed incompressible. Then the muscle force can be expressed as [Eq. (4)]

$$P = \alpha A C_1 M_1 = \alpha A \left(\frac{mskh^2}{2l} \right) Q_1. \tag{B-1}$$

The assumed incompressibility of muscle implies that $AL = A_0 L_0$, where A and L are the current cross-sectional area and length and A_0 is the cross-sectional area in a reference state when the length is L_0 . Further, as the total length of the contractile tissue is proportional to the sarcomere length s , we may write $L_0/s_0 = L/s$, where s_0 is the sarcomere length when the muscle is at the reference length L_0 . Inserting these two relations into Eq. (B-1), we obtain

$$P = \alpha A_0 \left(\frac{ms_0 kh^2}{2l} \right) Q_1. \quad (\text{B-2})$$

Equations (B-1) and (B-2) show that if the activation and the first moment of the bond distribution are constant, then the muscle force (and the Lagrangian stress, which is the force per unit *reference* area) remain constant, while the Eulerian stress (the force per unit *current* area) increases with muscle length. It is assumed that variations in the number of effective cross-bridges are accounted for by the length dependence of the activation parameter α .

According to Eq. (B-2) the force is jointly proportional to α and Q_1 ; the latter variable in turn is determined from a solution of the equations (A-4) together with a fourth equation

$$\frac{dL}{dt} = - \left(2h \frac{L_0}{s_0} \right) u \quad (\text{B-3})$$

which accounts for changes in the muscle length L . In (A-4) the unbonding rate parameters were given the values $g_1 = 10 \text{ sec}^{-1}$, $g_2 = 210 \text{ sec}^{-1}$, and $g_3 = 100 \text{ sec}^{-1}$, while the bonding rate parameter f_1 was assumed to vary with L as shown in the inset to Fig. 8. When f_1 is given its highest assumed value of 40 sec^{-1} , the equations (A-4) yield the isometric value $Q_1 = 0.413$, so it was assumed that

$$A_0 \left(\frac{ms_0 kh^2}{2l} \right) = 5.08 \text{ kg}, \quad (\text{B-4})$$

which gives a value of 2.1 kg for the tetanic force when $\alpha = 1$ (this value is typical for cat soleus). Finally the assignment was made that

$$\left(2h \frac{L_0}{s_0} \right) = 1.45 \text{ mm}. \quad (\text{B-5})$$

With these parameters specified, the equations (A-4) were integrated to produce the tension-length trajectories exhibited in Fig. 8.

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