Virtual Muscle 4.0.1
MUSCLE MODEL FOR MATLAB

User's Manual

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For updates and program downloads:

http://ami.usc.edu/projects/ami/projects/bion/musculoskeletal/virtual_muscle.html

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Contents

What is new in Virtual Muscle 4.0?

This section will explain the changes between version 3.1.5 and version 4.0. The detailed model development and implementation is described in a journal paper (Song et al. submitted).

Global Changes

1) *Upgraded software version:* Virtual Muscle version 4.0 runs under Matlab 6.5 and Simulink 5.1 (R13) above
2) *Addition of CMEX S-function Virtual Muscle models:* In addition to creating the Simulink basic-block based Virtual Muscle models '**Natural Discrete (Brown & Cheng)**', which is the 'Natural' model created by the previous VM 3.* versions, VM4.0 included CMEX S-function Virtual Muscle models with additional recruitment strategies.
3) *Additional Recruitment Strategies:* The S-function muscle models include three recruitment strategies: **a).** '**Natural Discrete**' which is equivalent to 'Natural Discrete (Brown & Cheng)', but removes the Activation delay effect modeled by effective length, L_{eff}, and this removal persists in the following recruitment models; **b).** "**Natural Continuous**", which is a new recruitment algorithm with a single motor unit of each fiber-type that is frequency modulated and weighted to approximate size-ordered physiological recruitment modeled in 'Natural Discrete' strategy. This new strategy substantially reduces the number of states for each integration step, thus improves the computation efficiency; **c).** '**Intramuscular FES**' which models the intramuscular FES stimulation for muscle force production. It includes a single motor unit of each fiber-type whose frequency of firing is specified by an input variable representing stimulus frequency. Force output is weighted equally among the motor units to approximate the random fiber-type recruitment reported for intramuscular electrical stimulation by (Singh et al.2000)

Changes to the BuildMuscles Function

1) *Change in submenu of 'Model' – 'Set Recruitment Strategy':* The additional CMEX s-function VM model and the additional recruitment strategies are reflected here. The options are: **'Natural Discrete (Brown & Cheng)'**, **'Natural Discrete'**, **'Natural Continuous'** and **'Intramuscular FES '**
2) *Changes in 'Help' menu:* Brief description of the newly added recruitment strategies, the parameter settings and inputs settings are explained.

Changes to Using the muscle blocks

1) *Changes in muscle parameters:* In the original Simulink basic-block based 'Natural Discrete (Brown & Cheng)' virtual muscle model, the model structures are reflected by different subsystems (**Recruitment block**, **Contractile element + Passive element subsystem, Series elastic element subsystem, Muscle mass subsystem**) which reflect the underlying mathematical model structure. The S-function based muscle model encoded the model in a state-space based formulation and imbedded into the CMEX S-function. The equations are described in Appendix E and the parameters are editable in the masks of the s-function block.

What was new in Virtual Muscle 3.1.5?

This section will explain the changes between version 3.1.4 and version 3.1.5.

Changes to the BuildMuscles Function

1) Changes introduced in version 3.1.4 unfortunately induced errors in the 'Rebuild' capabilities of the BuildMuscles function. This bug has been fixed
2) Various incompatibility problems with Matlab 6.0 have been corrected.

What was new in Virtual Muscle 3.1.4?

If you are not familiar with Virtual Muscle 3.0, skip this section as all information here has been updated in the following manual. Otherwise, this section will explain the changes between version 3.0.5 and version 3.1.4.

Changes to the BuildMuscles Function

1) CreateSimulinkBlocks has been separated from the BuildMuscles function. This change has no effect on the user interaction, but when installing Virtual Muscle, the user will now notice a third .m file.
2) When creating or rebuilding Simulink blocks the program now ensures that m, L_0, L_0^T and Whole-muscle maximal length are greater than zero.
3) Minor correction to the estimation of L_{max}. (Previous calculations assumed that the tendon was stretched to L_0^T, when in fact it should only be stretched by the passive forces present in the muscle).
4) Changes to the PCSA allotted to a fibertype are now always reflected in the individual motor units PCSAs for that fibertype. Previously, individual unit PCSAs were only updated when a fibertype's PCSA first became non-zero. The last method used to apportion a fibertype's PCSA is now stored so that changes which are made are appropriate.
5) If a change is made to a single unit's PCSA then the total PCSA for that fibertype is adjusted automatically in the Manual Distribute screen.

What was new in Virtual Muscle 3.0.5?

If you are not familiar with Virtual Muscle 2.0, skip this section as all information here has been updated in the following manual. Otherwise, this section will explain the changes between version 2.0 and version 3.0.5.

Changes to the Fiber Type Databases

1) A small error in the slow-twitch fibertypes rise- and fall-time parameters (both human and feline) was corrected here (originally corrected in version 2.0.1).

Changes to the BuildFiberTypes Function

1) We have added an additional comments box which is database specific.
2) The parameters for passive forces have been made fiber-type independent (i.e. one set of parameters per database). This was done because there is no evidence to suggest otherwise, and because it results in fewer calculations/muscle, hence an increased simulation speed.

Changes to the BuildMuscles Function

1) We have corrected an error in the initialization of the S variable for sag calculations.
2) We have corrected a small error in the implementation of the F_{PE2} relationship. This will only effect forces at lengths less than ~0.6 L_0.
3) We have corrected an error in the implementation of the a_{S1} vs. a_{s2} choice for Sag.
4) We have added a limiting function to ensure that $F_{total} \geq 0$.
5) We have added an additional comments box which is database specific.
6) The Recruitment block has been moved from out of each motor unit and changed so that there is a single block for each muscle. Thus it is now separate from CE, PE, SE and the muscle mass facilitating replacement with different recruitment strategies.
7) We have eliminated numerous redundant calculations. For example certain calculations (e.g. FL, FV etc.) are identical for all motor units of a single fiber type within one muscle. Previously these calculations were determined for each motor unit whereas now they are done once for each fiber type (in each muscle). Additionally we have removed Yielding and Sag calculations for those motor units of those fibertypes which do not have them. Lastly, we only calculate the passive forces once for each muscle. The result is a significant improvement in simulation speed.
8) We have added a new option for different recruitment strategies. Thus far the only new recruitment type is for intramuscular FES.
9) Additional Outputs can now be chosen for the muscle block (e.g. activation, fascicle length, velocity) facilitating the connection of these muscle blocks with feedback to control systems.
10) We have added two new types of automatic Motor-Unit PCSA distributions (equal sizes and geometrically increasing sizes)
11) The program now warns users when creating or re-building Simulink blocks if there are any motor units with 0 PCSA.
12) The user can now edit the PCSA and # motor units allotted to each fiber type when manually editing motor unit PCSAs.

What was new in Virtual Muscle 2.0?

If you are not familiar with Virtual Muscle 1.0, skip this section as all information here has been updated in the following manual. Otherwise, this section will explain the changes between the first version and 2.0.

Changes to the Fiber Type Databases

2) We have replaced the old feline fiber types database with a newer, updated one. The old version had 4 fiber types, the new one has 3 fiber types (only one fast-twitch fiber type). The new database more accurately reflects the scaling between different fiber types. Furthermore, the fast-twitch FV relationship has been re-fit to the original data to ensure a higher degree of accuracy at higher shortening velocities.
3) We have included a human fiber types database. Details on how this was generated from the feline fiber types database and existing data on human muscle properties can be found in Cheng et al. (submitted).

Changes to the BuildFiberTypes function

1) $V_{0.5}$ has replaced V_{max} as one of the input parameters for scaling velocity related parameters.
2) Changing $V_{0.5}$ or $f_{0.5}$ now includes the option to scale the other parameter by the same amount and also the fiber-type properties associated with that other parameter.
3) There is a new input on the main dialog window: 'Optimal Sarcomere Length'. Changing Optimal Sarcomere input gives the user the option to scale the FL and PE2 relationships appropriately. When a fiber is imported, if its Optimal Sarcomere length is different from that of the current database, the user is queried on whether or not to scale the FL and PE2 relationships
4) Specific Tension, tendon properties and viscosity inputs have been moved to the BuildFiberTypes function. These are now part of a new sub-menu window in which you can edit these properties.
5) Passive Viscosity is now an editable feature of Virtual Muscle.
6) The help function is a wee bit more explanatory.
7) Fixed a bug in the Delete Fiber Type command (when deleting the last 1 or 2 fiber types, the wrong one was deleted).

Changes to the BuildMuscles function.

1) If a new fiber type database is chosen to replace one currently being used, the BuildMuscles function looks to see if the fiber-types already in use by the current Muscle Model database are present. If not, and if there are new fiber-types or existing ones that are not used by any muscle currently the Muscle Model database, then the program allows the user to replace the 'missing' fiber-type with a new one.

2) Fiber-types are now listed in the BuildMuscles window in order of their recruitment rank.
3) Specific tension, viscosity and tendon properties have been removed from this function to the BuildFiberTypes function, and the required changes for building the Simulink blocks have been made.
4) The starting position of the muscle mass is now almost exactly correct. It is impossible to get an exact solution to the equations to provide this number, but the approximation provided is correct to within less than 0.1% if passive forces are less than 5% of maximum.

Introduction

Why a muscle model?

The models presented here were designed to meet the needs of physiologists and biomechanists interested in the use of muscles to produce natural behaviors. The model system provides a framework for constructing accurate muscle models that can be incorporated easily into complete neuromusculoskeletal systems. The muscle model includes the following components which can be scaled according to commonly available morphometric data:

- Motor nuclei that accept a single command input (e.g. net synaptic drive or EMG envelope) and apportion it into recruitment and frequency modulation of subgroups of motor units with type-specific properties
- Type-specific contractile elements that produce force as a function of firing frequency (past and present), length and velocity
- Passive elastic elements for passive muscle force.
- Passive elastic elements for series-compliance of tendons and aponeuroses

We have found it useful, where possible, to divide the model into components that have an obvious one-to-one correspondence with anatomical entities and physiological processes that occur in motoneurons, muscle and tendon. The experiments on which this model is based were designed to identify the specific structures and processes within muscle that give rise to complex phenomena (e.g. passive vs. active force, series-compliance, recruitment and frequency modulation, frequency-length interactions, yield, sag, etc.). The functions that comprise the model were chosen to describe those structures and processes explicitly and their coefficients were determined by best-fit procedures using data from experiments that explored these processes under a wide range of physiological conditions. This strategy improves the likelihood that the model will extrapolate accurately to deal with ranges and combinations of input conditions that may occur during normal use of muscles but may not have been tested explicitly in the source experiments. It also makes it simpler to identify the terms and coefficients that must be changed to describe muscles with different morphologies or different fiber type properties such as from different species.

Our goal is to capture accurately the complex mechanical properties of real muscles and tendons so that the user can understand the consequences of those properties for the control of musculoskeletal systems.

System requirements

The muscle model has been implemented in SIMULINK to be platform-independent, and requires only that your platform be able to run the following software:

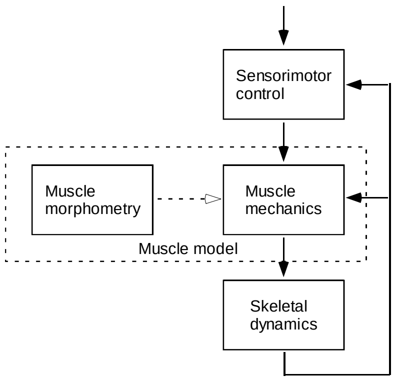
- MATLAB 5.2 or higher[1]
- SIMULINK 2.2 or higher

This muscle model can be customized to interface with a wide range of MATLAB or SIMULINK (Mathworks; http://www.mathworks.com/) compatible packages, which can be used to model other aspects of the hierarchical system.

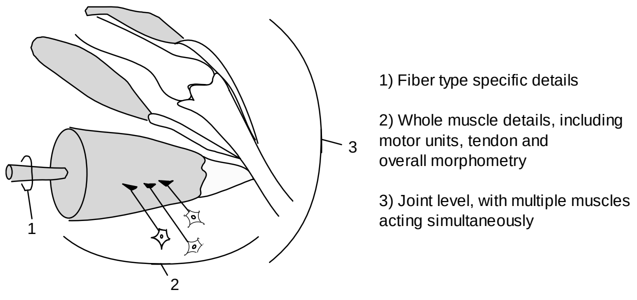
Instructions provided herein regarding using the MATLAB and SIMULINK software itself are directed towards the Windows based PC platform. For other platforms, use of the muscle package should be the same, but details regarding file paths, sequences of mouse clicks and so forth may differ slightly.

[1] To ensure that you have the correct version number, you can type the command `ver` at your MATLAB prompt (>>)

The structure of the muscle model



Our muscle modeling system is intended for use in a hierarchical framework. The mechanical dynamics of the skeletal segments comprise the lowest level, and are acted on by a realistic representation of physiological muscle properties at the middle level. At the top level, the muscles are controlled by any arbitrary set of activation commands, ranging from pre-recorded EMG data to dynamic, feedback driven reflex models, to high level simulations of cortical commands. Our software provides the middle level of the hierarchy. It enables users who may have only minimal interest in the details of muscle physiology to create realistic mathematical representations of muscles. At the same time, it is possible for those who wish to delve into and modify the mathematics of the muscle model to do so. The hierarchical database structure described below was designed to facilitate such modifications.


1
2
3
1) Fiber type specific details
2) Whole muscle details, including motor units, tendon and overall morphometry
3) Joint level, with multiple muscles acting simultaneously

Fiber type level

It has been shown that the behavior of the contractile element of the muscle scales well from the sarcomere level up to the whole muscle fiber level and again up to the level of an entire recruitment group of motor units (Zajac, 1989). There are two critical assumptions behind “lumping” of individual sarcomeres into a single group:

- All the sarcomeres in such a group must operate homogeneously, with similar activation, length and velocity. While some phenomena are believed to arise specifically because of intra-fiber sarcomere heterogeneity and/or damage (e.g. persistent stretch-induced force changes), these changes are small or rare under physiological use conditions (Brown and Loeb, Ms. III).

- The sarcomeres must all have the same contractile properties, i.e. their force-length-velocity relationship, parallel elasticity, and so forth. These characteristics have been shown to be homogenous within a single histochemical fiber type.

By defining the properties of each fiber type that will be used throughout the model in a single database, the muscle model can reference these properties when these fiber types are later combined into typical mixed-fiber-type muscles. The creation of the fiber type database is handled in a MATLAB function called `BuildFiberTypes`, which is a graphical user interface (GUI) described below.

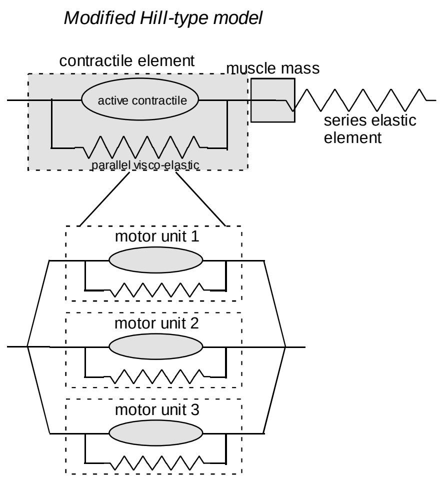
Whole muscle level

Muscles are organized into motor units, each of which consists of a motoneuron and the several hundred muscle fibers that it controls. All fibers in a unit are the same type. Groups of similar motor unit types tend to be recruited together. Different types of motor units tend to be recruited in a fixed order. This fact provides an ideal way to simplify the model. Each whole muscle is broken into motor units consisting of a single fiber type, with each unit being defined by its fiber type, its order of recruitment and its force-producing capacity (which is proportional to its total physiological cross-sectional area). It is assumed that the motor nucleus of the whole muscle receives a single, time-varying neural activation command signal, which is the apportioned by the model to activate each unit in turn, according to its defined recruitment order. Within each motor unit, the frequency of motoneuronal firing is modulated in a realistic manner.

Normally a muscle has about 100 or more motor units. While it is possible to create such a detailed muscle model with our software, this resolution will make the model run very slowly and is not usually necessary. For most uses, it will be sufficient to create a small number of model motor units (perhaps 3-5 for each fiber type), where each unit represents a group of “real” motor units with a total physiological cross-sectional area (PCSA) of around 10% of the muscle (first recruited units should be smaller than later recruited ones, as in real muscle). This will generally produce an acceptably smooth force modulation because of two features built into the model:

1. The model motor units always produce a smooth output force even at sub-tetanic frequencies, simulating the force that would have been produced by a large number of asynchronously active motor units all firing at the same sub-tetanic frequency.
2. The normal range of frequency modulation results in about a 4:1 range of force modulation, so the force step contributed by a newly recruited motor unit is relatively low until it gradually increases its firing frequency as activation of the muscle increases further.

If a muscle is compartmentalized in its mechanical actions and/or different neural activation is desired for each compartment, each such compartment should be treated as a separate muscle within the model. For simplicity throughout this document, the term muscle will be used to denote a single neuromuscular entity with a unidimensional command signal and a homogeneous mechanical action.



A given muscle consists of three interacting elements: the contractile element, a series elastic element, and a muscle mass. The contractile element and series elastic element both act on the muscle mass, which has inertial properties to prevent instabilities from arising within the muscle. The contractile element, in effect, consists of as many smaller contractile elements as are defined by the number of motor units, each of which has a passive parallel elastic element, an individually defined firing frequency, and force-length-velocity relationships as determined by the fiber type properties. The parallel elastic element includes a small viscosity for the purposes of stability. These active sub-compartments sum together to produce the total contractile element force. Muscles are created using a GUI designed in MATLAB called `BuildMuscles` which outputs those muscles as SIMULINK blocks as described below.

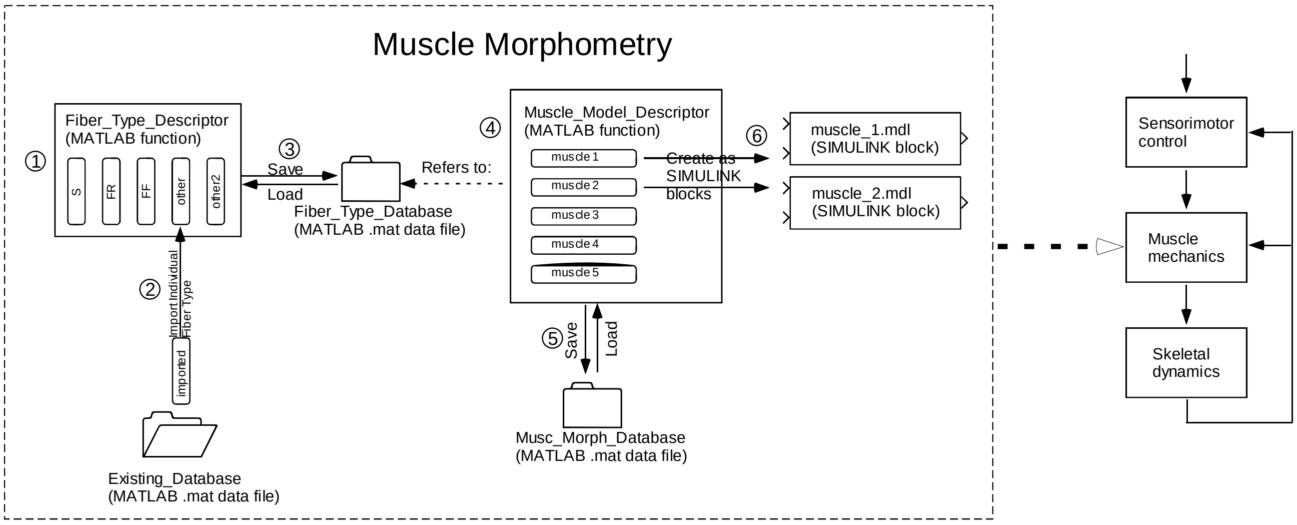
Interactions with Neural and Skeletal Elements

Each SIMULINK block representing a muscle must be joined to an appropriate model of the segment dynamics, which is not provided here. The interaction between the muscle model and dynamics model is two-way. The muscle blocks produce output force, which is used by the dynamics model to produce changes in kinematics. These kinematic changes are then passed back to the muscle model as changes in muscle length, which in turn result in changes in muscle force. Concurrent with this data exchange must be a source of neural activation for the muscles. This presumably will arise either from a data file of pre-recorded or pre-generated activations, possibly from EMG data, or from a control model built in SIMULINK or MATLAB that will generate the activation for each muscle. As discussed later, it may be necessary or appropriate to create a nonlinear scaling function between the source data and the activation applied to the model (see Appendix C).

The dynamics model can be created either within MATLAB or SIMULINK, or it can be linked to an external application via MATLAB's DDE interface.

Creating the muscle model

Overview



Muscle Morphometry
①
Fiber_Type_Descriptor (MATLAB function)
S
FR
FF
other
other2
③
Save
Load
Fiber_Type_Database (MATLAB .mat data file)
Refers to:
②
Import Individual Fiber Type
imported
Existing_Database (MATLAB .mat data file)
④
Muscle_Model_Descriptor (MATLAB function)
muscle 1
muscle 2
muscle 3
muscle 4
muscle 5
⑤
Save
Load
Musc_Morph_Database (MATLAB .mat data file)
⑥
Create as SIMULINK blocks
muscle_1.mdl (SIMULINK block)
muscle_2.mdl (SIMULINK block)
Sensorimotor control
Muscle mechanics
Skeletal dynamics

This software package provides a means to simulate the middle layer of the hierarchical model; that is, the muscle structure and the underlying mechanical function. The steps to use this software are relatively straightforward.

1. Use the `BuildFiberTypes` function to define the necessary muscle fiber types in MATLAB. This function is a GUI that allows the user to define fiber types either from scratch, or to import existing fiber types from file.
2. Once all fiber types to be used in a given muscle model are defined, they are saved to a `Fiber_Type_Database` file. This database can be loaded and edited again, or can have its fiber types imported into other databases.
3. Use `BuildMuscles` function to specify a set of muscles composed of varying proportions of the fiber types defined in steps 1) and 2).
4. Once the desired muscles have been defined they may be saved as a `Muscle_Model_Database` file. As before, this file can be opened and edited later.
5. Create muscle SIMULINK blocks using the `Create` function in the `BuildMuscles`. Subsequent changes to an existing simulation can be effected by the `Rebuild` function, which searches for and replaces all muscle blocks in a SIMULINK model file with blocks using updated parameters.

The `BuildFiberTypes` function

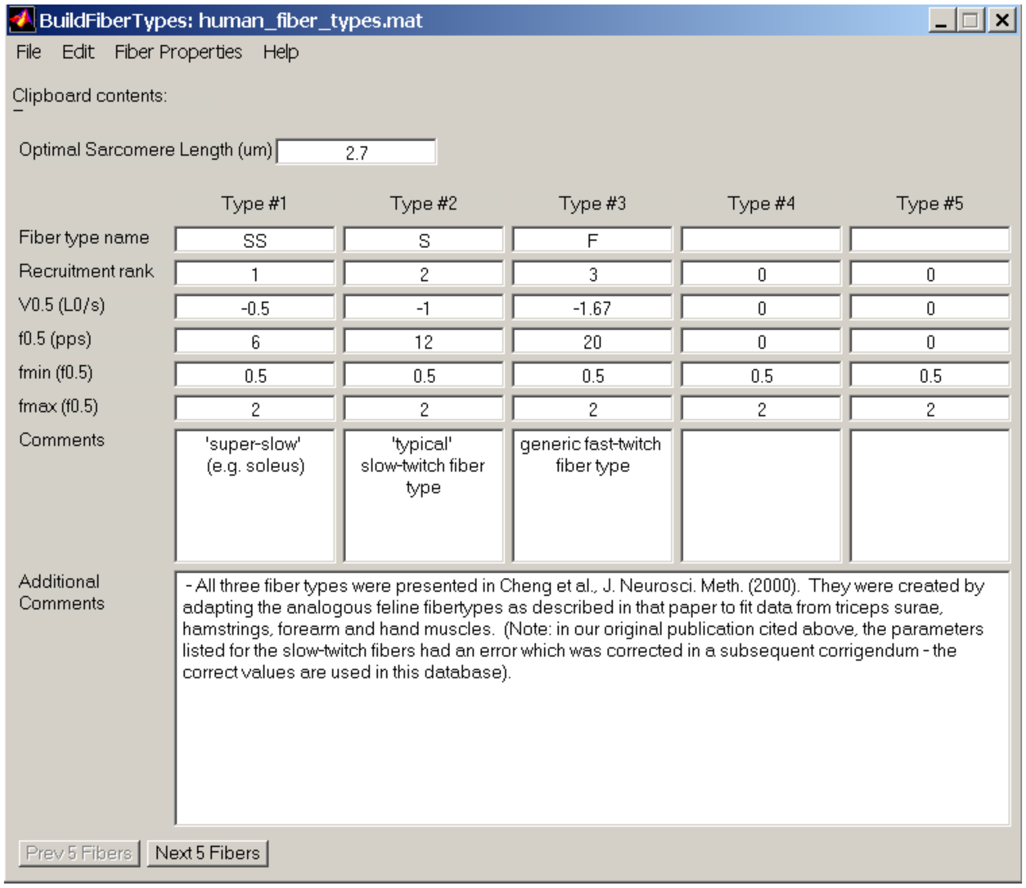
This function allows the user to create and modify the `Fiber_Type_Database.mat` files required for the `BuildMuscles` function within a GUI. Fiber types may be imported from existing databases and modified or created entirely from scratch.

Starting up the function

This function is called within MATLAB, so the first step is to run the MATLAB program. The `BuildFiberTypes` function is invoked by typing[2]:

```
>> BuildFiberTypes
```

Creating and editing fiber types in the main descriptor window



Clipboard contents:

Optimal Sarcomere Length (um) 2.7

	Type #1	Type #2	Type #3	Type #4	Type #5
Fiber type name	SS	S	F		
Recruitment rank	1	2	3	0	0
V0.5 (L0/s)	-0.5	-1	-1.67	0	0
f0.5 (pps)	6	12	20	0	0
fmin (f0.5)	0.5	0.5	0.5	0.5	0.5
fmax (f0.5)	2	2	2	2	2
Comments	'super-slow' (e.g. soleus)	'typical' slow-twitch fiber type	generic fast-twitch fiber type		

Additional Comments: - All three fiber types were presented in Cheng et al., J. Neurosci. Meth. (2000). They were created by adapting the analogous feline fibertypes as described in that paper to fit data from triceps surae, hamstrings, forearm and hand muscles. (Note: in our original publication cited above, the parameters listed for the slow-twitch fibers had an error which was corrected in a subsequent corrigendum - the correct values are used in this database).

[2] You must ensure that the `BuildFiberTypes.m` file is in your current working directory or is in a directory that is part of your path (the list of directories that MATLAB automatically searches for files). You can do the former by using `dir` to obtain a list of the files in your working directory, and `cd` to change your working directory at the >> MATLAB prompt. You can check which directories are part of your path with MATLAB's `path` command.

The main descriptor window allows you to load, save and import from database files, as well as edit the general parameters for each fiber type. The fiber types are arranged into columns, with up to five types being displayed on screen at once. If more than five types are created, the user can scroll to next and previous groups of five fibers using the Prev 5 Fibers or Next 5 Fibers button.

Editing fiber types

The main descriptor window allows the user to define optimal sarcomere length for the database (i.e. we force all fiber types in a single database to have the same optimal sarcomere length). If this value is changed, the user will be prompted as to whether or not they would like the active and passive force-length relationships scaled appropriately with changing optimal sarcomere length (the assumption is that the thick filament length stays constant).

In addition, the main descriptor window allows the user to define the following general parameters for the fiber type:

- **Fiber type name:** Each fiber type must be given a unique name. Other functions will search the names in the database for a space and case sensitive match, so consistent naming is important. *If this field is left blank, then no data from this column will be retained when the database is saved to disk.*
- **Recruitment rank:** The values in this row determine the order in which the fiber types are recruited within a given muscle. Any numerical value is acceptable, including non-integers. Those with lowest rank are recruited first; only when all the fibers of this rank are recruited are the types with the next higher rank recruited. The absolute values of the recruitment ranks have an effect on the algorithm for automatic apportioning PCSA among simulated motor units of different fiber types, as discussed below. For most simulations, small integer values for recruitment rank will work best (e.g. S=1, FR=2, FF=4).
- **$V_{0.5}$ (L_0/s):** This is the shortening velocity velocity necessary to reduce force to 0.5 F_0 during a maximal, tetanic contraction. This value is initially calculated from the detailed FV coefficients, however, changing this value will automatically rescale the related FV coefficients in the muscle coefficients level. The terms that are specifically affected are b_V and V_{max}. As an option, if you change $V_{0.5}$, you will be prompted as to whether or not you wish to also scale $f_{0.5}$ (and related rise and fall time constants) in proportion, because in normal muscles these values appear to scale proportionally to each other.
- **$f_{0.5}$ (pps):** The frequency in pulses per second at which the fibers in the compartment produce half of maximal isometric tetanic force at 1.0 L_0 (see Brown et al., 1999). Similar to $V_{0.5}$ field described above, you will be prompted as to whether or not to allow automatic rescaling of any related coefficients for rise and fall times (see Brown and Loeb, MS IV) and also if you wish to scale $V_{0.5}$ in proportion. Again, the default is to allow automatic rescaling. The terms specifically affected are T_{f1}, T_{f2}, T_{f3}, and T_{f4}.
- **f_{min} ($f_{0.5}$):** The minimal frequency at which a given recruitment compartment is activated upon threshold activation, relative to the $f_{0.5}$ frequency. A default value of 0.5 is provided.
- **f_{max} ($f_{0.5}$):** The maximal frequency at which a given recruitment compartment is activated upon maximal activation, relative to the $f_{0.5}$ frequency. A default value of 2 is provided.
- **Comments:** Entry into this field is optional. It is a user field that can contain any information the user desires.

Underneath these parameters for each fiber type there is a "hidden layer" of fiber coefficients (see below).

Loading and saving your database

The `Save Database` and `Open Database` options under the `File` menu item allow you to store the contents of your `Fiber_Type_Database` at any time, and then reload them for further editing. Both bring up a standard dialog that prompts you to select a filename to load or save. Files can have any name, with any number of characters. The name of the database you have saved or loaded will be reflected in the title bar of the main descriptor window. The only caveat is that MATLAB may have difficulty identifying files which are not saved with a `.mat` extension, so this is automatically appended on to the save filename. It is recommended that you leave this extension intact so that the save file is easily loaded during future use.

Just before saving, the program will ensure that you have assigned unique fiber names to each of the fiber types, and prompt you if this has been done incorrectly.

Creating fiber types in your own `Fiber_Type_Database` file

There are several methods that you can typically use when creating a `Fiber_Type_Database` file for your own use.

1) The first method is to open the `BuildFiberTypes` function and type in all the parameters and coefficients for each fiber that you wish to use. However, as there are thirty coefficients for each fiber type, this method is both tedious and prone to data entry errors. Most users will wish to avoid building their fiber types this way.

2) Another method is to start with an existing `Fiber_Type_Database`, such as the included database containing feline fiber properties, make whatever minor changes are desired to the existing fiber types, and then save it under a new file name.

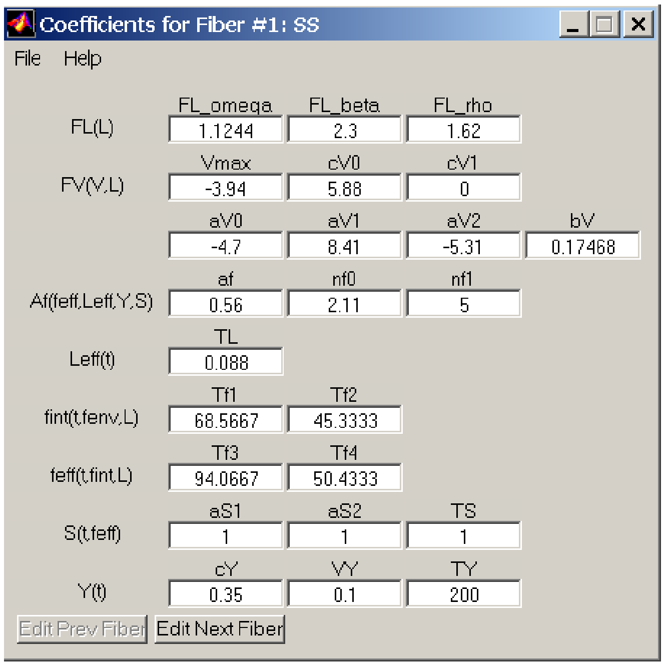
3) If you wish to use more fiber types than are provided in an existing database, you may wish to add new fibers based on other fibers already in the database. This can be done by selecting the `Copy` or `Cut` items from the `Edit` menu. Either action will open a dialog thatlists the names of the fibers in the current database. Selecting a fiber type will put the fiber type along with its parameters and coefficients into the clipboard, which will be reflected in the `Clipboard contains:` text string near the top of the window. Note that the `Cut` option will delete the selected fiber subsequent to storing it in the clipboard. At this point, selecting the `Paste` command will copy whatever fiber type is in the clipboard into the target column. You will be prompted for a column number to copy the clipboard fiber type in to. The `Paste` function will overwrite any contents in the destination fiber type. Note that the clipboard is not a standard Windows clipboard; thus, fiber type data can not be pasted into other Windows applications using this function. Note also that the copy, cut and paste operations include both the visible parameters and the hidden coefficients for a given fiber type.

4) Should you wish to combine fiber types from more than one `Fiber_Type_Database`, you can start with an existing database and use the `Import` action from the `Edit` menu. This will bring up a standard file selector dialog. From here, you should select the name of the database that you wish to import a fiber type from. Next, a list of fiber types in that file will be presented, allowing you to copy one of those fiber types into the clipboard. The fiber can then be pasted into your current database.

Editing fiber coefficients

For most purposes, users should be able to obtain a reasonable approximation of the function of most mammalian muscle fiber types by modifying the `V0.5` and `f0.5` properties of the fiber types imported from the two databases we provide, and allowing the `BuildFiberTypes` function to rescale any related coefficients.

However, should you wish to access the details of each equation at a lower level, selecting the `Edit Coefficients` item from the `Fibers` menu will bring up the fiber specifics window, allowing modification of any of these coefficients. The equations related to these coefficients are available in Appendix B of this document (see Brown et al., 1999, Brown and Loeb, 2000 and Cheng et al., 2000 for a detailed description of these coefficients).



	FL_omega	FL_beta	FL_rho	
FL(L)	1.1244	2.3	1.62	
	Vmax	cV0	cV1	
FV(V,L)	-3.94	5.88	0	
	aV0	aV1	aV2	bV
	-4.7	8.41	-5.31	0.17468
	af	nf0	nf1	
Af(feff,Leff,Y,S)	0.56	2.11	5	
	TL			
Leff(t)	0.088			
	Tf1	Tf2		
fint(t,fenv,L)	68.5667	45.3333		
	Tf3	Tf4		
feff(t,fint,L)	94.0667	50.4333		
	aS1	aS2	TS	
S(t,feff)	1	1	1	
	cY	VY	TY	
Y(t)	0.35	0.1	200	

Clicking the Edit Prev Fiber or Edit Next Fiber buttons will allow you to modify the coefficients for the previous or next fibers respectively. To return to the main window, click on the Back to main page button.

Editing generic coefficients

Specific tension, tendon properties and passive force properties (including viscosity) have their own sub-menu in the `BuildFiberTypes` function.. These properties are assumed to be constant for all fiber types in a given database.

Help

Selecting the `Help` menu item will bring up a window describing the definition of each property listed in the current window. For a more detailed explanation of the equations and their related coefficients used in the muscle model, please see Brown et al. (1999), Brown and Loeb (2000), Cheng et al. (2000) or see Appendix B.

The BuildMuscles function

Once a `Fiber_Type_Database.mat` file has been created, these fiber types can be combined in varying proportions to produce SIMULINK blocks that model muscle force output, complete with sequentially recruited motor units of varying size and fiber type, and intra-muscle interactions between active contractile elements and parallel and series elastic elements.

The function allows muscle data to be stored in two representations. The first is as a `Muscle_Database.mat` data file in MATLAB. This stores the current configuration of each muscle and can be loaded into the `BuildMuscles` function to be edited again. This database file is only used by this function and will not constitute part of your simulation. In order to use the muscles, you must generate the second representation as a SIMULINK block.

Starting up the function

From within MATLAB, this function is invoked by typing[3]:

```
>> BuildMuscles
```

Creating a new muscle model database

If you wish to create a new muscle model database, you should select a `Fiber_Type_Database.mat` file to use, from the `Select Fiber Type Database` item from the `File` menu. If you have not yet created one, return to the previous section and create one using the `BuildFiberTypes` function. The `Fiber_Type_Database.mat` file selected at this point is permanently associated with the created muscle database, and any changes made to the fiber type database will be reflected in the muscle model, so long as the fiber type names remain consistent.

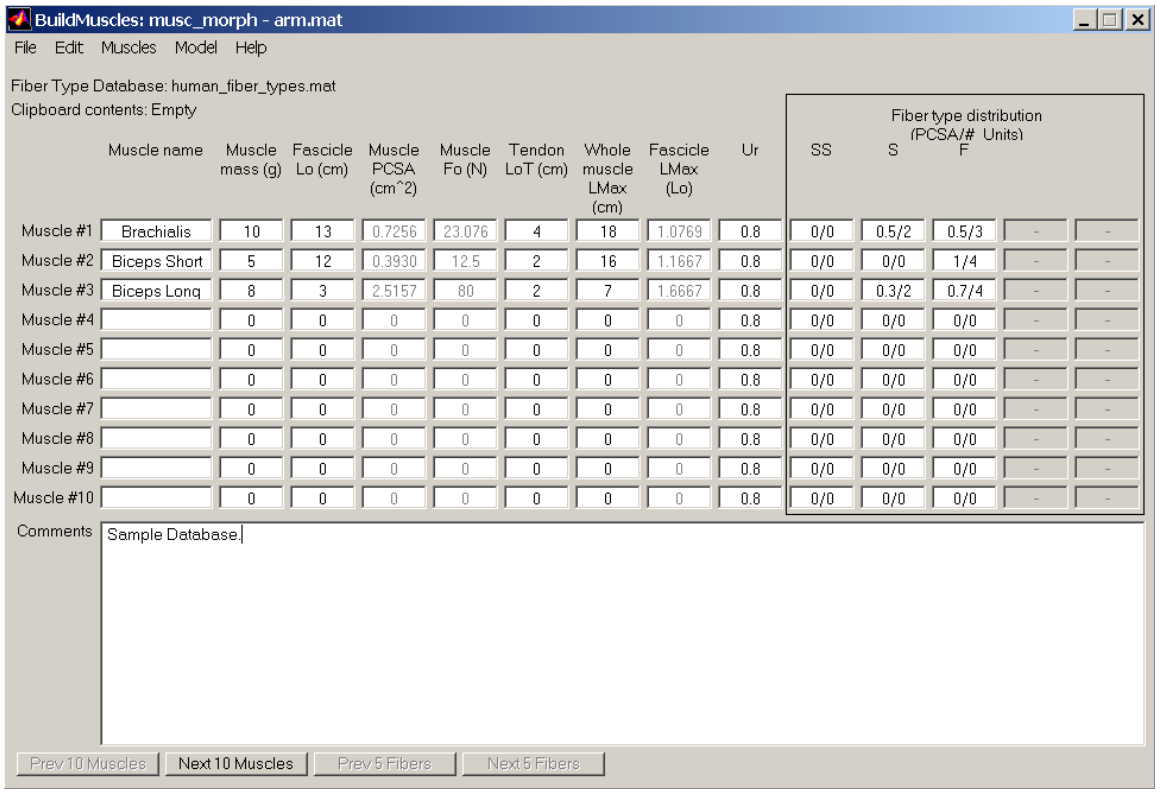
Once a `Fiber_Type_Database` file has been selected, or an existing `Muscle_Database` has been loaded, the name of the associated fiber type database file will be reflected in the `Fiber Type Database:` text string near the top of the window.

It is possible to change the `Fiber_Type_Database.mat` file associated with a `Muscle_Database` by choosing the `Select Fiber Type Database` option when a muscle model database is already open. The limitation is if existing fiber types present in the original muscle model database are not present in the new fiber type database, there must be enough new or unused fiber types that can replace the old ones, else an error will occur.

It is not recommended that you keep multiple copies of a single `Fiber_Type_Database` in different directories of the MATLAB path, as this will make it difficult to track which file is being used at any given time.

[3] As with the `BuildFiberTypes` function, the `BuildMuscles.m` file must be either in the current directory or in the MATLAB path.

Editing muscle types in the main descriptor window


BuildMuscles: musc_morph - arm.mat
File Edit Muscles Model Help
Prev 10 Muscles
Next 10 Muscles
Prev 5 Fibers
Next 5 Fibers

Fiber Type Database: human_fiber_types.mat
Clipboard contents: Empty

	Muscle name	Muscle mass (g)	Fascicle Lo (cm)	Muscle PCSA (cm^2)	Muscle Fo (N)	Tendon LoT (cm)	Whole muscle LMax (cm)	Fascicle LMax (Lo)	Ur	Fiber type distribution (PCSA/# Units) SS	S	F		
Muscle #1	Brachialis	10	13	0.7256	23.076	4	18	1.0769	0.8	0/0	0.5/2	0.5/3	-	-
Muscle #2	Biceps Short	5	12	0.3930	12.5	2	16	1.1667	0.8	0/0	0/0	1/4	-	-
Muscle #3	Biceps Long	8	3	2.5157	80	2	7	1.6667	0.8	0/0	0.3/2	0.7/4	-	-
Muscle #4		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #5		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #6		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #7		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #8		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #9		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-
Muscle #10		0	0	0	0	0	0	0	0.8	0/0	0/0	0/0	-	-

Comments: Sample Database.

The main descriptor window allows users to load, save, and edit a `Muscle_Database`, each of which is constructed of a combination of fiber types as described in the fiber type database. Each muscle from the database can be created as a SIMULINK block for use in a biomechanical model.

Loading and saving

If you choose to `Load` an existing database from the `File` menu, a dialog will open asking for the name of the existing database file. Note that the `Fiber_Type_Database.mat` file you used in the creation of this muscle database must either be in the current directory or in the MATLAB path. If the expected `Fiber_Type_Database.mat` file cannot be found, you will be prompted to select one. This database must contain at least as many fiber types as are used by the muscle database. The program will prompt you to choose which fiber types to associate with which if the names do not match. Ensure that a valid database file has been loaded before proceeding to edit your muscles or errors will result.

The `Save` item in the `File` menu allows you to store your muscle parameters for later modification. It is recommended that muscle model files be saved using a `.mat` extension.

Copying, cutting and pasting muscles

It is possible to `Copy`, `Cut`, and `Paste` muscles to and from the clipboard using the items from the `Edit` menu. Contents of the clipboard will be reflected in the `Clipboard contents:` string at near the top of the window.

Importing muscles from another database

As with fiber types, muscles can also be imported from other `Muscle_Database.mat` files. Selecting `Import muscle` from the `Muscles` menu will open a file selection dialog, allowing you to select another muscle model database file, and select a muscle from that file. This muscle data will then be stored in the clipboard for pasting into the currently open database.

Editing muscles

The main descriptor window allows ten rows of muscles to be viewed and edited simultaneously. Scrolling through muscles if more than five are used is accomplished with the Prev 10 Muscle and Next 10 Muscle buttons. The muscle parameters that may be modified are:

- **Muscle name:** A unique name for each muscle must be input here. Muscle data for each row will be saved to the database file only if a name is entered.
- **Muscle mass (g):** Mass of the muscle belly in grams.
- **Fascicle L_0 (cm):** Average length of the fascicles in the muscle belly, when the muscle is at its optimal length for production of isometric tetanic force (note that this value is typically 10-30% less than the length at which optimal twitch force is generated, Close, 1972; Roszek et al., 1994; Brown and Loeb, 1998).
- **Muscle PCSA (cm^2):** Physiological cross-sectional area of the muscle. This value cannot be input directly, and is instead calculated from values input for muscle mass and fascicle length. A muscle density of 1.06 g/cm^3 is assumed (Mendez and Keys, 1960).
- **Muscle F_0 (N):** The maximal amount of force that the muscle can produce isometrically. This value cannot be entered directly, and is calculated from the muscle PCSA, multiplied by a standard value for specific tension of muscle. The default specific tension for mammalian muscle (defaults to 31.8 N/cm^2, Brown et al., 1996) can be modified by selecting the `Change specific tension` item from the `Muscles` menu.
- **Tendon L_0^T (cm):** Length of the tendon at the muscle's optimal force. This term should consist of the total amount of connective tissue in series with the muscle fascicles, including both internal aponeurosis and external tendon. This value must be greater than zero; this value will default to 0.1 cm if no value is entered. The coefficients for the properties of the tendon can be modified from their defaults with the `Edit tendon properties` item from the `Muscles` menu. The tendon is modeled on a log/linear relationship (Brown et al., 1996). L_0^T is the length of the tendon when stretched with force F_0; this is well up in the linear stiffness range. As the tendon shortens by 3.6% from length L_0^T, force drops linearly to about 20% of F_0, followed by an exponential decrease to slack (essentially zero tension) at 95% of L_0^T. While the total range of length of tendon is small, it can exert large effects on muscle force because it changes the way in which velocity of the whole-muscle length appears at the contractile elements, which are very velocity-sensitive. This is particularly true in muscles that have substantially longer tendon+aponeurosis than fascicle length.
- **Max. whole-muscle length (cm):** Maximum length of the whole-muscle (entire musculotendon path length) at the most extreme anatomical position. This value is used to calculate the following L_{max} parameter, which controls passive tension.
- **Fascicle L_{max} (L_0):** The maximal length of the fascicles at extreme anatomical position of the skeleton, measured in terms of the optimal fascicle length. This value cannot be entered directly, and is calculated from the difference of the Max. whole-muscle length and the

Tendon L_0^T, scaled by fascicle L_0. Reasonable values of L_{max} are typically greater than 1, but less than 1.3.

- **U_r:** Fractional activation level at which all motor units for a given muscle are recruited (i.e. it is the threshold of the last motor unit) for the 'Natural' Recruitment algorithm provided Once activation has reached U_r, further increases in activation result only in frequency modulation up to f_{max} for each motor unit at U=1. A reasonable default value of 0.8 is provided. Lower values are more appropriate for muscles with unusually homogenous fiber type composition.
- **Fiber type distribution (PCSA/# of motor units):** The fraction of total muscle PCSA and the number of motor units assigned to each fiber type. The fiber types named at the top are determined by those present in the selected `Fiber_Type_Database`. The two values are separated by a forward-slash (/) for each fiber type. Note that the PCSA assigned to the fiber types for each muscle must total 1.0, otherwise an error will be reported when attempting to save your database. Should this occur, you will be presented with an opportunity to either 1) have the `BuildMuscles` function automatically redistribute the PCSA among the fiber types in the same proportions, but such that they total 1.0, 2) to save the muscle with the incorrect PCSA total, or 3) to cancel the save and manually redistribute the PCSA. Scrolling through more than the five visible fiber types is accomplished by clicking the Prev 5 Fibers or Next 5 Fibers buttons near the top of the window. In the example of Figure 7, Muscle #1 (Brachialis) is composed of 50% S type fibers, and 50% FF type fibers, with the names being taken from the fiber type database the user has loaded. Of these fiber types, 2 motor units are allocated to the S fibers and 3 to the FF fibers.

Size of motor units

Each real motor unit innervates a fraction of the muscle's total PCSA. Realistic recruitment of biological motor units during activation occurs in a fixed sequence, with smaller and slower motor units being recruited first according to Henneman's size principle. For example, motor units innervating slow-twitch muscle fibers are typically smallest, while motor units for the larger fast-twitch fibers are recruited later. To reproduce this orderly recruitment based on fiber type, the `Recruitment_Rank` parameter in the `BuildFiberTypes` function determines the order of recruitment of motor units composed of different fiber types, if the 'Natural' recruitment strategy is selected (as described below) .

Within motor units of the same muscle fiber type, Henneman's size principle still applies in real biology; for example, motor units that innervate a smaller number slow-twitch fibers will tend to be recruited before motor units that innervate a larger number of slow-twitch fibers. However, in the muscle model motor units within a fiber type are recruited in the order in which they are listed (e.g., `Unit #1`, `Unit #2`, `Unit #3`, etc.) and PCSA is assigned to each motor unit individually. So to maintain Hennemann's size principle in a model, motor units should be listed in order of size (smallest to largest), at least for 'Natural' recruitment strategies.

In a perfect muscle model, each motor unit would be represented individually, and thus each slow-twitch motor unit would have a smaller PCSA assigned to it than a fast-twitch motor unit. This would make the computations unnecessarily lengthy, however. The model allows the number of simulated motor units (and hence resolution of the simulation) to be specified by the user. It then apportions the PCSA of the muscle among those units according to one of several algorithms. In a typical simulation with 10 motor units, each motor unit would actually reflect the contribution of about 10 "real" motor units.

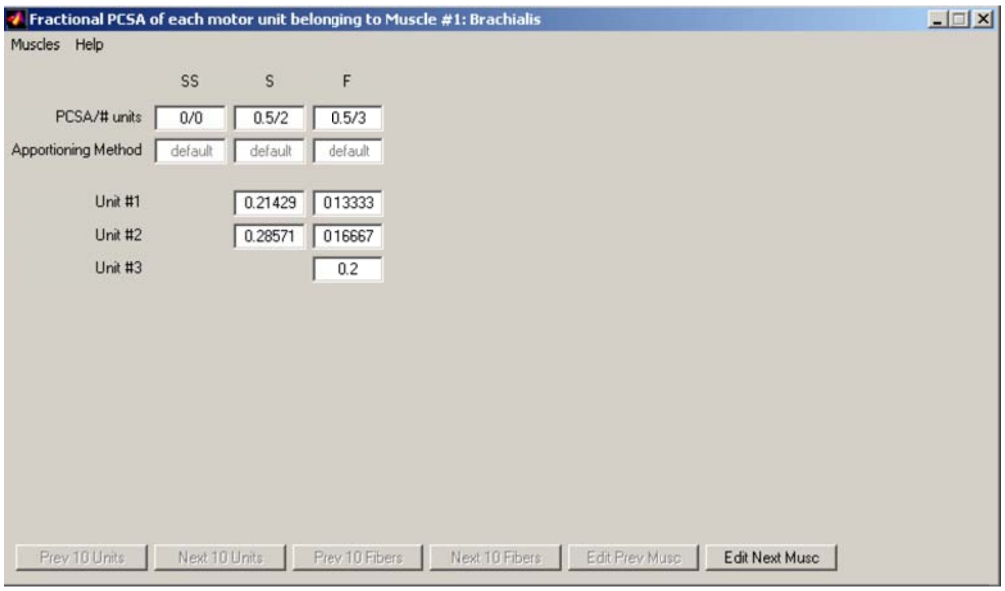
The allocation of the total PCSA of the muscle to each simulated motor unit can be viewed and edited by choosing the `Manually distribute unit PCSAs` item from the `Muscles` menu. A dialog will allow you to select the muscle to modify. A muscle specific window will open, listing the proportion of the muscle's PCSA that is apportioned to each motor unit and each different fiber type.

By default, assigning PCSA and number of motor units to a previously unassigned fiber type (i.e., with a previous PCSA/# motor units of 0/0) will result in an automatic distribution of PCSA for the motor units of that muscle and fiber type using the 'default' apportioning algorithm. For the 'default' apportioning scheme, the proportion of PCSA automatically allocated to each motor unit is based on the `Recruitment_Rank` parameter for the fiber type and on the total number of units of that type; as in the following equation:

$$\mathrm{PCSA}_{n^{th}\ \text{motor unit}} = \mathrm{PCSA}_{\text{assigned to fiber type}} \times \frac{\text{Recruitment\_Rank} + n}{(\text{Recruit\_Rank} + 1) + (\text{Recruit\_Rank} + 2) + \ldots + (\text{Recruit\_Rank} + \text{total \# motor units})}$$

Effectively, this distribution scheme assigns a larger proportion of PCSA to later recruited motor units of a given type. Increasing the absolute value of the `Recruitment_Rank` parameter for the fiber type reduces the differences in PCSA between consecutively recruited motor units. Because the `Recruitment_Rank` values of late recruited fiber types must always be greater than those of early recruited types, the distribution will always represent the physiological phenomenon whereby fast-fatigable units (which have a higher `Recruitment_Rank`) have a smaller range of sizes than slow-twitch units (Burke et al., 1973). Note that if you change the `Recruitment_Rank` parameter to change the automatic redistribution properties, you must ensure that the `Recruitment_Rank` for all other fiber types still accurately reflects the order of their recruitment. If a user wishes, he/she can manually enter in the PCSA of each motor unit to override the automatic distribution.

The user can also choose one of two other automatic apportioning schemes, each of which can be applied to either a single muscle or multiple muscles. The 'geometric' one will ask the user for the fractional increase between one motor unit and the next, and will then distribute the PCSAs appropriately for each fiber type. The 'equal' one simply makes all motor units of each fiber type equal in size to the other motor units of that fiber type.


Fractional PCSA of each motor unit belonging to Muscle #1: Brachialis

Muscles Help

	SS	S	F
PCSA/# units	0/0	0.5/2	0.5/3
Apportioning Method	default	default	default
Unit #1		0.21429	013333
Unit #2		0.28571	016667
Unit #3			0.2

The above figure depicts the automatic (‘default’) distribution of the PCSA in Muscle #1 (Brachialis) using 50% Type S in 2 motor units and 50% type FF in 3 groups. Thus, the two S units were sized to 21.4% and 28.6% of the total PCSA each, and the three FR units were sized to between 13.3% and 20% each. Note that consecutive FF motor units have a smaller change in proportion of PCSA, because FF fibers have a higher `Recruitment_Rank`. This model would be more realistic, particularly at low recruitment levels, if the relatively large fraction of total PCSA occupied by S units were divided into a larger number of smaller units such that the largest S unit was smaller than the smallest FF unit. The sudden recruitment of a relatively large unit at the beginning of muscle activation will create an unphysiologically large step in force (although the problem is not as severe as might be thought because of the ongoing frequency modulation of the units after their initial recruitment).

These numbers can be manually edited by typing new values into each field. If you change the total PCSA allotted to a fiber type, the individual unit PCSAs will be updated using the Apportioning method for that fiber type. If one of the unit PCSAs is manually updated, then the total PCSA for that unit will be updated automatically, and the apportioning method for that fibertype will change to ‘manual’. Different apportioning methods can be chosen by chosen under the `Muscles` menu.

If there are more than ten motor units of a given fiber type, the Prev 10 Units and Next 10 Units can be used to scroll through them. If more than five fiber types are used, the Prev 5 Fibers or Next 5 Fibers buttons are used. When changes are completed, select the `Close` option from the `File` menu.

Recruitment of motor units

Currently, two different recruitment strategies can be chosen from: ‘Natural’ and ‘Intramuscular FES’. Each one results in the creation of a SIMULINK block within the muscle block that takes the appropriate activation input and divides it into the recruitment and frequency outputs for each motor unit. For ‘Natural’ recruitment the activation input is assumed to be the relative strength of the net synaptic drive or EMG envelope. The 'Natural' recruitment strategy recruits all motor units of a lower Recruitment_Ranked fiber type before recruiting any motor units of the next highest Recruitment_Ranked fiber type. Within each fiber type, motor units are recruited in the order in which they were listed (i.e. it assumes that the motor units were listed in order of size). The frequency of each unit begins at f_{min} when that unit is first recruited and reaches a maximum of f_{max} when input activation equals 1.

The 'Intramuscular FES' strategy requires both an activation and a frequency input. The frequency input is assumed to be the frequency of stimulation being applied to the muscles and is the same (in units of pps) for all motor units. The activation is the relative strength of the stimulus. Motor units within each fiber type are recruited in the order in which they were listed, however, no distinction is made between recruitment rank. Instead the motor units are recruited so as to equalize the fraction of each fiber type recruited. A linear relationship between the fractional PCSA recruited and activation is maintained.

Additional Outputs

There is an option to add one or more of several outputs to each SIMULINK block, in addition to the force (N) output. These have been added because some of them may be necessary to provide as feedback to a neural circuit. The current choices are: activation, fascicle length (L_0), fascicle velocity (L_0/s) and Force (F_0).

Creating a SIMULINK block of one muscle

Once all details have been finalized to your satisfaction, a SIMULINK block which has been assigned the name of your muscle can then be created by selecting the `Create SIMULINK Muscle Block` item from the `Model` menu. This will launch SIMULINK and create a block that can be drag-and-dropped into your working SIMULINK figure. A SIMULINK block can be created as many times as desired, and for as many different defined muscles as desired. If you wish to utilize the `Rebuild Existing SIMULINK Model` function described below, it is necessary that the SIMULINK block name be kept the same. The use of these blocks is explained in the subsequent section.

Rebuilding an existing SIMULINK model

After you have used the SIMULINK muscle blocks in a model, you may wish to modify the parameters for each muscle or for the fiber types comprising the muscle blocks. The `Rebuild existing SIMULINK model` option from the `Model` menu allows you to select an existing SIMULINK model and will replace each muscle block in that model. This function works by searching the SIMULINK model for any blocks with names that match the muscle names in the currently open `Muscle_Database`. Any blocks with matching names will be replaced with a newly created SIMULINK block of that muscle, using the current parameters in the muscle model database and its associated fiber type database.

This facility allows you to easily modify the parameters for your muscles and test the effects of their changes on your simulation.

Using the muscle model

Structure of the SIMULINK block

Once you have created your `Muscle_Database`, you can create blocks of physiologically functioning muscle from the `BuildMuscles` function. The SIMULINK blocks are based on a modified Hill-type muscle model, which is described in detail in Brown *et al*. 1996. Although it is not necessary to understand the internal details of the muscle block, they are summarized here briefly. If you are not interested in the internal details, proceed to the next section.

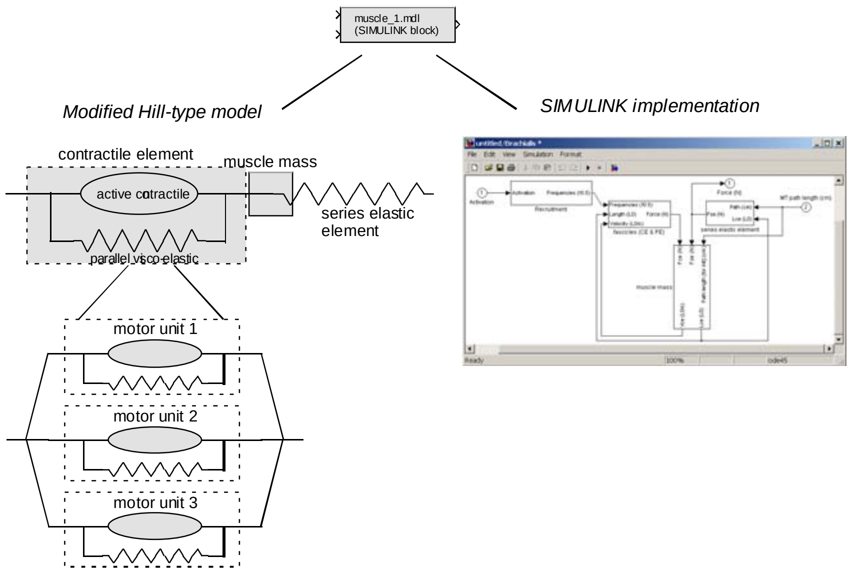
In summary, each SIMULINK muscle block contains a contractile element (which is composed of an active element and a parallel visco-elastic element) and a series elastic element. For modeling purposes, a muscle mass is interposed between the contractile and series elastic elements to prevent unrealistically large, instantaneous accelerations and instabilities that occur if the velocity dependent contractile element is connected directly to the series elastic element. Descriptions of SIMULINK subsystems used to model each of the elements are given below:

- **Recruitment block:** This element represents the motor pool (for natural recruitment) or stimulators (for FES). A single activation input (plus a frequency input for FES) is transformed into frequency outputs for each motor unit of that muscle. The combined vector is sent to the CE + PE element to calculate active force.
- **Contractile element + Passive element subsystem:** This element represents the fascicles in the muscle belly. Its output, force, is determined by three inputs; activation, fascicle length and fascicle velocity. Note that the fascicle length input to this subsystem is different from the entire musculotendon path length value which is input to the whole-muscle block. It is assumed that pennation angle is negligible for this model. Fascicle velocity is computed within the SIMULINK block by integrating the calculated acceleration. Also note that this element calculate the active and passive forces for the fascicles.

  The block representing the contractile element subsystem consists of one sub-block for each fiber-type within that muscle. Each of those fiber-type specific blocks then contains blocks that calculate those muscle properties which are the same for all motor units (of that fiber-type) as well as one sub-block for each motor unit as defined in the `BuildMuscles` function. The force blocks for each motor unit sum together to produce a force output for each fiber type block, which then sum to produce a single force output for the entire contractile element.
- **Series elastic element subsystem:** This element represents the effective length of the internal and external tendons; aponeurosis elements should be included. The force produced by this element is dependent only on length, and has been shown to have no significant velocity dependence at physiologically relevant frequencies. For this reason, changes in the musculotendon path length are made to act directly on the series elastic element.

  A single function block provides all the calculations for this element. Note that the length of this element is calculated by subtracting the length of the contractile element from the musculotendon path length.
- **Muscle mass subsystem:** The muscle mass was included to prevent the system from becoming unstable as the series elastic element and contractile element act on each other.

Position of the muscle mass within the block is tracked by first converting the force produced by the contractile and series elastic elements into a net acceleration, based on the size of the mass. Acceleration is then integrated to give a velocity, and integrated again to give the position of the mass. Velocity and position of the mass are fed back into the contractile element, and position is subtracted from the musculotendon length and fed back into the series elastic element.



Using the muscle blocks

Each SIMULINK whole-muscle block has at least two inputs and at least one output. A few common implementations are briefly discussed, but these will vary based on the form of the segment and activation data provided in your simulation. The two required inputs are:

- **Length:** The musculotendon path length is required in units of meters. *Note that this value may have to be calculated from the available data in the skeletal dynamics model, as often only segment coordinates or joint angles are provided.*
- **Neural activation:** This is a value for activation of the active part of the contractile element. This value is clipped between 0 and 1. The recruitment element of the muscle converts this activation (and possibly using other inputs, e.g. frequency for the case of FES recruitment) into an effective firing frequency of the motor units of the muscle. Typical inputs for 'natural' recruitment might be from EMG data scaled to the level of maximal voluntary contraction, or a simulated α-motoneuron that is controlled by reflex feedback or a neural network.

- **Frequency:** This value is only required for FES recruitment and is the stimulus frequency (pps) being applied to the motor pool.

A single required output is provided from the SIMULINK block:

- **Force (N):** The force is measured at the series elastic element. If the muscle is to act at a joint to create a torque, it is important that the moment arm which the muscle acts through is realistic.

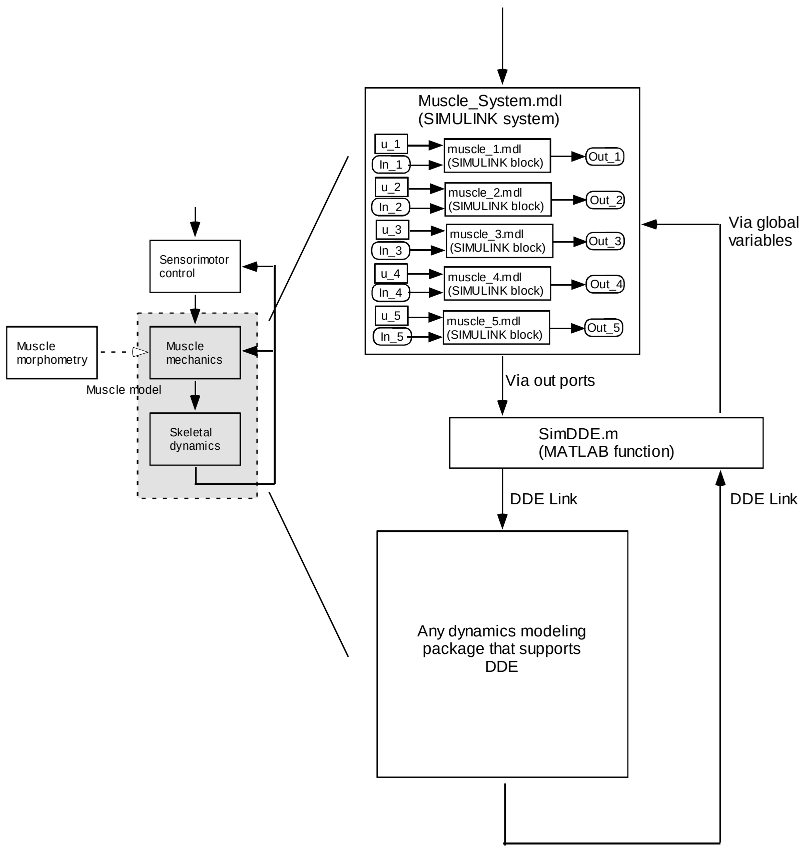
  The force produced by the muscle is positive in sign. Thus, the output may have to be multiplied by –1 depending on the implementation of the skeletal mechanics portion of your model.
- **Force (F_0), Activation, Fascicle Length (L_0) and Fascicle Velocity (L_0/s):** These outputs are optional, and may be of use when providing feedback to a controller. The activation is just a wire through of the activation input. Force, Length and Velocity are simply the normalized versions of these variables.

Interacting with models of segment dynamics

As discussed previously, a model of the segment dynamics is not included, as this model was intended to provide only realistic muscle forces, and the segment systems are typically so specific that a generic model would not be useful for most users. This muscle model fits best with systems that have been designed hierarchically; i.e., that have existing handles for muscles that would allow forces to act directly on segments. Especially with SIMULINK based models, incorporating this muscle model would be trivial, as the force outputs from the desired muscles could easily be summed, modified by any requisite moment arm or other scalars and connected to the segment dynamics model.

Model integration will work well with any hierarchically designed models in other packages that can interface with MATLAB. But Virtual Muscle is now an integral part of a new musculoskeletal modeling software known as MSMS (developed in our laboratory) that provides graphical interface to build complete models of musculoskeletal systems and simulate them in Simulink. For more information about MSMS please visit:

http://ami.usc.edu/projects/ami/projects/bion/musculoskeletal/msms.html



Interacting with a controller model

A control block created within SIMULINK is well suited to providing the activation levels needed for each muscle block. This controller can easily receive input from the segment dynamics model to provide feedback control of the muscles. This control can be supplemented by or replaced with pre-generated muscle activation levels, such as those recorded from EMG signals. SIMULINK allows simple access to data such as EMG signals recorded over time via either a `From Workspace` block or a `From File` block. Essentially, the data must be in tabular form with time values as one column, and any other values to be passed into SIMULINK as other columns. Detailed instructions are given in the SIMULINK documentation.

External software that can exchange data with MATLAB can also be used as the controller model. In Windows, DDE is a common standard to facilitate inter-software communication. The SimDDE example given in the following section can be modified to suit this role.

Editing the muscle blocks

Each SIMULINK muscle block contains fixed equations and constants as defined in the original `Fiber_Type_Database.mat` and `Muscle_Database.mat` files at the time of the creation of the block. Once the muscles have been created and linked into a SIMULINK model, their parameters can be changed by modifying the information in the original `Fiber_Type_Database.mat` and `Muscle_Database.mat` files and using the `Rebuild Existing SIMULINK Model` from the `BuildMuscles` functions. In this way, it is simple to observe the effects of different muscle and fiber type parameters on the behavior of your system. As described previously, the names of the muscle blocks in your SIMULINK model should match the names of the muscles in your `Muscle_Database.mat` file should you wish to use the rebuild function.

To examine the structure of the muscle model, double-click on the whole muscle block. This will reveal the SIMULINK blocks that make up the muscle model. At this level editing the details directly is not recommended, but is possible. For conceptualization purposes, the blocks are loosely grouped into a contractile element subsystem of blocks, a series elastic element subsystem, and a muscle mass subsystem. The visible lines control the flow of data between the subsystems.

Running your simulation

The muscle block that you have created behaves like any other standard SIMULINK block.

Inserting it into any existing system or .mdl file will allow you to click on the ▶ icon in SIMULINK or to use the `SIM` command from within MATLAB to start your simulation.

Initial conditions for the muscle mass block

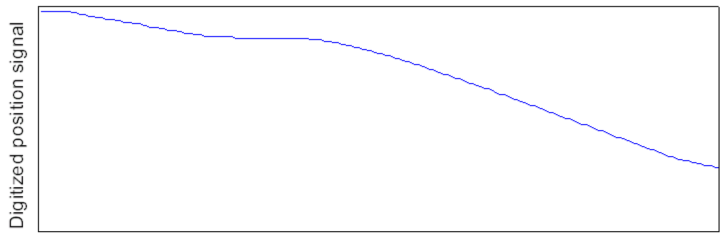
At the first time-step of the simulation, positions of all internal muscle masses and hence the starting lengths of each contractile and elastic element are chosen based on the initial conditions predefined by the model. The initial fascicle length conditions can be modified within the muscle mass subsystem by changing the default conditions for the muscle mass position integrator. By default, the position is set to a position that is almost exactly in equilibrium (if the passive force of the muscle is less than 5% of maximum, this position will be accurate to better than 0.1%). At extremely long lengths or if the passive force equations are changed such that there is significant passive force at the start of a simulation, the system will have to be allowed to reach equilibrium.

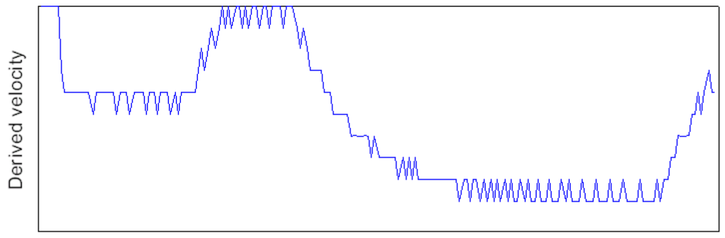
After the first time-step, the positions of all the internal muscle masses are stored in a state vector that is continuously updated by SIMULINK. These state values are important so that SIMULINK can remember the lengths and velocities of each contractile and elastic element. If your simulation is run uninterrupted, this state vector is completely transparent to the user and does not need to be considered. However, if you plan on stopping your simulation and restarting it at different times, this state vector will have to be stored on stop and reloaded on restart to avoid going through a new settling period. Doing this may be necessary if you are interfacing with an external simulation package, such as to model system dynamics. An explanation of this procedure is given in the following section describing a sample implementation of this model.

Common problems

Using experimental data

One typical use of muscle models is to predict muscle force from experimentally recorded data for activation and length. Kinematic data often have noise or quantization errors that are magnified when the length data are differentiated to produce velocities of muscle stretch, as shown below. Note that while the position signal appears smooth, when differentiated in the SIMULINK model, the velocity is not smooth. Because muscle fiber velocity has such a large effect on force output, it is usually desirable to apply a modest smoothing function to your length data before sending it to the SIMULINK muscle model block.

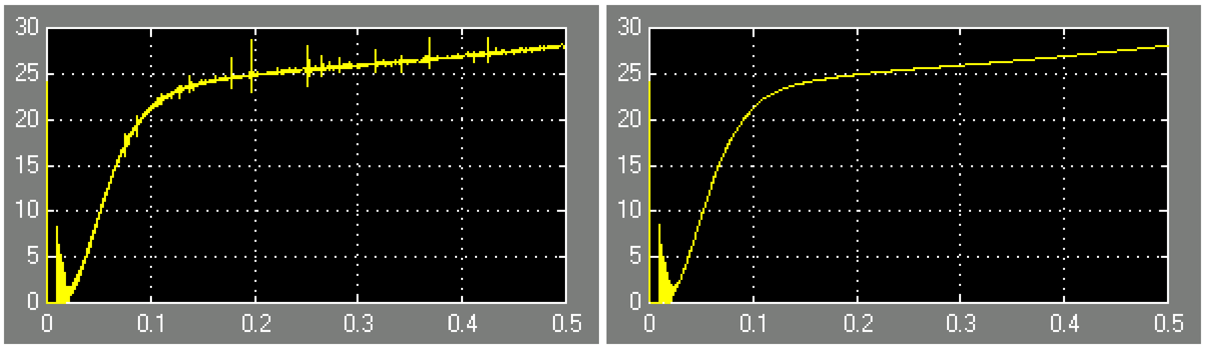




Insufficient accuracy

The tolerances for inaccuracy that SIMULINK uses can be viewed in an open .mdl document under the `Simulation`→`Parameters`→`Solver` menu. The default relative tolerance for SIMULINK 3.0 is 1e-3. Any errors in integration detected when the simulation runs above this value will result in SIMULINK automatically reducing its time step sizes. For most muscle models, a relative accuracy of 1e-6 is sufficient to prevent instabilities from arising under physiological conditions. If accuracy conditions are not stringent enough, SIMULINK may not return any errors, but the force output between time steps may be change drastically, as opposed to gradually. This may be reflected in the kinematics of the system you are modeling by instability or jerkiness. Try tightening tolerances by an order of magnitude to see if this resolves the issue.

An example is depicted below. On the left, a muscle is given a constant level of activation and has a constant velocity ramp stretch applied, using the default relative accuracy in SIMULINK of 1e-3. Note the spikes in the force trace corresponding to inaccuracies in integration. On the right, the same conditions but with relative accuracy tolerance tightened to 1e-6. In both cases, for the first 20 ms, there are initial force transients relating to the "settling" of the contractile element and the tendon. This is unrelated to the integrator tolerances, and is discussed in a following section.



Inappropriate initial conditions

Muscles with a zero tendon length will not function properly. To counteract this, a minimum tendon length of 0.1 cm is attributed to muscles specified in the `BuildMuscles` function.

Scaling of activation inputs with multiple motor units

A consequence of simulating multiple motor units is that the recruitment function used in this model produces a non-linear response in the conversion from input activation into effective muscle activation such as might be measured by EMG. This arises because increasing activation linearly increases the frequency envelope of any currently recruited motor units and also recruits additional motor units. Suggested solutions are described in Appendix C.

Unrealistic simulation conditions

If muscles are stretched to extremely long lengths (i.e., if the contractile element of the muscle exceeds 1.85 L_0), SIMULINK will likely return the following warning.

```
Warning: Attempt to raise negative value to a non-integer power in
'untitled/Brachialis/contractile element/Fiber 1/Af'.
```

This results from the method used to determine rise and fall times for the effective activation of the muscle. While exact solutions for A_f would not produce these errors, numerical solutions can be inaccurate. If this warning arises, check the lengths for the muscle indicated by SIMULINK.

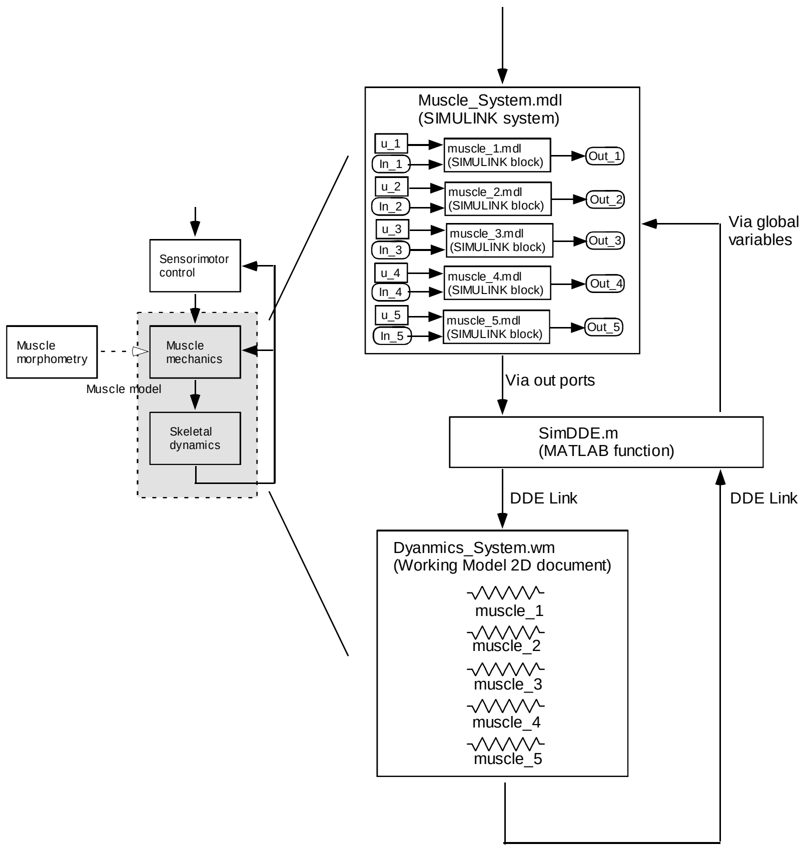
Simulation running too slowly

While the use of multiple motor units allows a combination of muscle fiber types and serves to increase accuracy of muscle force production, an inherent drawback is the increased computational time required for your simulation. Depending on the level of accuracy desired, the use of multiple motor units may not be necessary to replicate relatively realistic muscle behavior. Additionally, for the purposes of familiarizing yourself with the muscle model software and to first set up your model, it may be desirable to use single motor unit muscles, which can later be replaced with muscles that have multiple units and fiber types using the `Rebuild Existing Muscle Model` option in the `BuildMuscles` function. To facilitate a simple but effective single motor unit muscle, you should modify the minimal firing frequency (f_{min}) of the fiber type to be used in your muscle to be zero (in the `BuildFiberTypes` function), and specify the U_r (in the `BuildMuscles` function) for that muscle to be zero.

Interfacing with non-MATLAB applications

Provisions are provided in many simulation packages for dynamic data exchange (DDE) that allow MATLAB to control one aspect of the simulation. In this case, it is possible to use MATLAB's DDE interface to allow SIMULINK to pass data to and from another application (SIMULINK cannot do this directly). This can be affected by writing a MATLAB "wrapper" function that acts as an intermediary between your external application and the SIMULINK model.

The MATLAB wrapper must call SIMULINK to run over a time-step that matches the time-step of the external application. Inputs to the MATLAB function will vary depending upon the specifics of the external application. As mentioned previously, for all time-steps except the first one, SIMULINK relies on a vector of saved state variables that allow the muscle model to resume its run with the lengths and velocities of the elements within the muscle being retained. Data is passed out of the MATLAB wrapper in the form of variables which may be in vector or scalar form. The way in which your application utilizes these will vary.



Appendix A: MATLAB database details

Fiber type database

The fiber type database file created by the `BuildFiberTypes` function contains two structures named `BFT_Fiber_Type_Database` and `BFT_FTD_General_Parameters` that are required by the `BuildMuscles` function (their names change to `BM_Fiber_Type_Database` and `BM_FTD_General_Parameters` respectively in the `BuildMuscles` function). The structure of these variables is pre-defined and must be conserved in order for the system to function properly. For most users, all editing of these structures is done transparently using the `BuildFiberTypes` function (i.e. the user never sees the structure explicitly). However, for users interested in the workings of the function, an explanation of these structures is given at the beginning of the `BuildFiberTypes` m-file.

The GUI for `BuildFiberTypes` relies on global variables including, but not limited to the two structure mentioned above. So while this function is running, it is best to avoid modifying variables in the global workspace within MATLAB. If you are not an experienced MATLAB user, you will not have to be concerned with this detail, as global variables cannot be modified unless you explicitly attempt to do so. These global variables are cleared after closing the `BuildFiberTypes` function.

Muscle database

The `BuildMuscles` function creates and saves a database file also containing two structures, `Muscle_Morph` and `Muscle_Model_Parameters`. The former variable tracks the values that are independently assigned to each muscle in the database, such as the muscle names, masses, and compartment PCSA distributions. The latter variable stores the variables that remain constant for all muscles in that database, such as the tendon properties, the filename of the associated `Fiber_Type_Database`, and the names of the fiber types used in the `Muscle_Database`. Both these variables are structures and are described at the beginning of the `BuildMuscles` m-file.

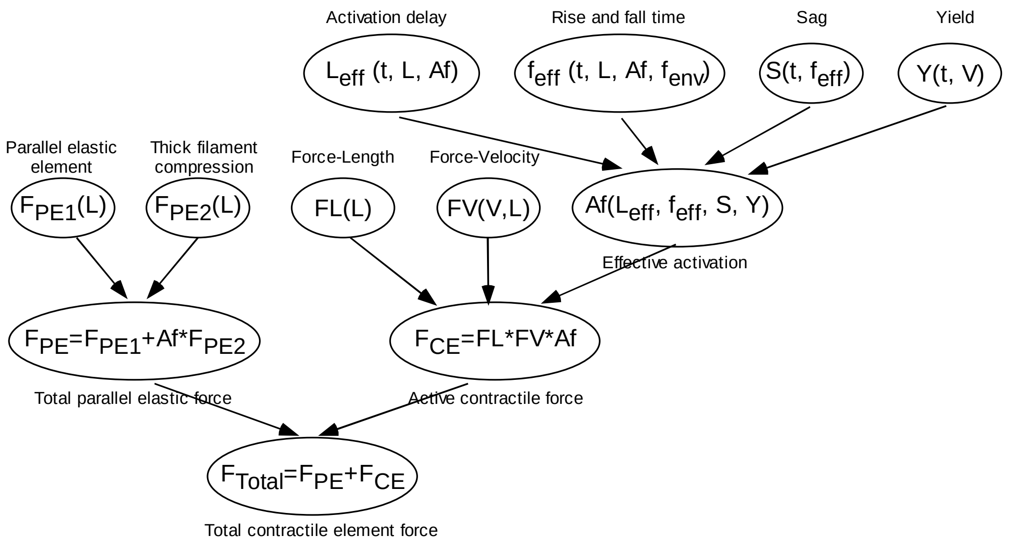
Upon loading an existing `BuildMuscles` database file, the `BuildMuscles` function searches for and attempts to load the `BuildFiberTypes` database file associated with the `BuildMuscles` database file, so ensure that this file can be found in the current directory or in the MATLAB search path.

Appendix B: Structure of Model and SIMULINK Blocks of 'Natural Discrete (Brown & Cheng)'

Representations of muscle properties and components

Our general approach to modeling is to create a set of functions and terms that have a one-to-one correspondence with known anatomical structures and physiological processes that occur in muscle and tendon. The experiments on which this model is based were designed to identify the specific structures and processes within muscle that give rise to complex phenomena (e.g. frequency-length interactions, yield, sag, etc.). The functions that describe those structures and processes or their input parameters were then modified to reflect the mechanisms underlying the phenomena. This strategy improves the likelihood that the model will extrapolate accurately to deal with ranges and combinations of input conditions that have not been tested explicitly in the source experiments. The resulting model has three representations providing increasing levels of detail, as described in the following sections.

Schematic diagram of functions



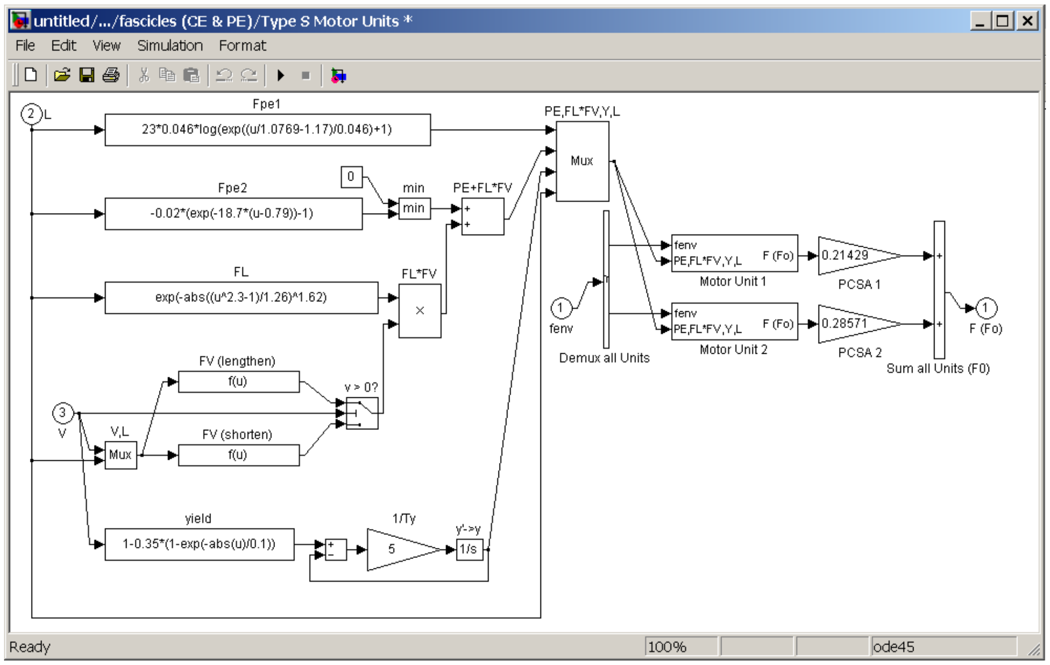
Each of the blocks represents a physiological process whereby input parameters are converted into output parameters according to that process, as described by a mathematical function. The output parameters of one process represent input parameters to other processes contained in other blocks of the hierarchy, which ends at the bottom with total force output of the contractile element. The label associated with each block is a short-hand name for the physiological process, which often reflects the experimental phenomenon whereby that process was first revealed or quantified. The corresponding SIMULINK component blocks and mathematical equations described in the next two sections are identified by the same labels.

SIMULINK muscle blocks

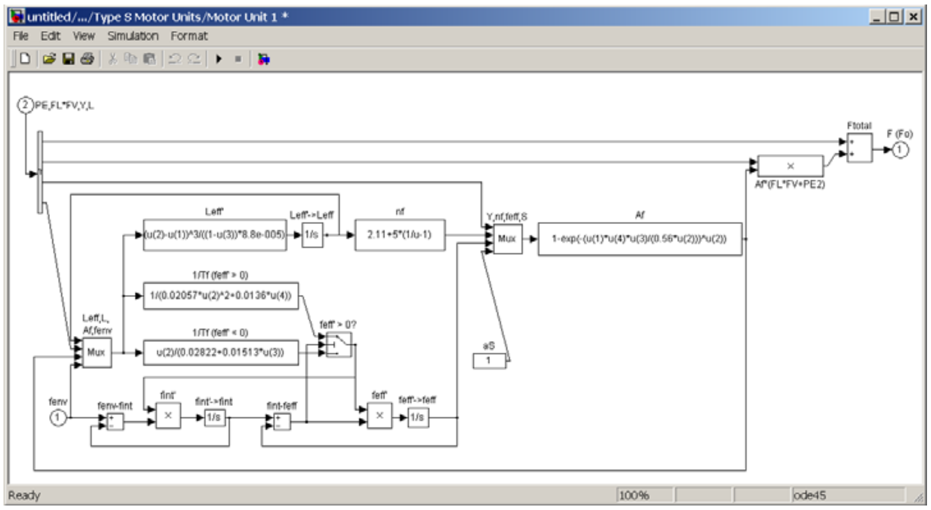
Each SIMULINK muscle block is composed of many individual blocks that perform the mathematical functions described above. The connectivity between blocks reflects the dependencies described schematically above. Each block contains a mathematical function whose constants were set when the muscle block was created, reflecting the muscle fiber type data and parameters used to create it. A sample function equation is given below:

```
1-exp(-(u(1)*u(4)*u(3)/(0.56*u(2)))^u(2))
```

These equations are somewhat unwieldy when manipulated directly. Changes are best effected by modifying the parameters and coefficients in the `BuildMuscles` function, and using the `Rebuild existing SIMULINK model` function.



The actual SIMULINK block for the motor units of a single fiber-type is depicted above, and is based on a structure provided by Jiping He (personal communication). Those properites (e.g. FL) which are the same for all of these motor units, are calculated only once. Those properties which are unit-specific, are calculated separately, as shown below in an example of a motor unit block.



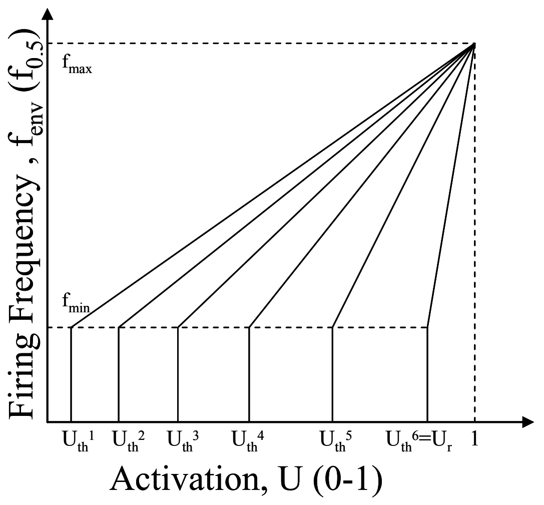
Appendix C: ‘Natural Discrete (Brown & Cheng)’ Recruitment details

The idea central to almost all recruitment functions for multiple motor units driven by a common input is the Henneman (1968) size principle, which states that smaller motor units are recruited before larger motor units. In our ‘natural’ recruitment function, this is applied to motor units of different histochemical fiber types, reflecting the normal tendency of slow-twitch motor units to be smaller than fast-twitch motor units, and thus recruited first. Recruitment order of different fiber types is tracked in the `BuildFiberTypes` function with the `Recruitment_Rank` parameter assigned individually to each fiber type.

Physiologically, motor units of the same fiber type are also recruited according to their sizes. In our model, recruitment order within a fiber type is determined by the sequence of the motor units as they are entered into the `Manually_Distribute_PCSAs` window of the `BuildMuscles` function. A strict PCSA based recruitment order was not enforced at this level for two reasons: 1) the user is able to simulate this behavior by apportioning smaller fractions of PCSA to the first motor units and larger PCSA to later motor units, and 2) the simulated motor units are not necessarily intended to model individual motor units; instead they represent groups of motor units to reduce computational time. The auto-distribution of PCSA in the `BuildMuscles` function actually replicates this behavior to an extent, by apportioning less PCSA to the earlier recruited motor units; this apportioning is detailed in the description of the `BuildMuscles` earlier in the manual. This also serves a practical purpose in that it makes the onset of force production more gradual by making the first recruited motor units of a given fiber type smaller than the later recruited ones.

The ideas behind the implementation of the ‘natural’ recruitment function are described by Brown (1998), with some minor variations. All the motor units in a given pool are driven by a common activation signal, U. Motor units are recruited sequentially, based on two properties: 1) the `Recruitment_Rank` of the fiber type for that motor unit, and then 2) the order determined in the `BuildMuscles` function. As U increases, more motor units are recruited until U_r is reached; this is the point at which all motor units have been recruited; increases in activation beyond this point result only in frequency modulation of motor units. Motor unit recruitment threshold is determined based on a combination of the cumulative fractional PCSA of all motor units recruited prior to the given motor unit, with range of recruitment between 0 and U_r, as depicted in the figure below.

As an example, the first two compartments are slow-twitch (and are thus recruited first), and the U_r for the muscle is 0.8. Note that while it appears that both slow- and fast-twitch motor units have the same firing frequency range, recall that f_{min} and f_{max} are in units of $f_{0.5}$, and that $f_{0.5}$ has different values depending on fiber type.



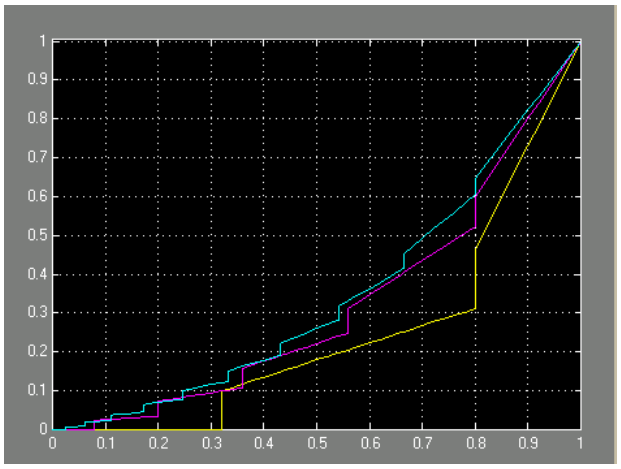
For each motor unit, the frequency modulates from a predetermined f_{min}, when the unit is first recruited, up to f_{max}, which occurs at a full activation for the muscle. This linear change in firing frequency change relative to change in EMG has been demonstrated experimentally (e.g., Milner-Brown et al., 1973). The common initial firing frequency for motor units of a given fiber type and the convergence of their firing frequencies to a single maximal firing frequency at maximal activation have been demonstrated experimentally (De Luca et al., 1996).

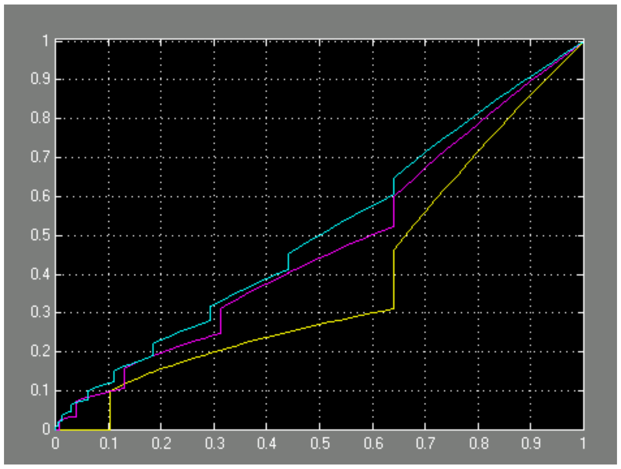
There is some suggestion that the frequency modulation of earlier recruited units is hyperbolic rather than linear (Monster and Chan, 1977). This can be approximated by setting F_{max} artificially high for such fiber types and taking advantage of the sigmoidal shape of the force-frequency relationship.

Multiple motor unit recruitment behavior

As a consequence of the interaction between having both an increased recruitment of motor units and an increase in the firing frequency of each motor unit with increasing activation, the relationship between activation and the frequency envelope driving the motor units becomes non-linear. As an example of why this occurs, consider first the simplest case; having a muscle modeled as a single motor unit. When activation reaches U_r, the motor unit is activated at a frequency of f_{min} and the frequency envelope for the whole muscle rises linearly until f_{max} is reached.

Next, consider a case with two compartments. When threshold for the first motor unit is reached, the frequency envelop for the portion of the muscle's PCSA allocated to that motor unit increases linearly from f_{min} to f_{max}. However, when the second motor unit reaches threshold, there is a jump in motor unit activation as the PCSA for the second motor unit becomes recruited, and also frequency modulates from its own f_{min} to f_{max}. Thus, the mean frequency driving the total muscle PCSA increases at a higher rate at this point. With more than two compartments, sudden transients in mean frequency are reduced in magnitude, but the non-linearity in frequency response remains.





The figure above on the left depicts the mean frequency driving the total PCSA for the entire muscle, when two (yellow), five (magenta) and ten (cyan) motor units are modeled. To linearize the response of the muscle, one method is to take the square root of activation input before applying it to the muscle. The figure above on the right depicts the effects of using a square root adjustment on the activation input. With fewer than 10 compartments, a lower exponent might be desired, such as $u^{1/3}$. However, $u^{1/2}$ fits relatively well for 5 or more compartments.

The relationship between recorded EMG and effective muscle activation is complex and probably depends on the recording method. If all regions and fiber types in the muscle are sampled without bias, then it should be possible to estimate this relationship from first principles:

- A single action potential in a single motor unit should produce a unitary potential whose amplitude corresponds approximately to the total physiological cross-sectional area of its muscle fibers. This assumes that the recorded action potential reflects the total action current, which is the sum of the synchronous action currents in each muscle fiber.
- The action current generated by a spike in a simple cylindrical conductor such as an unmyelinated axon tends to depend on diameter (i.e. surface area) rather than cross-sectional area, but the action currents of muscle fibers may scale more closely to their cross-sectional area because of active conduction down the transverse tubules. Fortunately, the range of muscle fiber diameters is relatively small, with more of the range in motor unit size related to innervation ratio (number of muscle fibers per motor unit).

Unfortunately, the recorded EMG is not a simple linear summation of these unitary action potentials because of occlusion – the tendency of biphasic action potentials to cancel each other when their opposite polarity phases happen to overlap. The higher the aggregate rate of action potentials, the more likely they are to be partially occluded before they can contribute to the recorded AC waveform whose area-under-the-curve is taken to represent activation. This would suggest that the recorded EMG should be squared to more accurately reflect the underlying total muscle activation. Thus, this effect might be expected to counteract the above-noted suggestion that you should use the square-root of a recorded EMG envelope in order to use it as an activation input.

There is one piece of evidence suggesting that the EMG envelope is, in fact, linearly related to the input signal to the motoneuron pool itself, as currently structured in the model. When such a recorded EMG envelope was scaled linearly and applied as an intracellularly-injected depolarizing current to individual motoneurons, those motoneurons reproduced the frequency modulation recorded from single motor axons recorded at the same time as the EMG envelope (Hoffer et al., 1987).

The appropriate theoretical relationship probably lies somewhere between linear and square-root of EMG envelope. Practically, the effects of electrode design and placement and underlying muscle architecture are likely to be much larger. For example, skin surface electrodes are highly biased toward large, superficial motor units that are recruited only at high activation levels, severely underestimating low-levels of recruitment. Such records would be better modeled by taking the square-root of the recorded envelope.

Appendix D: 'Natural Discrete' recruitment model

Difference between 'Natural Discrete (Brown & Cheng)' and 'Natural Discrete' algorithms

The 'Natural Discrete' muscle model is different from 'Natural Discrete (Brown & Cheng)' in two aspects: basic model structure and model implementation.

Basic model structure: 'Natural Discrete' does not include the 'Activation delay' effect, which is modeled in 'Natural Discrete (Brown & Cheng)' by introducing an intermediate muscle fascicle length variable, effective length, L_{eff}.

Model implementation: The functions of 'Natural Discrete (Brown & Cheng)' model is implemented by interconnecting Simulink basic blocks as described in Appendix B, whereas, 'Natural Discrete' model is implemented by state-space functions in CMEX S-function represented by a customized Simulink block.

Updated Equations and coefficients for the muscle model

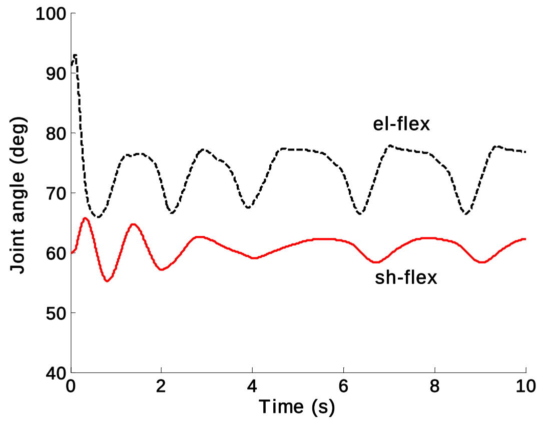
Corresponding to the change of model structure, the equations for Activation delay is removed and the Activation frequency relation (Af) is formulated as function of current muscle fascicle length instead of effective length (see the table for equations and coefficient at the end of Appendix E).

Computational Efficiency

The model is computationally more efficient because of the reduced number of states due to removal of L_{eff}. This is a motor unit specific state thus if the muscle is modeled with large motor neuron pool, the reduction of the state numbers will be substantial.

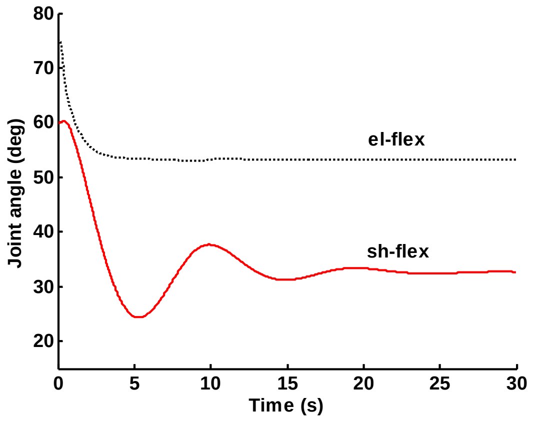
Model performance

The intermediate state variable, effective length (L_{eff}) was introduced to the original VM model (Natural Discrete (Brown & Cheng)) to model the effect of delayed length dependency on activation-frequency relationships (*Af*). This forms an internal negative feedback loop with an *Af* dependent delay, which may produce instability of the musculo-skeletal dynamics even without reflex feedback. This is demonstrated in a dynamic simulation using two-joint six-muscle musculo-skeletal human arm model given constant motor commands. The figure on the left shows the shoulder (sh_flex) and elbow (el_flex) joint kinematics as functions of time, the instability results from the delayed length feedback in Af relations. Removing this complication resulted in a stable open-loop response as shown in the right figure below. The comparison of model performances showed little if present discrepancy of force production with the modified VM.



100
90
80
70
60
50
40
0
2
4
6
8
10
Joint angle (deg)
Time (s)
el-flex
sh-flex

(a)



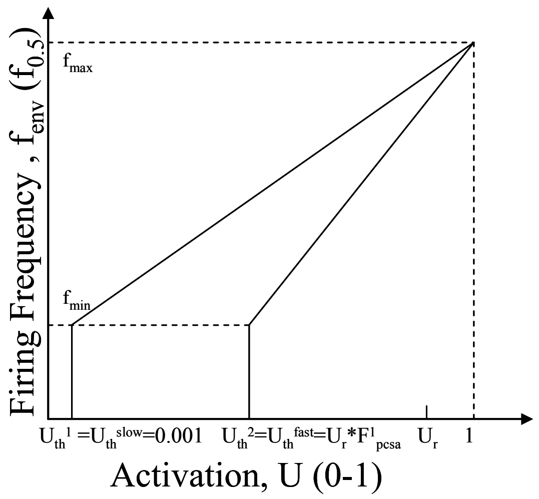
80
70
60
50
40
30
20
0
5
10
15
20
25
30
Joint angle (deg)
Time (s)
el-flex
sh-flex

(b)

Appendix E: 'Natural Continuous' Recruitment details

Natural Continuous algorithm in Virtual Muscle

'Natural Continuous' Recruitment is designed to match the average behavior of 'Natural Discrete' Recruitment strategy.



Instead of modeling each unit explicitly, the Natural Continuous algorithm lumps the multiple units according to the corresponding fiber types, thus requiring only one unit per fiber type. Each unit or fiber type becomes active at a threshold U_{th}^{i} that depends on the distribution of fractional PCSA (F_{pcsa}) among all the fiber types and their recruitment orders:

$$\begin{cases} U_{th}^{i} = 0.001 & i = 1 \\ U_{th}^{i} = U_r \cdot \sum_{k=1}^{i-1} F_{pcsa}^{k} & i > 1 \end{cases} \tag{1}$$

Once recruited, the lumped motor unit modulates its frequency according to the usual calcium dynamics as in the Natural Discrete algorithm. There are three important aspects of the new algorithm. Firstly, the total muscle activation and contraction dynamics depend on the proportions of slow and fast fibers. The continuous algorithm accounts for this effect by linearly combining Af and FL, FV properties of each fiber types (*Eq.2*) multiplied by a weighting factor, W^i, representing proportions of the fiber type among the overall active muscle portion (*Eq.3*). Secondly, the discrete algorithm simulates force modulations in physiological muscles by sequentially adding or substracting fractional PCSA scaled forces of newly recruited or derecruited motor units. As the number of units increases, this additional process is equivalent to multiplication by the activation level (U_{eff}), which formulates the continuous version of neural modulation of muscle forces in the new Natural Continuous algorithm (*Eq.2*). Thirdly, the activation frequency (Af) relationship includes the dynamics of calcium activation and this effect must also be represented in the multiplication of activation. We thus introduced a first order dynamics to convert activation input *U* to effective activation U_{eff} (*Eq.4*). The values of rising and falling time constants (T_U) were chosen to simulate the dynamic force responses of Natural Discrete system to sinusoidal activation inputs over the range of physiological neural modulations (0-10Hz).

The normalized active force from contractile element (CE) with n fiber types (units) is calculated as:

$$\overline{F}_{ce} = U_{eff} \cdot \sum_{i=1}^{n} \left[W^i \cdot Af^i \cdot \left(FL^i FV^i + \overline{F}_{pe2} \right) \right] \tag{2}$$

Where n is the number of active muscle fiber types, and the W^i is calculated based on the threshold of each fiber type or unit, $U_{th}^{\ i}$, and the effective activation, U_{eff},:

$$W^i = \frac{U_{eff} - U_{th}^i}{\sum_{k=1}^{i} \left(U_{eff} - U_{th}^k \right)}, \forall U_{eff} \geq U_{th}^i \tag{3}$$

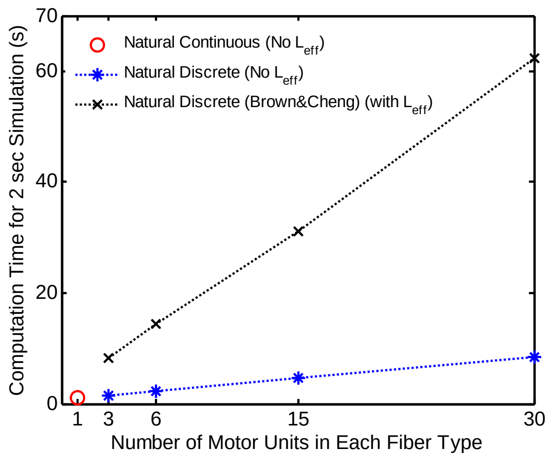
The amount of muscle actually recruited is specified by an intermediate muscle activation signal, effective activation, U_{eff}, which incorporates first order dynamics simulating the rise-fall effect modeled in calcium dynamics:

$$\dot{U}_{eff} = \frac{U - U_{eff}}{T_U}, \quad T_U = \begin{cases} 0.03(\sec) & U \geq U_{eff} \\ 0.15(\sec) & U < U_{eff} \end{cases} \tag{4}$$

Computational Efficiency

The continuous algorithm is computationally much more efficient because of the reduced number of states: four fiber-type-specific states and three muscle states. In the discrete algorithm, each motor unit is independently frequency modulated, and then VM must keep track of the history of activation of many units to deal with the nonlinear relationship between frequency and force output. Since there are 4 motor unit specific state variables, thus each increase of number of motor unit will have 4-fold increase on the number of states. The continuous algorithm approximate the physiological muscle by assigning one unit for each fiber type with its size reflecting the percentage of PCSA occupied by that fiber type, thus significantly reduced the total number of state variables for each integration step. Consequently, the computation time is greatly reduced.

The time elapsed for full activation simulation with the three models (Natural Continuous, Natural Discrete, Natural Discrete (Brown & Cheng)) are compared in the figure below. The 2 second single muscle simulations were carried out with Matlab 7.1/Simulink 6.3. Operating System: Microsoft Windows XP Version 5.1 (Build 2600: Service Pack 2). Machine: Intel(R) Pentium (R) 4 CPU 3.20 GHz, 2.00 GB of RAM. In the two discrete models, the computation time increases linearly with number of motor units, and removing the effective length substantially reduces the CPU time. The natural continuous model has 15 fold reduction of computation time compared to the discrete model (no L_{eff}) with 30 motor units.



Comparison between Natural Discrete and Natural Continuous Recruitment modes

To test the effectiveness of Natural Continuous algorithm, we compared the performance of it with physiological "Natural Discrete" algorithm in force product on both static and dynamic neural modulation and muscle length changes. Specifically, we built a VM model with a motor neuron pool composed of 60% of slow and 40% of fast fiber types. The muscle architectural parameters were: muscle mass= 122.4 g (i.e.F0=266 N), optimal fascicle length=13.8 cm, optimal tendon length=4.2 cm, max musculotendon length=18.4 cm. Muscle force outputs with sinusoidal activation (U=0-1) at constant musculotendon length (Lmt=16 cm) (a and c), and sinusoidal musculotendon length (Lmt=14-18cm) at constant activation (U=0.5) were also compared between Natural Continuous and Natural Discrete algorithms in the figure below:

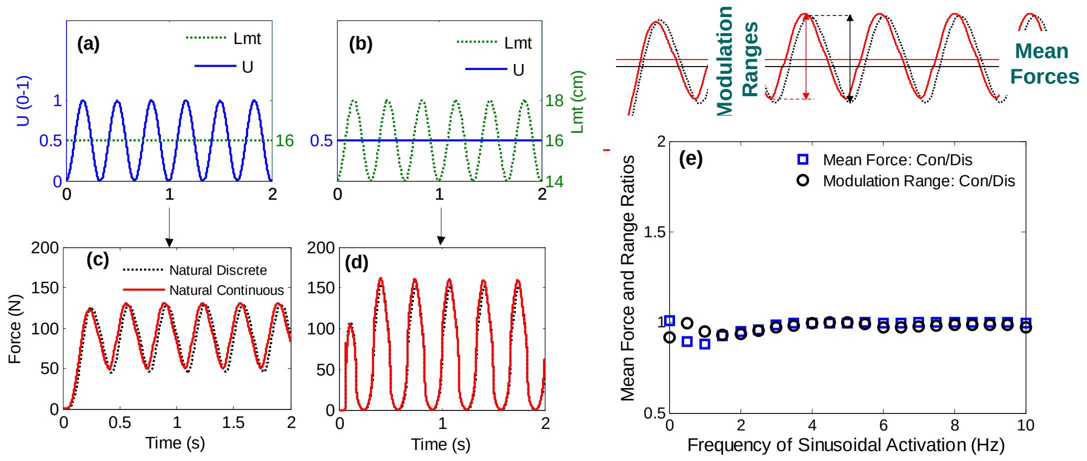


Figure legend: Natural Continuous VM produces force transients approximating those of Natural Discrete, with slight phase lead compared to discrete during relatively rapid modulation of neural activation *U* (c). In neural modulation of movement dynamics, the important control variables of muscle motor output usually include the mean force and force modulation ranges (top panel of e). The ratios of natural continuous to discrete algorithm for these two variables are

almost constant at one over a wide range of frequencies of sinusoidal neural activation *U* (1-10 Hz) , which demonstrates the ability of MTCR to account for the dynamics of motor neuron modulation.

Equations and coefficients for the muscle model

The equations and their coefficients that are used in this model are drawn from Brown et al. (1996; 1999), Brown and Loeb (2000), Cheng et al. (2000) and Song et al. (submitted). A summary of the equations is listed below, as well as their coefficients in human fiber types slow- and fast-twitch fibers (extrapolated from feline muscle described in Brown and Loeb, 2000 and Brown et al., 1999).

Curve	*Slow-twitch muscle constants*	*Fast-twitch muscle constants*
Tendon elasticity $\bar{F}_{se}\left(\bar{L}_{se}\right)=c^T k^T \ln\left\{\exp\left[\frac{\bar{L}_{se}-L_r^T}{k^T}\right]+1\right\}$	c^T k^T L_r^T 27.8 .0047 0.964	c^T k^T L_r^T 27.8 .0047 0.964
Parallel elastic element $\bar{F}_{pe1}\left(\bar{L}_{ce},\bar{V}_{ce}\right)=c_1 k_1 \ln\left\{\exp\left[\frac{\bar{L}_{ce}/\bar{L}_{ce}^{\max}-L_{r1}}{k_1}\right]+1\right\}+\eta\bar{V}_{ce}$	c_1 k_1 L_{r1} η 23 0.046 1.17 0.01	c_1 k_1 L_{r1} η 23 0.046 1.17 0.01
Thick filament compression $\bar{F}_{pe2}\left(\bar{L}_{ce}\right)=c_2\left\{\exp\left[k_2\left(\bar{L}_{ce}-L_{r2}\right)\right]-1\right\}, \qquad \bar{F}_{pe2}\le 0$	c_2 k_2 L_{r2} -0.02 -21.0 0.70	c_2 k_2 L_{r2} -0.02 -21.0 0.70
Force-length $FL\left(\bar{L}_{ce}\right)=exp\left(-\left\|\frac{\bar{L}_{ce}^{\ \beta}-1}{\omega}\right\|^{\rho}\right)$	ω β ρ 1.12 2.30 1.62	ω β ρ 0.75 1.55 2.12
Force-velocity $FV\left(\bar{V}_{ce},\bar{L}_{ce}\right)=$ $\begin{cases}\left(V_{\max}-\bar{V}_{ce}\right)/\left[V_{\max}+\left(c_{v0}+c_{v1}\bar{L}_{ce}\right)\bar{V}_{ce}\right], & \bar{V}_{ce}\le 0\\ \left[b_v-\left(a_{v0}+a_{v1}\bar{L}_{ce}+a_{v2}\bar{L}_{ce}^{\ 2}\right)\bar{V}_{ce}\right]/\left(b_v+\bar{V}_{ce}\right), & \bar{V}_{ce}>0\end{cases}$	$V_{\max}$ c_{V0} c_{V1} -7.88 5.88 0 a_{V0} a_{V1} a_{V2} b_V -4.70 8.41 -5.34 0.35	$V_{\max}$ c_{V0} c_{V1} -9.15 5.70 9.18 a_{V0} a_{V1} a_{V2} b_V -1.53 0 0 0.69
Activation delay modeled by effective length $\dot{\bar{L}}_{ce}^{eff\ i}(t)=\frac{\left[\bar{L}_{ce}(t)-\bar{L}_{ce}^{eff\ i}(t)\right]^3}{T_L\left(1-Af^{\,i}\right)}$	T_L (ms) 0.088	T_L (ms) 0.088
Yield $\dot{Y}(t)=\frac{1-c_Y\left[1-exp\left(-\frac{\left\|\bar{V}_{ce}\right\|}{V_Y}\right)\right]-Y(t)}{T_Y}$	c_Y V_Y T_Y (ms) 0.35 0.1 200	– – –
Sag $\dot{S}^i\left(t,f_{eff}^{\,i}\right)=\frac{a_S-S^i(t)}{T_S}, \qquad a_S=\begin{cases}a_{S1}, f_{eff}^{\,i}(t)<0.1\\ a_{S2}, f_{eff}^{\,i}(t)\ge 0.1\end{cases}$	– – –	a_{S1} a_{S2} T_S (ms) 1.76 0.96 43

Rise and fall time $\dot{f}_{int}^{i}\left(t, f_{env}^{i}, \bar{L}_{ce}\right) = \frac{f_{env}^{i}(t) - f_{int}^{i}(t)}{T_{f}^{i}}$ $\dot{f}_{eff}^{i}\left(t, f_{int}^{i}, \bar{L}_{ce}\right) = \frac{f_{int}^{i}(t) - f_{eff}^{i}(t)}{T_{f}^{i}}$ $T_{f}^{i} = \begin{cases} T_{f1}\bar{L}_{ce}^{2} + T_{f2} f_{env}^{i}(t), \; \dot{f}_{eff}^{i} \geq 0 \\ \left(T_{f3} + T_{f4} Af^{i}\right)/\bar{L}_{ce}, \; \dot{f}_{eff}^{i} < 0 \end{cases}$	T_{f1} (ms) T_{f2}(ms) 34.3 22.7 T_{f3}(ms) T_{f4}(ms) 47.0 25.2	T_{f1}(ms) T_{f2}(ms) 20.6 13.6 T_{f3}(ms) T_{f4}(ms) 28.2 15.1
Activation-frequency relation, with effective length $Af^{i} = \begin{cases} Af^{i}\left(f_{eff}^{i}, \bar{L}_{ce}^{eff\,i}, \bar{V}_{ce}\right) = 1 - \exp\left[-\left(\frac{Y f_{eff}^{i}}{a_f n_f}\right)^{n_f^i}\right], & slow \\ Af^{i}\left(f_{eff}^{i}, \bar{L}_{ce}^{eff\,i}\right) = 1 - \exp\left[-\left(\frac{S^{i} f_{eff}^{i}}{a_f n_f}\right)^{n_f^i}\right], & fast \end{cases}$ $n_f^i = n_{f0} + n_{f1}\left(\frac{1}{\bar{L}_{ce}^{eff\,i}} - 1\right)$ Activation-frequency relation, no effective length $\begin{cases} Af^{i}\left(f_{eff}^{i}, \bar{L}_{ce}, \bar{V}_{ce}\right) = 1 - \exp\left[-\left(\frac{Y f_{eff}^{i}}{a_f n_f}\right)^{n_f^i}\right], & slow \\ Af^{i}\left(f_{eff}^{i}, \bar{L}_{ce}\right) = 1 - \exp\left[-\left(\frac{S^{i} f_{eff}^{i}}{a_f n_f}\right)^{n_f^i}\right], & fast \end{cases}$ $n_f^i = n_{f0} + n_{f1}\left(\frac{1}{\bar{L}_{ce}} - 1\right)$	a_f n_{f0} n_{f1} 0.56 2.11 5.00	a_f n_{f0} n_{f1} 0.56 2.11 3.33
Effective activation $\dot{U}_{eff} = \frac{U - U_{eff}}{T_U}$, $T_U = \begin{cases} T_{U1} & U \geq U_{eff} \\ T_{U2} & U < U_{eff} \end{cases}$	T_{U1}(ms) T_{U2}(ms) 30 150	T_{U1}(ms) T_{U2}(ms) 30 150
Notes: Top bar $\bar{x}$ denotes the normalized variable *x* (forces by maximum isometric tetanic muscle force F_0 , lengths and velocities by optimal fascicle length or optimal tendon length [L_{ce0} or L_{se0}]); superscript x^i denotes the i^{th} motor unit specific variable x.		

Appendix F: ‘Intramuscular FES’ Recruitment details

The FES recruitment algorithm simulates Intramuscular FES and is computationally more efficient than the original FES recruitment in Virtual Muscle 3.1.5.

The new algorithm for Intramuscular FES recruitment is based upon the assumption that motor axon branchlets within a muscle belly are not recruited in any preferential fiber type order (this assumption is based on the Data of Singh et al., 2000). The algorithm recruits a fraction of the muscle's PCSA equal to the activation input. In order to decrease the amount of computation for real time applications, there is only one motor unit per fiber type representing the entire population of motor units. Consider, for example, a muscle composed of 30% slow fibers and 70% fast fibers, then the numbers 0.3/x and 0.7/y should be added under S and F columns respectively. The value of x and y after the “/” specify the number of motor unit for that fiber type. No matter what that number is (besides zero), we have modeled only one motor unit for each fiber type. In case that the user has defined a fiber type but would like to shut down that fiber type without having to redefine a new fiber type database, the following should be inserted: 0/x and PCSA distribution should be readjusted. Frequency of FES recruited units is set by a second input to each motor unit, which is the stimulus frequency applied by the user (the algorithm converts the frequency from pps input to internal dimensionless units of f0.5).

Stimulation Frequency

The stimulation frequency chosen for fixed frequency FES is usually a compromise between a frequency high enough to avoid tremor from unfused twitches and low enough to minimize fatigue. Both constitute a moving target in clinical patients undergoing FES training, because trophic factors tend to shift muscle fiber properties towards slower twitch properties and greater fatigue resistance (Malmivuo et al., 1995). It is recommended to use 20Hz as excitation frequency for realistic clinical FES applications, but VM now provides an explicit input for frequency as well as intensity of stimulation, and it should represent total muscle force correctly if the appropriate physiological parameters are set for the unit types (f0.5 = frequency that produces half of maximal tetanic, isometric tension at L0 for each unit type). (It is useful to remember that a fixed firing rate tends to be much higher on the force/frequency relationship of slow twitch muscle than fast twitch muscle, so the relative force contributions will not be simply related to their relative PCSA.)

Computational Efficiency

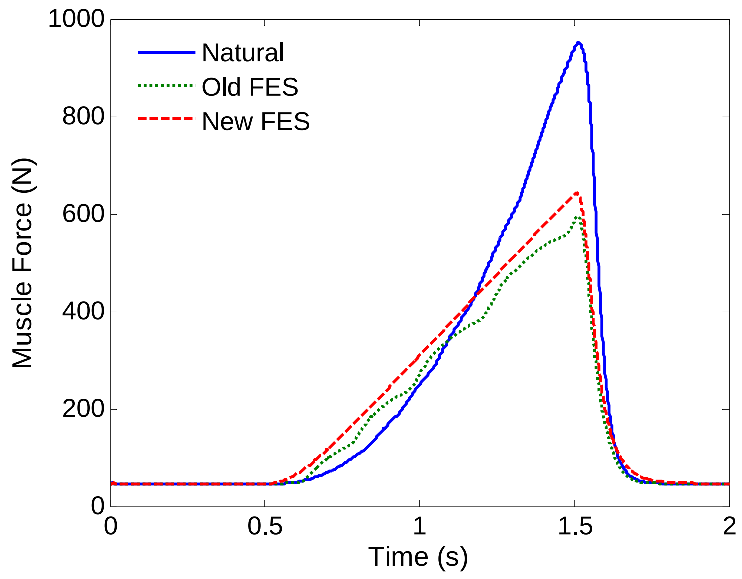
Most of the computational time is dedicated to the dynamics of the Virtual Muscle. If each motor unit is independently frequency modulated (as in physiological recruitment), then VM must keep track of the history of activation of many units to deal with the nonlinear relationship between frequency and force output. But if all recruited motor units are firing at a constant rate set by the stimulus frequency, then it is only necessary to keep track of the effects of that rate on different fiber types, not all motor units. Thus, a muscle can be built from one motor unit for each fiber type, with its size reflecting the percentage of PCSA occupied by that fiber type. The model simply assumes that these few (typically 2-3) motor units are always firing at the stimulus rate but that their force output is scaled by the stimulus intensity (i.e. by the percentage of motor units recruited at the current stimulus strength). A simple rise and fall time (representing a composite of the different times typical of different fiber types) must be added to deal with the dynamics of muscle activation, which are effectively bypassed in this model.

The previous version of VM was originally designed to represent physiological recruitment. Its resolution depends on having a reasonably fine-grained representation of the various motor units present in the muscle, which are then recruited discretely and frequency modulated after recruitment. As mentioned in the Virtual Muscle manual, for each iterative step, the algorithm determines which fiber type has the smallest fraction (by PCSA) of its units recruited. The next motor unit recruited will be of that fiber type. It will become recruited when the activation reaches a threshold equal to the total muscle fractional PCSA that will be recruited (including the current unit). Motor units in the model are recruited in an all-or-none fashion. The problem is that if we model only few motor units in Virtual Muscle using the FES algorithm, the threshold of the first recruited fiber type would be equal to the total muscle fractional PCSA that will be recruited, which will be 100% (activation = 1) if I use only 1 motor unit, 50% (activation = 0.5) if we use 2 motor units with equally distributed PCSA, 33% (activation = 0.33) if we use 3 motor units with equally distributed PCSA etc. Thus if we want to reduce the computational time in FES mode, the minimum activation level for the smallest motor unit (based on PCSA) is based on that threshold, which is based on the percentage of CSA covered by that motor unit.

Comparison of Intramuscular FES with original FES and Natural Discrete (Brown & Cheng) recruitment modes

Figure below show a comparison between Natural, old Intramuscular FES, and new Intramuscular FES recruitment modes with ramp activation from U=0 to 1. The muscle has 30% slow-twitch fibers and 70% fast-twitch fibers. For both natural and old FES, there were 10 slow and 5 fast MUs. The muscle architectural parameters are: mass=614.4 g (i.e.F0=1130.7 N), optimal fascicle length =16.3 cm, optimal tendon length =17 cm, max musculoskeletal muscle length =32.9 cm. A ramp activation input (U=0~1 when t=0.5~1.5) at constant musculotendon length at 33.3 cm were given to check the dynamic response of FES algorithm to stimulation intensity. The firing frequency input to FES muscles was fixed at 20 Hz.

We observed a good match between the new efficient Fes algorithm and the original FES algorithm. Natural recruitment curves are higher because of frequency modulation above the stimulation rate specified for either type of FES recruitment. We also observed the equal series of bumps for old FES showing the non preferential recruitment fashion, whereas the new FES a smooth line because there is only one motoneuron per fiber type present in the model and the activation is multiplying the total output force for each motoneuron.


1000
800
600
400
200
0
0
0.5
1
1.5
2
Muscle Force (N)
Time (s)
Natural
Old FES
New FES

Appendix G: Tips for building your model

Obtaining morphometric measures

The first step in using this package is to create a database of fiber properties. For most purposes, the included database of feline muscle fiber types will provide a good starting point. By knowing a few key parameters it may be possible to estimate values for other species by scaling the coefficients provided for feline muscle. If you wish to collect your own data and fit it to the equations provided, this is beyond the scope of the present text; see Brown et al., (1999) and Brown and Loeb (2000) for a more detailed discussion. Assuming you already have a satisfactory set of fiber type parameters that match the subject you are trying to model, the next step is to provide information on the muscle you are attempting to model. A brief description of the function of and methods to obtain the parameters required by the `BuildMuscles` function follow:

Muscle mass: In the muscle model, this value serves two purposes. The first is to provide the volume of the muscle (in conjunction with the density of muscle, which is fixed at 1.06 g/cm^3 [Mendez and Keyes, 1960]), which is then used to calculate physiological cross-sectional area (PCSA). PCSA relates to F_0, or maximal tetanic force, which in turn scales all of the force output of the muscle. The specific tension of muscle is effectively constant across different fiber types (see Brown et al., 1998), so it is set as a single value for each `Muscle_Database`. The second purpose of muscle mass is to provide stability in the simulation for the interaction between the visco-elastic contractile element and the elastic tendon element (see Loeb and Levine, 1990). In our model, half of this value is incorporated to provide inertial damping – i.e. the muscle mass is assumed to centered halfway along the length of the fascicles. The stability of the model proved relatively insensitive to the amount of muscle mass used; a change in the stabilizing mass by an order of magnitude only changed rise and fall times of force production by a few milliseconds.

The only stipulation for collecting this value is that the wet weight be used, not the weight of desiccated muscle. If you already have a muscle volume, multiply by the density of muscle (1.06 g/cm^3) to obtain a mass.

Fascicle length (L_0): Fascicle length (not muscle belly length!!!) is important for three purposes. As previously discussed, it is important for determining PCSA, and hence F_0. Second, it scales the velocity and length dependence of the contractile element of the muscle, and thus changes the sensitivity of the contractile element to changes in total musculotendon path length. Thus, a shorter fascicle will show greater changes in force output with the same total length change. Finally, it is used in conjunction with optimal tendon length (L_0^T) and maximal musculotendon path length (L_{max}^{MT}) to determine fascicle L_{max}. This term scales the passive force produced by the contractile element, which will be discussed later.

It is important that the actual fascicles for the muscle you are studying are measured, and not simply the muscle belly length or the whole musculotendon path length. Commonly, muscle belly length is reported in literature, but this is usually an inaccurate representation of fascicle length for muscles with even a minimal pennation angle. An additional factor is that the fascicles must be at L_0, the length that provides maximal tetanic force. It is inaccurate to assume that L_0

will occur when muscle is at the midpoint of its range of motion; for example, cat hindlimb muscles typically function at lengths slightly below L_0. Similarly, it is inaccurate to assume that L_0 is the length at which peak twitch force is evoked, as that length is typically 10-30% longer than L_0 (Close, 1972; Roszek et al., 1994; Brown and Loeb, 1998).

Short of using actual tetanic stimulation and force recordings from the subject muscles, we use the following technique to obtain L_0. Fix the muscle *in situ* and measure its fascicle length. Next, excise bundles of a few muscle fibers, mount them with glycerol and coverslip them, and examine them under a light microscope at approximately 400x magnification. Using a calibrated measuring graticule, it is possible to obtain measures of sarcomere lengths in the fixed muscle. This value can then be compared with literature values for optimal sarcomere lengths. For example, if average sarcomere length from your muscle was 2.0 μm and optimal sarcomere length for skeletal muscle in the same species is 2.4 μm, then you would have to multiply your *in situ* fascicle length by 1.2 to obtain L_0.

Tendon length (L_0^T): This is the sum of any external tendon plus all in-series aponeurosis, as this has been shown to have similar mechanical properties to external tendon (Scott and Loeb, 1995). This value scales the length of the tendon for the purposes of series elastic force production. This parameter differs from Zajac's (1989) model, which uses tendon slack length. The L_0^T length is a measure of tendon length when the tendon is stretched by the maximal tetanic force of the fascicles (Brown et al., 1996). As mentioned above, this value is also used in the calculation of the fascicle L_{max}.

The external tendon component of L_0^T can be measured directly from the tendon using a ruler *in situ*. Unfortunately, it is impossible to measure L_0^T from a typical dissection without a system to stimulate the fascicles and measure the length of the tendon when the fascicles are producing an isometric force of F_0. In the absence of direct L_0^T measures, it can be approximated by using 105% of tendon slack length.

The aponeurosis component of L_0^T is the mean amount of aponeurosis that is in series with each fascicle. This can be approximated by halving the sum of the total aponeurosis length at the origin plus the insertion (scaled by 105% if measured when the muscle was slack). If you have a measurement of musculotendon path length at the skeletal posture where the muscle produces optimal force, (L_0^{MT}), then $L_0^T = (L_0^{MT} - L_0)$.

Maximal musculotendon path length (L_{max}^{MT}): The sole purpose of this value for the muscle model is to calculate maximal fascicle length. Maximal fascicle length (L_{max}) is calculated as ($L_{max}^{MT} - L_0^T$), which is then divided by fascicle L_0 to provide a scaled value for L_{max}. It has been shown that a separate L_{max} term is more appropriate than simply L_0 for scaling passive forces produced by muscle (Brown et al., 1996).

The value L_{max}^{MT} is measured by moving the appropriate joints to the extreme anatomical positions that produce a maximal *in situ* musculotendon path length (L_{max}^{MT}). The manner in which L_{max} is calculated (subtracting L_0^T and then dividing by L_0) is based on two assumptions. The first is that L_0^T will represent the length of the tendon when the muscle is fully stretched; this is reasonable considering that L_0^T represents the tendon length when it is already stretched to a certain degree. The second is that pennation angle is negligible; this assumption will be discussed later.

If this value cannot be measured and is unavailable in literature, reasonable values for L_{max} have been shown to be between 1.1 and 1.42 L_0 in five cat hindlimb muscles (Brown et al., 1996). Maximum musculotendon path length values can be entered *ad hoc* so that the calculated L_{max} value equals any approximation that you wish to use. This is the only function of the maximum musculotendon path length input value, so it does not need to correspond to a physiological measure, so long as the calculated L_{max} is reasonable. In fact, if the range of motion used in your model is in the midrange of motion of the muscles involved, passive force from the fascicles is minimal. At L_{max}, it has been measured at typically less than 7% of F_0; at L_0 or shorter, it is negligible.

Pennation angle: This muscle model assumes that there is no pennation angle in the muscles. This appears to be accurate when pennation angle is less than 10-15° (e.g., Zajac, 1989). In most such muscles, the main effect of pennation is to provide a long aponeurosis for insertion of large numbers of relatively short muscle fibers whose forces combine in parallel. This important feature is now well captured by the ability to set L_0 and L_0^T independently. In more highly pinnate muscles, the angle changes with the length of the muscle. This necessitates a dynamic pennation angle to modify both the length and the velocity of the fascicles, as well as to compute the portion of the force vector that acts on the line of pull of the muscle. For small ranges of motion, the force output of the muscle can be adjusted with the cosine of a fixed pennation angle, but with the current muscle model, large ranges of motion may not be correctly modeled using this simple approximation. This condition is beyond the scope of the current discussion.

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