LifeMOD/Fitness IQ Male Shake Weight Report

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This report details the analysis preformed using LifeMOD to compare muscular reactions for the Shake Weight and a normal dumbbell curl exercise.

MALE REPORT

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1.0 Introduction

This report details the analysis preformed using LifeMOD to compare muscular reactions for the Shake Weight and a normal dumbbell curl exercise. It compares total body energy intake and various muscle group force firing patterns for the Shake Weight and a dumbbell of comparable mass. The analysis was performed for a period of 3 seconds for each exercise for both the **5 lbs male model**.

3.0 Project Scope

LMI performed human simulations for the following cases:

- 5 lbs (male model) Shake Weight for 3 seconds
- 5 lbs dumbbell curl for 3 seconds (1 complete repetition)
- 5 lbs dumbbell curl for 3 seconds (1 complete repetition)

For each event specified above, the following results are reported:

- Total body energy consumption
- Muscle force time history for
  - Right deltoid
  - Right biceps
  - Erector spinae group (back muscles)

2.0 Modeling

LMI will use the LifeMOD Human Modeling program to set up the models for the Shake Weight event and the dumbbell curl event. The human models will be a 50% generic male model. In order for a consistent comparison between events, one model will be use to perform the exercise events listed above. For an in-depth discussion on LifeMOD see www.lifemodeler.com/LM_Manual_2008 and Appendix A.

1. Human model will be a standard 19 segment, eighteen joint LifeMOD model.
2. Segment length and inertia properties will be based on GeBOD model scaling for a generic 50% male.
3. The standard human muscle set will be used. Muscle parameters (Hill) were selected based on a 50% human male.
4. A CAD model of the Shake weight was imported.
   a. Mass properties were determined from the CAD models
   b. The Shake Weight mechanism was created with proper constraints, spring rates, and jounce bumpers.
   c. The model was attached to the left and right hands using bushing elements.
5. A dumbbell part was created
   a. The same human model was then positioned in a curl exercise posture
   b. The dumbbell was of the same mass as the Shake Weight
   c. The dumbbell was attached to the right had of the human model via bushing elements.
6. The feet were secured to the ground using bushing elements.

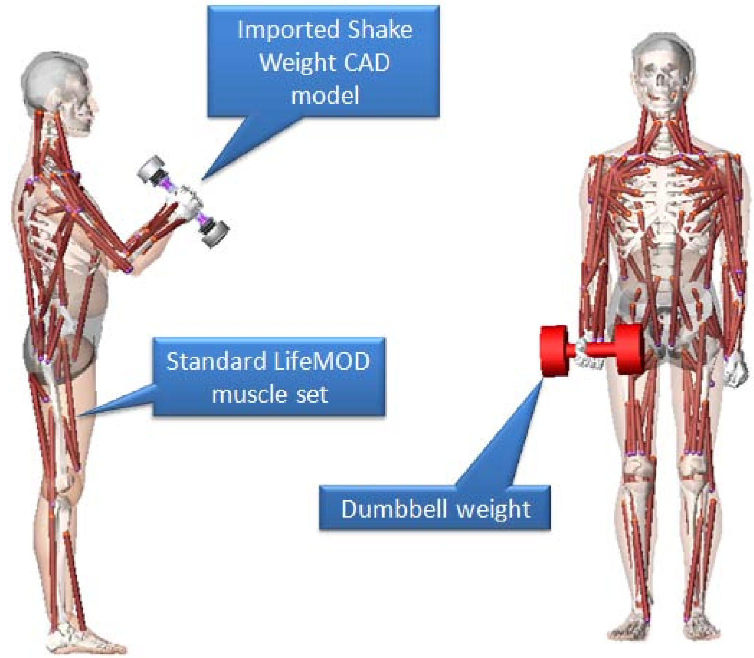

Figure 1. Generic male human models in exercise posture for the Shake Weight (left) and the dumbbell (right).

3.0 Simulations

Simulations were performed for both exercises for a period of 3 seconds. The same human model was used for both the Shake Weight and the dumbbell curl to maintain a consistent comparison.

1. Shake Weight
    a. Using inverse dynamics (see appendix), the muscles were trained to produce a shaking motion of 4 cycles/sec (240 cycles/minute).
    b. A forward dynamics analysis was performed to drive the Shake Weight.
    c. Muscle activity was recorded for the exercise.
2. Dumbbell
    a. Using inverse dynamics, the muscles were trained to produce a dumbbell curl exercise patter of 3 sec/cycle (complete flexion/extension)
    b. A forward dynamics analysis was performed.
    c. Muscle activity was recorded for the exercise.

4.0 Results

For both the Shake Weight exercise and the dumbbell curl specific muscular activity and whole body energy consumption were compared.

1. General Muscle Activation

   a. Figure 2 displays a sequence in the simulation for both models. The graphical images representing the muscles increase in thickness during higher muscular activity. It can be noted that the Shake weight simulations displays muscular activity for both arms, while the dumbbell displays activity for the arm being exercises (right).
2. Biceps Muscle Activity
   a. Figure 3 displays the right biceps activity for both exercises for 3 seconds. It can be noted that the magnitude and frequency is greater for the Shake Weight compared to the dumbbell curl. Also, this graph is only for the right biceps. The simulation also reports an equivalent left biceps force for the Shake Weight, with little activation for the dumbbell curl.
3. Anterior Deltoid Activity
   a. Figure 4 displays the anterior deltoid activity for both exercises for 3 seconds. It can be noted that the magnitude and frequency is greater for the Shake Weight compared to the dumbbell curl. Also, this graph is only for the right deltoid. The simulation also reports an equivalent left deltoid force for the Shake Weight, with little activation for the dumbbell curl. It can also be noted by comparing figure 4 to figure 3, that the deltoid produces more force than the deltoid.
4. Lumbar Region Muscular Activity
   a. Figure 5 displays the muscle activity in the lumbar region of the back (erector spinae group) for both exercises for 3 seconds. It can be noted that the magnitude and frequency is greater for the Shake Weight compared to the dumbbell curl.
5. Total Body Energy Consumption
   a. Figure 6 displays the energy consumed by all the muscles in the body for the 3 second exercise time.

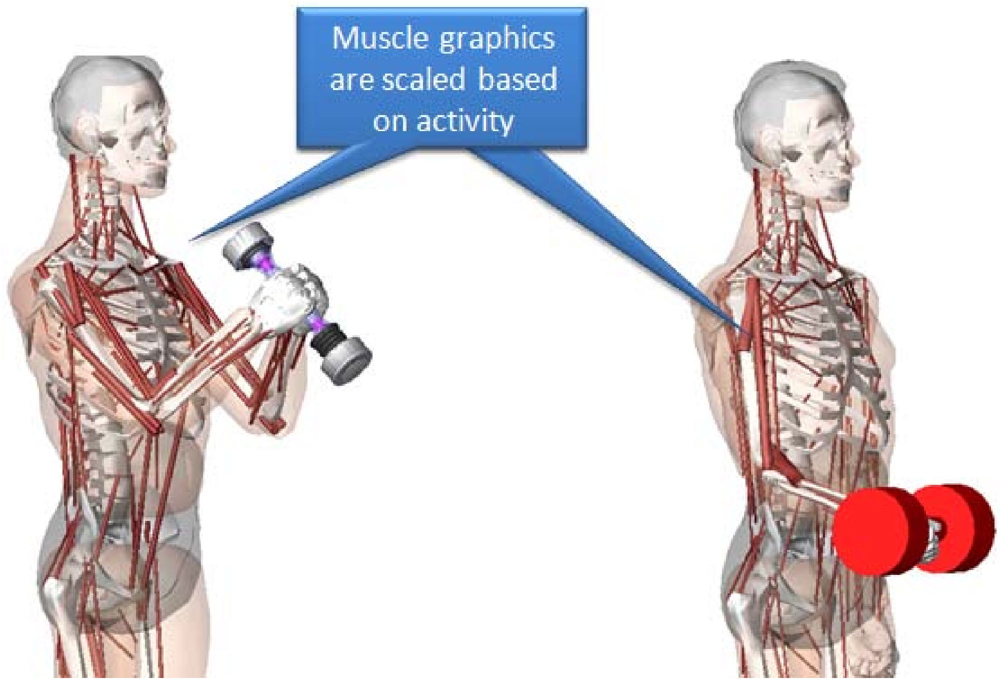

Figure 2. Shake Weight model showing muscle pattern (larger width denote higher activity) for the Shake Weight (left) and the dumbbell (right)

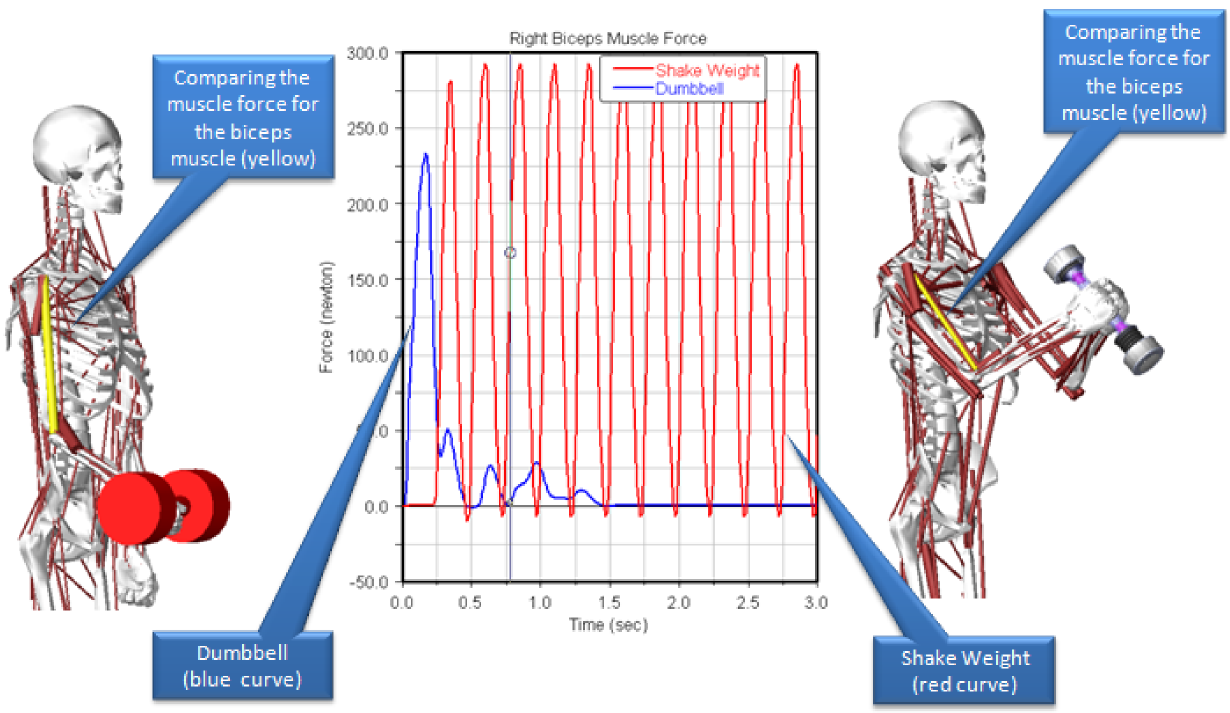

Figure 3. Comparing the right biceps muscle force for each activity for 3 seconds of exercise.

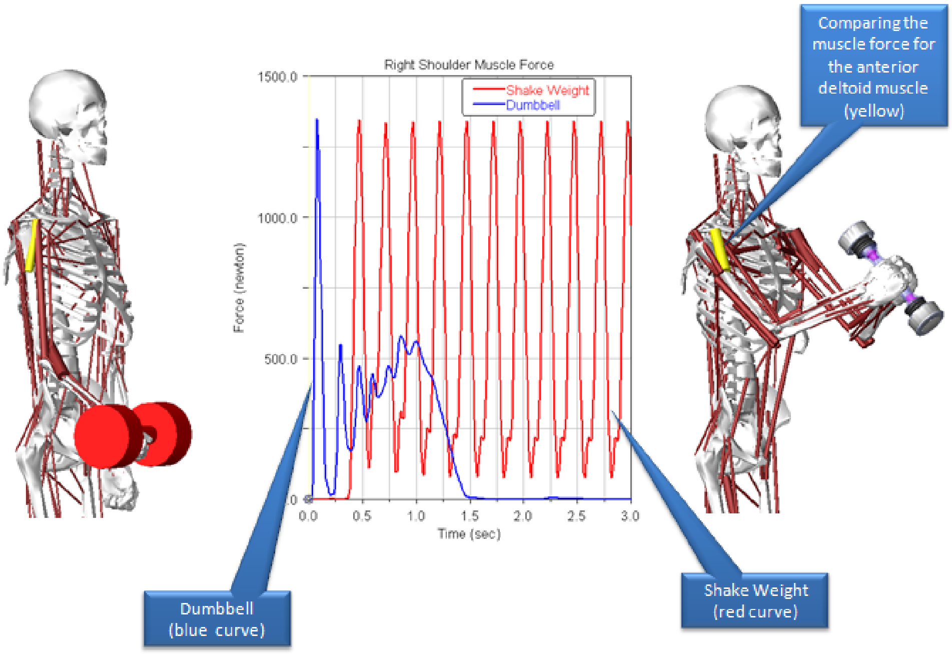

Figure 4. Comparing the right anterior deltoid muscle force for each activity for 3 seconds of exercise.

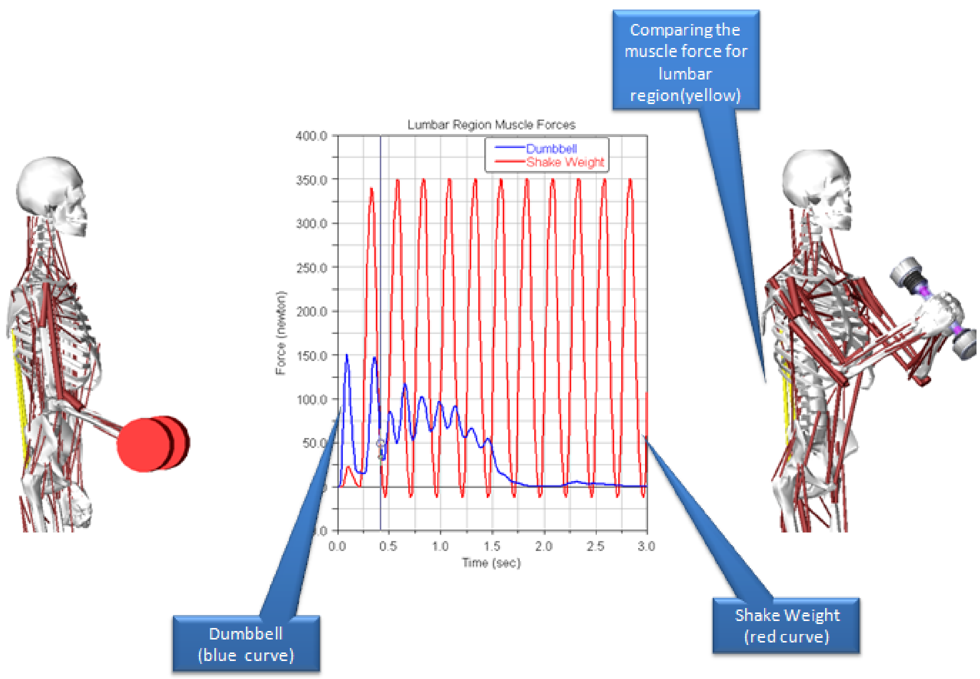

Figure 5. Comparing the muscle forces in the lumbar region (erector spinae group) for each activity for 3 seconds of exercise.

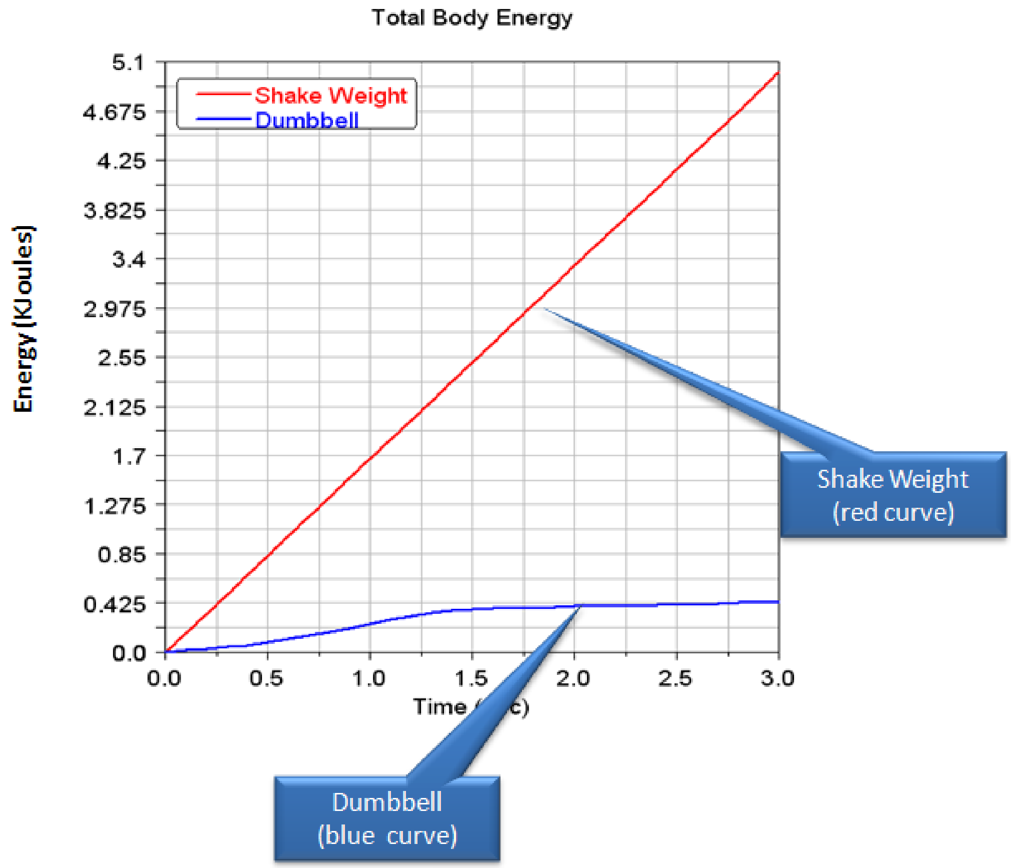

Figure 6. Comparing total body energy consumption for each exercise for a period of 3 seconds.

Exercise	Calories (nutritional) Consumed / minute
Shake Weight	**36.5**
Dumbbell	**4.54**
Walking	**4.7**
Running	**21**

Table 1 Nutritional calories consumed for the Shake Weight as compared to traditional exercises.

5.0 Conclusions

Energy consumption results are displayed in figure 6. When comparing the Shake Weight exercise event to the dumbbell curl event it is reasonable to conclude from the LifeMOD analysis that

1. You would have to exercise ~7 times longer with the dumbbell to expend the same total energy as the Shake Weight
2. You would have to increase the weight of the dumbbell over ~10 times to expend the same energy in the same time as the Shake Weight.
3. The Shake Weight is a total body energizer. There is more full body muscular activation for the Shake Weight versus the Dumbbell curl.
4. The Shake Weight generates higher peak muscle forces in the main driving muscle groups.
5. The frequency of contraction is much higher for the Shake Weight.

A. Appendix

Muscle Formulation

LifeMOD™ muscles follow a series of physiologically-determined equations in order to produce the necessary forces that replicate the desired motion of the body, while staying within each muscle's physiological limit. The assumption is that if enough muscles are included, the calculated muscle forces will be very close the the physical muscle force values for the same activity. To decrease the problem of redundancy -- cases where there are several muscles contributing to the motion of a given joint -- the user may condition the output of any muscle from 0 to 200%. This is also defined as the muscle "tone."

Aside from the passive recording muscle -- which functions based on a user-tunable spring damper that records motion during a training simulation -- the muscles in LifeMOD all stem from two basic control algorithms and fit into one of two strength-conditioning (or force-limiting) muscle types, as shown in Figure 1.

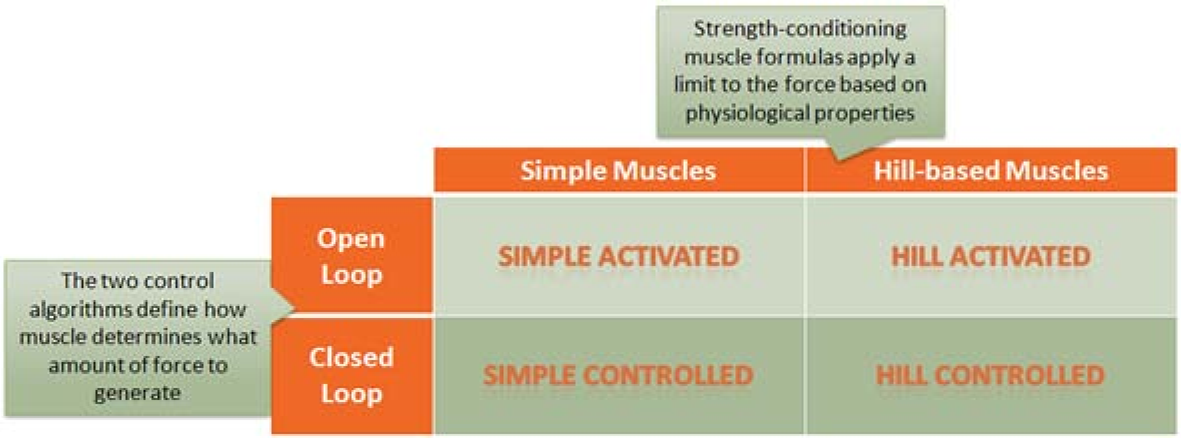

Figure 1: Muscle Matrix outlining the control algorithms and strength_conditioning muscle factors.

The Hill-type muscle formulation is the traditional combination of a contractile element (CE) and a parallel elastic element (PE) describing the passive force. The contractile element contains an muscle activation state which controls the active muscle force capability for the muscle. Data from an EMG test may be used as activation curves for the contractile element.

Various muscle parameters may be adjusted. See Parameters to tune the model for simulation including also see Choosing Model Parameters for data sources and information on how to select the parameters mentioned in this section.

Sections:

- Open Loop Control
- Closed Loop Control
- In-depth Hill Formulation
- References

Open Loop Simple Muscle Formula

Open loop muscles fire via a user-defined activation curve, A(t), between 0 and 100% with no contraints or target values. The simple muscle limits the force admitted by the A(t) through the formula:

$$F = A(t) \bullet F_{max} \bullet tone \bullet preload$$

Where the terms meet the following conditions:

- **A(t)** = activation curve with values between 0 and 1
- **F_{max}** = product of the physiological cross sectional area and maximum isometric muscle stress (σ_{max})
- **Tone** = muscle force output filter value between 0 and 2
- **Preload** = user-defined constant force value

Open Loop Hill Muscle Formula

The open Hill muscle formulas combine the A(t) curve and the physiological characteristics of the Hill-based muscles [Hill, '38], which operate on the traditional combination of active contractile elements (CE) and parallel passive elements (PE) with force-length and force-velocity contraints.

$$F = (f_{CE} + f_{PE}) \bullet tone$$

Equation 2 shows the formula used to place the strength-conditioning limits on open loop Hill muscles where F_{CE} can be found using the formula shown in Equation 3.

$$F_{CE} = A(t) \bullet F_{max} \bullet f_H(v_r) \bullet f_L(l_r)$$

Where:

- **A(t)** = activation state (normalized between 0 and 1)
- **F_{max}**= product of the physiological cross sectional area and maximum isometric muscle stress (σ_{max})
- **f_H**= the normalized active force-velocity relation (Hill-curve)
- **f_L**= the normalized active force-length relation
- **v_r**= dimensionless lengthening velocity
- **l_r**= dimensionless muscle length

For more detail on the definitions and terms in this equation, see the formula in the detailed Hill Muscle Formulation section.

Closed Loop Muscle Formulas

Closed loop muscles contain proportional-integral-differential (PID) controllers. The PID controller algorithm uses a target length/time curve to generate the muscle activation and the muscles follow this curve. Because of this, they require an inverse dynamics simulation using passive recording muscles prior to simulation with closed loop muscles. The closed loop algorithm is governed by the following formula:

$$F = p_{gain}(p_{error}) + I_{gain}(I_{error}) + d_{gain}(d_{error})$$

Where

$$P_{error} = (targetValue - currentValue) / rangeOfmotion$$

And

- D_{error} = first derivative of P_{error}
- I_{error} = time integral of P_{error}

The maximum force generated by a closed loop muscle is limited by the muscle strength conditioning formulas, listed in the open loop section, with A(t)=1. If the PID calculations result in a larger value than this, the force is limited and the controller will not force the model to exceed this physiological limit.

To apply maximum force limits to closed loop muscle groups, set A(t)=1 and compare the open loop strength conditioning formulas against the closed loop formula. In open loop muscles, A(t) is always an input into the formulations. For closed loop muscles, however, it serves as a calculated output value.

See Choosing Model Parameters for data sources and information on how to select the parameters mentioned in this section.

In-depth Hill-Based Muscle Formulation

The Hill-type muscle model is developed from the material behavior of the muscle model adapted from the original work by [Hill, '38] which results in a popular state equation applicable to skeletal muscle that has been stimulated to show tetanus. Reviews of this model and extensions can be found in [Winters, '88] and [Zajac, '89]. The Hill-type muscle model (Figure 1), consists of a contractile element (CE) which is in series with a series elastic element (SEE) both of which are in parallel with a passive element (PE). The SEE, shown in grey in figure 1 is often neglected when a series tendon is added. The main assumptions of the Hill model are that the contractile element is entirely stress free and freely distensible in the resting state, and is described by Hill's equation. When the muscle is activated, the series and paralell elements are elastic, and the whole muscle is a simple combination of identical sarcomeres in series and parallel.

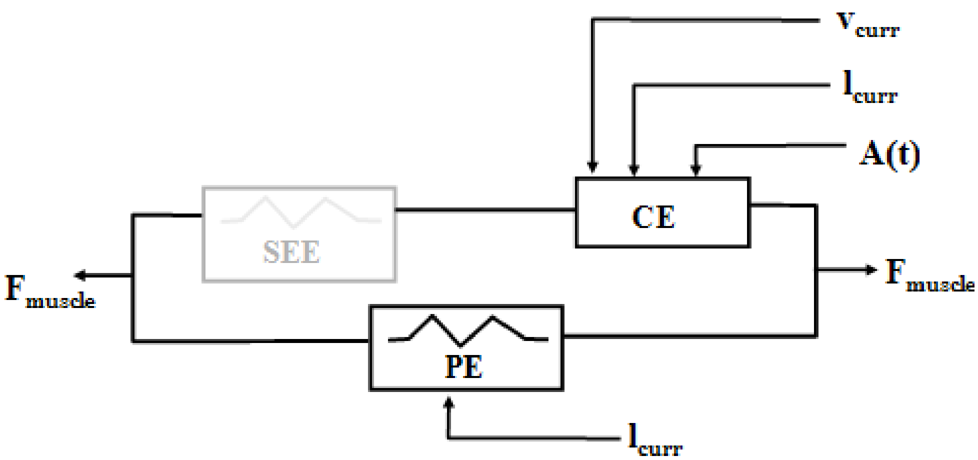

Figure 1: Discrete model for muscle contraction dynamics based on a Hill-type representation. The total force F_{MUSCLE} is the sum of a passive force F_{PE} and an active force F_{CE}. The passive element (PE) is a function of the instantaneous muscle length, l_{curr}. The contractile element (CE) is a function of the instantaneous muscle length, l_{curr}, instantaneous muscle shortening velocity v_{curr} and the time dependent activation state A(t).

When ignoring the SEE, The total muscle force calculated from the Hill formulation comes from the sum of a passive element force F_{PE} with an active element force F_{CE}. F_{MUSCLE} is the sum of both forces, thus:

$$F_{MUSCLE} = F_{CE} + F_{PE}$$

Passive Element F_{PE}

The passive element (PE) is a function of the instantaneous muscle length, l_{curr}.The muscle input parameters for the passive element are displayed in Figure 2.

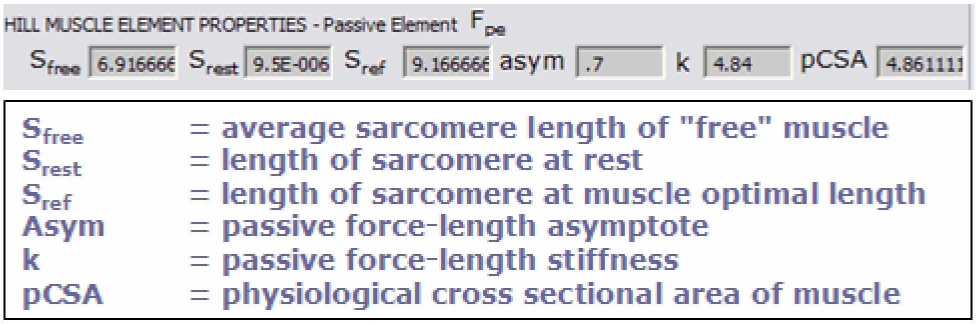

Figure 2: Section of the Hill muscle dialog box with descriptions of the input parameters for the passive element.

The passive element force $\mathbf{F_{PE}}$ is modeled with a passive muscle stress, **σ,** value multiplied by the physiological cross sectional area, **pCSA**, of the particular muscle.

$$F_{PE} = \sigma \cdot pCSA$$, where

σ = passive muscle stress
pCSA = physiological cross sectional area

Passive muscle stress, **σ**, modeled by the nonlinear stress-strain relationship [Deng, '87]

$$\sigma = (k \cdot \varepsilon)/(1-\varepsilon/asym)$$, where

ε = strain defined as the elongation relative to the resting length of the muscle,
k = passive muscle stiffness
asym = strain asymptote

The strain is defined by:

$$\varepsilon = (l_{curr} - l_{free}) / l_{free}$$, where

$\mathbf{l_{curr}}$ = current (instantaneious) length of the muscle
$\mathbf{l_{free}}$ = free length of the muscle at rest when it is removed from the body

The $\mathbf{l_{free}}$ results in a smaller free length than the muscle length in its initial position in the model. The initial position in the body is define by $\mathbf{l_{rest}}$. Assuming a linear relationship between the sarcomere length **s** [Magid, '85, Meyers, '98, Rack, '69], and the muscle length, the free length of the muscle can be calculated as:

$$l_{free} = l_{rest} \cdot (S_{free}) / (S_{rest}),$$

where the muscle reference length $\mathbf{l_{ref}}$ is based on [Brelin-Fornari, '98]

$$l_{ref} = l_{rest} \cdot (S_{ref}) / (S_{rest})$$, where

$\mathbf{S_{free}}$ = average sarcomere length of "free" muscle
$\mathbf{S_{rest}}$ = length of sarcomere at rest
$\mathbf{S_{ref}}$ = length of sarcomere at muscle optimal length

Active Element F_{CE}

The active or contractile element (CE) is a function of the instantaneous muscle length (l_{curr}) instantaneous muscle shortening velocity (v_{curr}) and the time dependent activation state A(t). The muscle input parameters for the contractile element are displayed in figure 4.

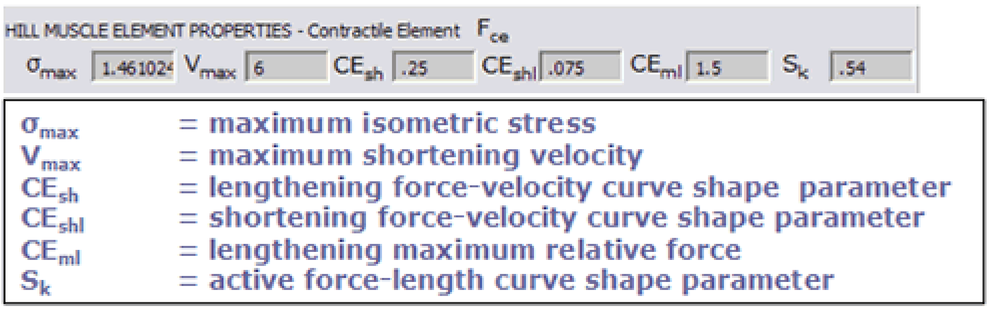

Figure 3: Section of the Hill muscle dialog box with descriptions of the input parameters for the contractile element.

Active muscle behavior (contractile element) is modeled with a normalized activation state and a maximum muscle force at activation.

$$F_{CE} = A(t) \cdot F_{max} \cdot f_H(v_r) \cdot f_L(l_r)$$, where

A(t) = activation state (normalized betwee 0 - resting to 1 - maximum activation)
F_{max}= muscle force at maximum activation isometric conditions
f_H= the normalized active force-velocity relation (Hill-curve)
f_L= the normalized active force-length relation
v_r= dimensionless lengthening velocity
l_r= dimensionless muscle length

The muscle force at maximum activation is calculated by:

$$F_{max} = \sigma_{max} \cdot pCSA$$, where

σ_{max} = is the maximum isometric muscle stress
pCSA = physiological cross sectional area

The function **f_H** is the normalized active force-velocity relation (Hill-curve). The default value used in LifeMOD was developed by [Delp, 1990]. Separate functions are defined for lengthening and shortening of the CE-element.

$$f_H(v_r) = \begin{cases} 0 & v_r \leq -1 \\ (1+v_r)/(1-v_r/CE_{sh}) & -1 < v_r \leq 0 \\ (1+v_r CE_{ml}/CE_{shl})/(1+v_r CE_{ml}) & v_r > 0 \end{cases}$$,

Where,

v_r = v_{curr} / V_{max}
v_{curr} = the instantaneous lengthening velocity **V_{max}** = the maximum shortening velocity of the muscle
CE_{sh}= shape force-velocity curve (shortening)
CE_{shl}= shape force-velocity curve (lengthening)
CE_{ml}= maximum relative force (lengthening)

The shape is determined by the parameters **CE_{sh}** and **CE_{shl}** , where **CE_{ml}** defines the maximum force the muscle can generate during lengthning relative to the maximum isometric force **F_{max}**.

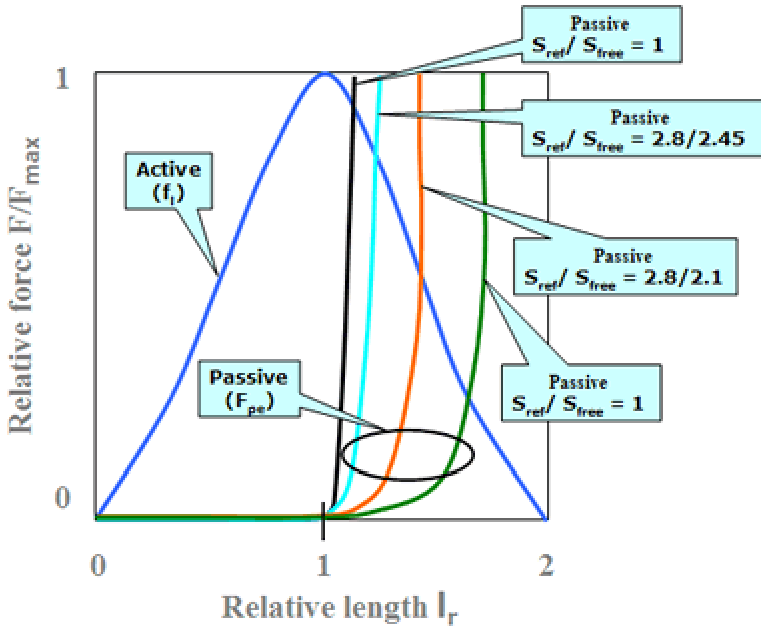

Figure 4: Normalized muscle force as a function of normalized muscle length (l_r) for both active, $f_l(l_r)$, (blue curve) and passive, F_{PE} , (other) element curves.

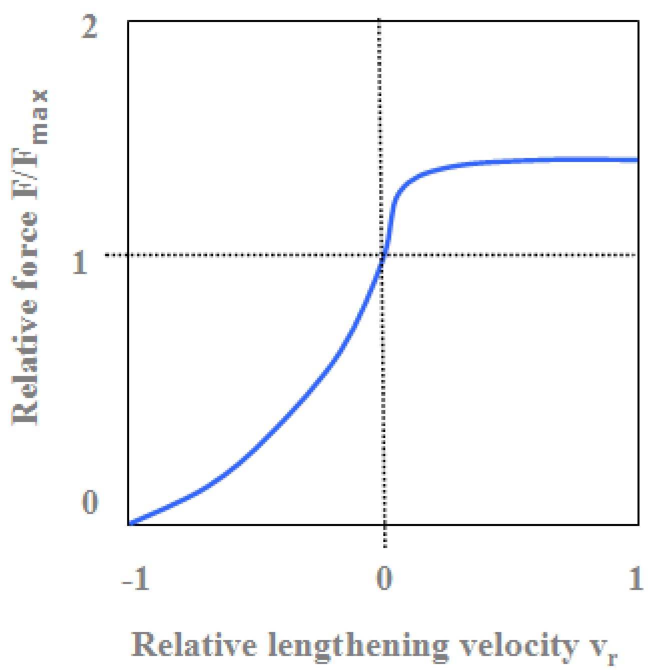

Figure 5: Standard force-velocity curve f_h for the conditions CE_{sh} = .5, CE_{shl} = .075, C_{ml} = 1.5

The function **f_l** is the normalized active fore-length relation.

$$f_l(l_r) = e - ((l_r - 1) / S_K)**2$$, where

$l_r = l_{curr} / l_{ref}$
l_{curr} = the instantaneous muscle length

$\mathbf{l_{ref}}$ = optimum reference length at which the active force is generate most efficiently
$\mathbf{S_k}$ = determines the shape of the curve (figure 2)

Muscle activation, **A(t)**, is described by a user-defined data spline. The data spline uses time as the independent variable and the normalized activation **A** as the dependent variable. A library of EMG data is avaliable via the XChange function in the main LifeMOD panel.

See Choosing Model Parameters for data sources and information on how to select the parameters mentioned in this section.

B. Appendix - References

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