

A COMPUTATIONAL FRAMEWORK FOR SIMULATING AND ANALYZING HUMAN AND ANIMAL MOVEMENT

Computer simulations provide a framework for exploring the biomechanics of movement. The authors have developed a software system that lets users create computer graphics simulations of human and animal movement. This software provides a platform on which the biomechanics community can build a library of simulations that can be exchanged, tested, and improved through multi-institutional collaboration.

An outline of the basic steps involved in the production of voluntary movement is quite simple. Commands initiated in the brain are transmitted along nerves to muscles. When activated by nerves, muscles generate forces. Muscle forces are transferred to bones and produce angular motions of the joints. When the nervous system properly coordinates the activation of many muscles, the result is smooth, purposeful movement.

Scientists fascinated by human and animal movement have examined each of these steps and performed an extensive range of experiments to record neuromuscular excitation patterns, characterize muscle-contraction mechanics, describe musculoskeletal geometry, and quantify movement dynamics. However, linking detailed knowledge of neuromusculoskeletal el-

ements to create an integrated understanding of movement remains a challenge.

Computational models of human and animal movement provide a framework for integrating facts about the biology of movement. Once researchers develop and test a computer model of the neuromusculoskeletal system, they can use it to explore movement control, analyze athletic performance, and simulate treatments for musculoskeletal and neurologic disorders. Researchers need simulations to complement experimental studies because important elements of movement, including neural signals and muscle forces, are extremely difficult to measure experimentally.

Developing accurate simulations of human and animal movement is challenging because of the intrinsic complexity of biologic systems. For example, the forces produced by muscles depend on their activation, length, and velocity. Muscles transmit forces through tendons, which have nonlinear properties. Tendons connect to bones that have complex geometry and span joints that have complicated kinematics. Understanding how the nervous system coordinates movement is especially difficult because many muscles work together to produce movement, and any individual muscle can accelerate all of the joints of the

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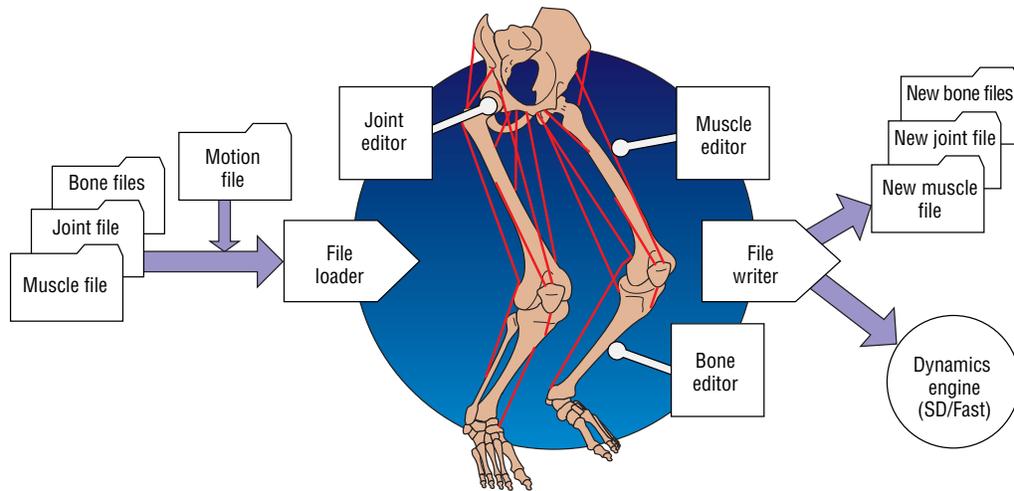


Figure 1. Structure of musculoskeletal modeling software. SIMM's File Loader reads input files describing bone surfaces (bone files), joint kinematics (joint file), and muscle–tendon parameters (muscle file). The File Loader also reads motion files containing the joint angles that describe a movement to animate a model. Users can alter a model using the Joint Editor, Muscle Editor, Bone Editor, and other tools. To extract information from the model, users make plots or export edited joint and muscle files. To create dynamic simulations, SIMM's File Writer creates an input file for SD/Fast, a dynamic simulation package that lets users perform forward simulations (computation of motions from forces) or inverse simulations (computation of forces from motions).

body.¹ These complexities have important functional consequences and must be represented accurately if computational models are to provide insights into musculoskeletal performance.

Developing and testing biologically realistic models requires collaboration between biologists and engineers. A software framework that allows investigators to work together on the development of computer simulations of movement is needed. This framework should let researchers develop models that faithfully reproduce known features of the neuromusculoskeletal system. Although the standard engineering software packages used in computer-aided design, finite element analysis, and computer animation provide an excellent environment for analyzing mechanical components, they are not well suited for developing models of biologic systems.

We have created Software for Interactive Musculoskeletal Modeling (SIMM), a software package that lets users develop, alter, and evaluate models of almost any musculoskeletal structure.² SIMM lets users build models that accurately represent muscle force generation, bone geometry, joint kinematics, and movement dynamics. SIMM is used in biomechanics laboratories around the world to provide a framework for the development and testing of models to study human and

animal movement. This software platform lets users exchange models and facilitates collaboration among individuals and research groups.

How SIMM works

SIMM lets users build and analyze computer models of a wide variety of musculoskeletal structures. A SIMM model consists of a set of rigid segments connected by joints. Muscles and ligaments span the joints, develop force, and generate movements of the joints. SIMM's File Loader loads a model by reading a set of bone files, a joint file, and a muscle file and creates a data structure that represents the musculoskeletal model (see Figure 1).

Users can edit and analyze models with several graphical tools. For example, a Muscle Editor lets users change a muscle's line of action and force-generating properties. A Plot Maker calculates the lengths and moment arms of muscles in a model, enabling users to analyze muscle functions for a range of body positions. Also, given muscle activation, a mathematical model of muscle computes the force and moments that each muscle generates. When SIMM is used in conjunction with SD/Fast, a dynamics engine (www.symdyn.com), users can compute the joint

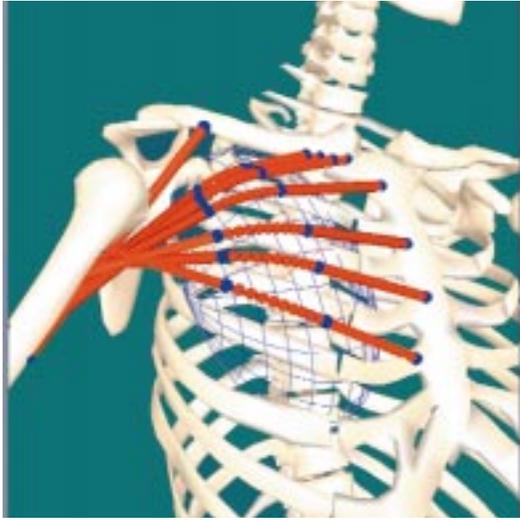


Figure 2. A SIMM model of the pectoralis major muscle. We divided the muscle into several lines of action to represent its broad area of attachment and introduced an ellipsoidal wrapping surface to prevent the muscle lines of action from penetrating the chest. The dotted regions of the muscle paths indicate where they wrap over the ellipsoid.

motions resulting from a pattern of muscle activations. Also, body motions measured during a movement can be read into the software to animate a model or evaluate simulation results. SIMM is written in C and uses the OpenGL graphics library; it runs on Windows and Silicon Graphics' Irix systems.

Model components

A musculoskeletal model is composed of body segments, joints, muscles, tendons, and ligaments.

A *body segment* consists of a reference frame that contains one or more bones. Each bone is stored in a file that lists the polygons comprising the bone surface. Users can create bone files from medical images or by digitizing bone surfaces.³ The vertices in each polyhedron are expressed in the Cartesian coordinate system that serves as the reference frame for the body segment. Inertial parameters of the body segment (mass, mass center, and inertia matrix) are expressed in this reference frame. The reference frame is also used to specify the position and orientation of the body segment with respect to other body segments in the model.

Users can connect body segments in any arrangement by defining *joints*. The joint file specifies the transformations that relate the position and orientation of one body segment to another.

The transformations consist of three translations and three rotations; thus, six degrees of freedom are allowed to represent a joint. This flexibility is important for joints with complex kinematics, such as the shoulder. For joints with simple kinematics, such as the elbow, users need to specify only the location and orientation of the joint's axis of rotation.

Users define a *muscle* and its associated *tendon* in a muscle file by specifying their geometry and force-generating properties. The geometry of a muscle-tendon unit is characterized by a series of points, which are connected by line segments. A minimum of two points is required to define a muscle-tendon path. Each point is fixed to one of the body segments. Any number of "via" points can be used to describe a muscle-tendon path that is constrained by bones or other anatomical structures. In addition, users can graphically define wrapping surfaces to simulate the wrapping and sliding of muscles over surrounding tissues (see Figure 2). Wrapping surfaces can take the form of cylinders or ellipsoids. When a muscle makes contact with a wrapping surface, its path is deflected to prevent the muscle-tendon unit from penetrating the wrapping surface. Wrapping surfaces are particularly useful for representing the paths of muscles that cross joints with multiple degrees of freedom, such as the shoulder or the hip.

SIMM represents the force-generating properties of a specific muscle-tendon unit by scaling a dimensionless model.⁴ To create a muscle-tendon model, users provide four dimensionless curves and five parameters that scale these curves (see Figure 3). The four dimensionless curves represent the mechanical properties of muscle and tendon; in dimensionless form they are generally considered to be invariant between muscles. The four curves are

- the active force-length relation of muscle,
- the passive force-length relation of muscle,
- the force-velocity relation of muscle, and
- the force-length relation of tendon.

The five parameters that scale these curves are

- the peak isometric muscle force (F_0^M), which is derived from the cross-sectional area of the muscle,
- the optimal muscle-fiber length (l_0^M), which is the length at which the muscle develops maximum force,
- the pennation angle at optimal fiber length

(α_0), which is the angle between the muscle fibers and the tendon,

- the tendon slack length (l_S^T), which is the length at which tendons begin to transmit force when stretched, and
- the maximum contraction velocity of muscle (V_{MAX}^M).

To reduce the information users must supply for each muscle, SIMM provides a default muscle that contains the four dimensionless curves that represent the mechanical properties of muscle and tendon. SIMM scales these dimensionless curves to represent a particular muscle–tendon actuator using the five parameters. The active force–length curve of muscle is also scaled by muscle activation, which ranges from 0 (no activation) to 1 (full activation).

Ligaments are passive structures that connect bones. Users can include them in a model by specifying their mechanical properties in the muscle file. SIMM represents ligaments as muscles that produce only passive force.

Graphical user interface

SIMM's user interface provides graphical tools to alter any parameter of a model (see Figure 1). The Joint Editor lets users graphically manipulate the kinematics of joints, for example, by relocating joint centers or axes of rotation. The Muscle Editor lets users graphically adjust muscle–tendon paths and parameters (F^M , l_O^M , l_S^T , α_0 , V_{MAX}^M). The Bone Editor lets users cut a bone to simulate a surgery or scale a bone to represent the geometry of an individual. Other graphical tools let users load experimental data for comparison with a simulation, manipulate the model for better visualization, or create plots for quantitative analysis of musculoskeletal function.

Dynamics

Once users develop a musculoskeletal model (by specification of the bone, joint, and muscle files), the File Writer creates a set of input files for SD/Fast, which generates the dynamic equations of motion (see Figure 1). With these equations and SIMM-generated Ccode, users can perform forward and inverse dynamic simulations of movement. For forward dynamics, users specify the timing and intensity of the muscle activations, and the dynamic model computes the resulting muscle forces, joint moments, and motions of the body segments. For inverse dynamics, users specify the time histories of the joint angles during an activity, and the dynamic model

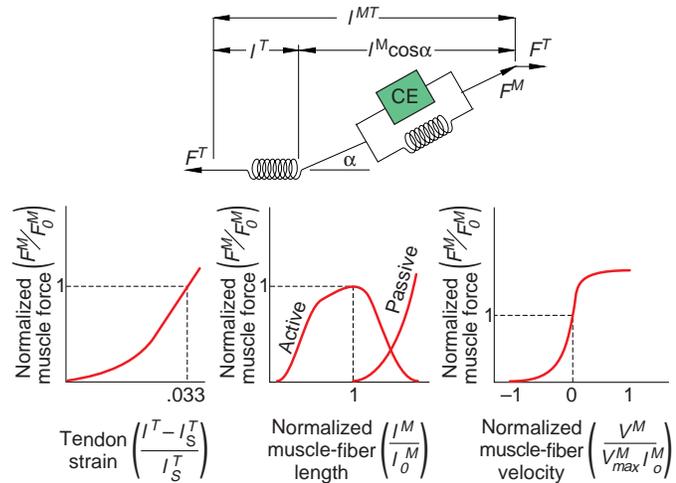


Figure 3. Dimensionless model of muscle and tendon. The model represents muscle properties by an active contractile element (CE) in parallel with a passive elastic element (top figure). Muscle force is the sum of muscle force when it is excited by the nervous system (active) and when it is passive (middle plot). This force is dependent on muscle fiber length (middle plot) and velocity (right plot). Muscle is in series with tendon, which is represented by a nonlinear elastic element (left plot). The pennation angle, α , is the angle between the muscle fibers and the tendon. The forces in muscle and tendon are normalized by peak isometric muscle force (F_0^M). Muscle-fiber length (l^M) and tendon length (l^T) are normalized by optimal muscle fiber length (l_0^M). Tendon slack length (l_S^T) is the length at which tendons begin to transmit force when stretched. Velocities are normalized by the maximum contraction velocity of muscle (V_{MAX}^M). For a given muscle–tendon length (l^{MT}), velocity, and activation level, the model computes muscle force (F^M) and tendon force (F^T).

calculates the joint moments required to produce the specified motion.

Applications

Developers have used SIMM to create highly accurate models of the human arm, leg, trunk, and neck; a cat neck; a primate neck; and a cockroach leg. Some models are simple geometric representations that let users visualize anatomical structures during movement. Other models include force-generating muscle properties and let users examine how surgical alterations affect muscle strength. SIMM users have developed complex models that include limb dynamics and nervous system control to help them explore principles of neural control and the dynamics of abnormal movement. In developing a musculoskeletal model for a specific application, users

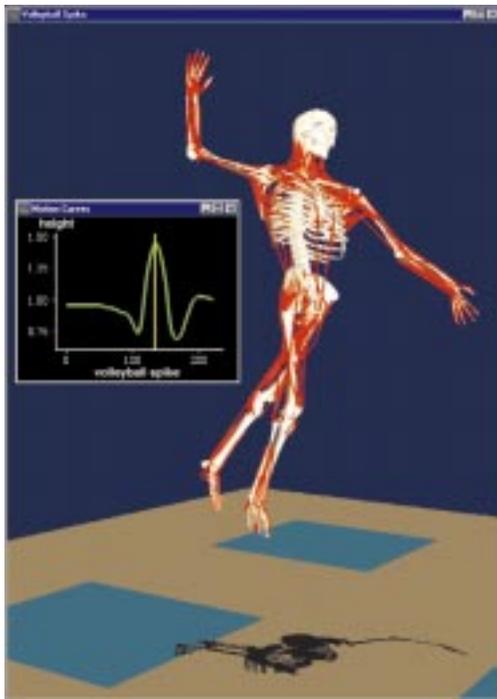


Figure 4. Single frame from an animation of a volleyball spike. Motion Analysis Corporation’s motion measurement system (www.motionanalysis.com) records the three-dimensional motions of the body segments. SIMM automatically scales the musculoskeletal model to represent the athlete and animates the athlete’s movement. The inset shows the height of the mass center (in meters) over the course of the activity. The vertical line on the plot shows the position on the graph corresponding to the animation frame.

must consider the level of complexity the analysis will require. To demonstrate the range of SIMM models and their applications, we offer a few examples.

Movement animation

Animating a musculoskeletal model from measured body motions is a simple and useful technique for studying human and animal movement. Experimental motion analysis uses stereophotogrametric techniques to track the location of markers on the body segments. These markers define the positions of the body segments during a movement. SIMM reads this motion-analysis data and creates a 3D animation showing the body motion (see Figure 4). The animation shows the timing and intensity of muscle activity and the magnitude and direction of external forces on the body. Clinical laboratories use animations to study pathologic movements and to help communicate the results of

their studies. Sports performance centers use real-time animations to compare an individual athlete’s motion with that of a world-class athlete’s. Trainers and athletes use this visual feedback to evaluate and improve performance.

Combining a graphics-based musculoskeletal model with motion-analysis data has several important advantages over using motion measurement systems alone. First, in contrast to video-based systems, users can view an animation of a movement from any perspective and at any speed. They can also remove body segments to improve visualization and superimpose otherwise invisible external forces and muscle activities and analyze them in the context of the movement.

Second, a graphics-based model lets users visualize and reduce errors in motion analysis data. Motion measurement systems typically use external markers to determine the location of bones. Errors in the localization of the markers or motions between skin-mounted markers and the bones result in unrealistic estimations of bone movements. An animation lets users detect these errors. A musculoskeletal model lets users reduce the errors, either by imposing constraints on joint motions, or by optimally fitting a set of markers to the body segments of a model.

Third, users can add new, untracked body segments to a model and animate them. For example, the patella’s motions are generally not monitored during motion analysis experiments but could be included in an animation if the patella’s kinematics are specified relative to a tracked body segment.

Finally, a musculoskeletal model lets users calculate other parameters that are not easily measured during movement, such as muscle lengths and moment arms. Knowledge of muscle lengths has clinical relevance, because a “short” muscle that restricts movement can often be surgically lengthened. Researchers have used SIMM to analyze motion analysis data describing various walking abnormalities to study how various pathologies affect the lengths and moment arms of muscles.^{5,6}

Surgical simulation

Biomechanical simulations that reveal the functional consequences of surgery are needed to design more effective procedures. Orthopaedic surgeons frequently operate to improve mobility and function in people with musculoskeletal and neurologic diseases. These surgeries are intended to restore the range of motion of joints,

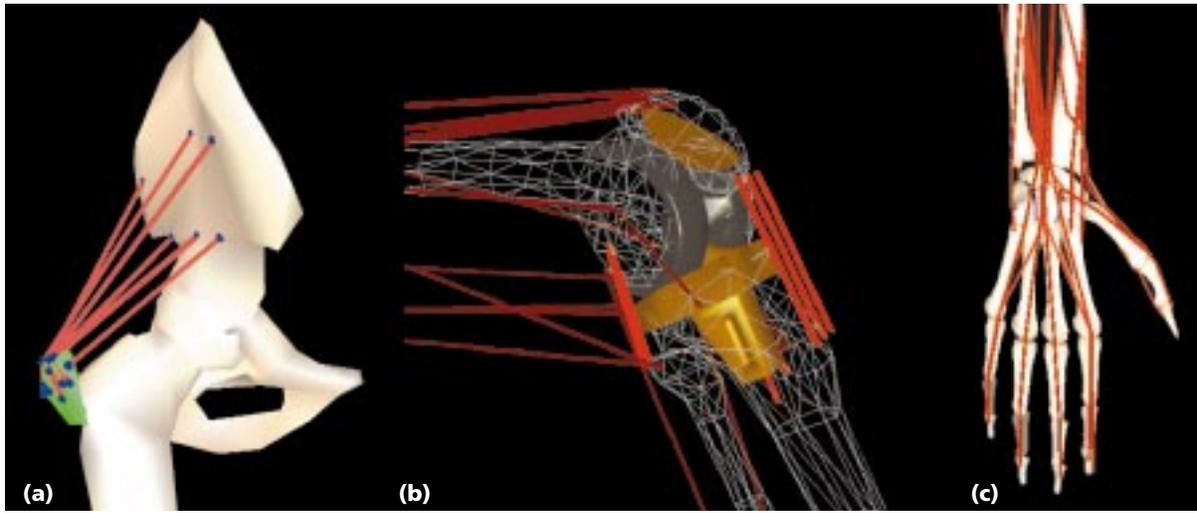


Figure 5. Models used in simulated surgeries. (a) Simulation of a surgery in which surgeons detach a bone fragment from the femur and transfer it to a new location. (b) Model used to study alterations in joint mechanics after knee replacement. (c) Model of the wrist used to analyze tendon transfer surgery.

the stabilizing properties of ligaments, or the force-generating capacity of muscles by altering the geometry of the musculoskeletal system. However, the outcome of such surgeries depends on complex, interacting geometric and biologic factors. Graphics-based simulations can provide insight into the functional consequences of surgery and serve as a basis for successful surgical design. Researchers have used SIMM to study the biomechanical consequences of bone reconstructions, joint replacements, and muscle-tendon surgeries.

For example, researchers used SIMM to develop a 3D computer model of the pelvis, femur, and hip muscles to study the effects of a surgical procedure in which surgeons transferred a fragment of the femur to a new location.⁷ Using the Bone Editor, they divided the bone model according to several different surgical plans (see Figure 5a). Next, they evaluated how the simulated surgery changed muscle moment arms and force-generating capacities. In contrast to clinical expectations, the simulations revealed that the surgery scarcely altered the muscles' moment arms. However, the surgery did increase muscle lengths and force-generating capacities. These results suggest that the surgeons should consider this procedure primarily to improve the muscles' force-generating potential and to prevent muscle weakness after surgery.

Researchers have also developed a computer

model of the knee and its surrounding tissues to study knee motions after the implantation of a knee prosthesis. They used the Joint Editor to alter the kinematics of the knee caused by insertion of a knee prosthesis. They also used the model to examine the effects of tilting the tibial component (the lower prosthetic component in Figure 5b), a common surgical error. The simulations showed that even a small amount of tilting of the prosthesis has the potential to substantially alter the kinematics of the knee and the tensions in the ligaments after surgery,⁸ emphasizing the need for accurate alignment of knee implants.

Herrmann and Delp used a computer model of the wrist to examine how muscle architecture and moment arms affect the moments generated by the muscles before and after a tendon transfer surgery (see Figure 5c).⁹ They used the Muscle Editor to alter the attachment of the tendon from one location to another based on anatomical measurements of the muscle-tendon paths before and after surgery. They then determined the maximum force and moment generated by the muscle before and after surgery using the musculoskeletal model. As expected, the simulations demonstrated that the surgery increased the muscle's mechanical advantage. The simulations also showed that surgeons must properly tension the tendon to maximize the force-generating potential of the transferred muscle over a functional range of motion.

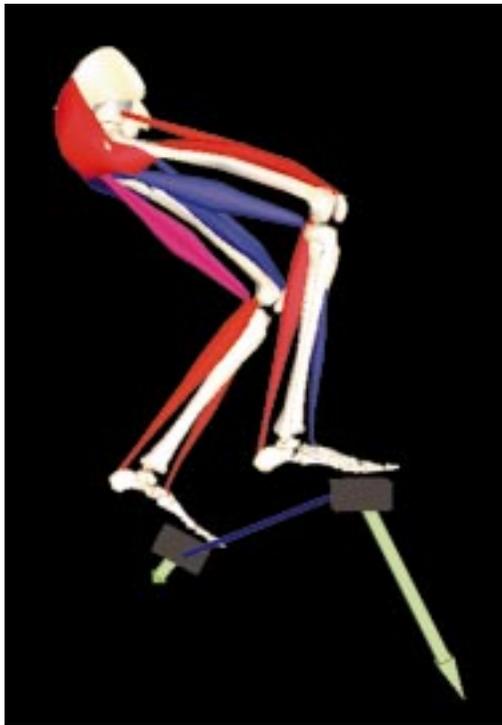


Figure 6. Model of bicycle rider developed by Neptune and Hull.¹⁰ The color of the muscles indicates the level of muscle activity, with red showing high activity and purple showing low activity. The model also shows the direction and magnitude of the pedal forces.

Dynamic simulation

Dynamic simulation is a powerful technique for studying human movement. In contrast to animations, dynamic simulations let researchers examine neural control of movement, calculate forces in joints, and study the dynamics of abnormal movement. Dynamic simulations are valuable because they provide quantitative measures of parameters that are very difficult to measure and manipulate experimentally.

Neptune and Hull used SIMM to develop a two-legged, dynamic model of a bicycle rider¹⁰ (see Figure 6). Each leg consisted of three rigid segments: thigh, shank, and foot. The hip was fixed above the seat and the foot was fixed to the pedal. They derived the equations of motion with SD/Fast and computed the joint motions and external forces from the activation patterns of 14 muscles. The timing and magnitude of the muscle activations were determined to optimally reproduce the mechanics of experimentally studied bicycle riders. The model represented leg mechanics during cycling and let the researchers conduct a detailed investigation into variables

that are not generally available from experiments.

In one study, Neptune and Hull simulated pedaling at three different rates (75, 90, and 105 rpm) to evaluate which neuromuscular variables the central nervous system uses to select pedaling rate.¹⁰ The model calculated muscle activations, forces, stresses, and neuromuscular fatigue and revealed that all of these quantities were minimized at 90 rpm, the pedaling rate that experienced cyclists typically choose. This suggests that cyclists may choose their pedaling rate to minimize these neuromuscular variables. In a second study, Neptune and Kautz developed simulations of forward and backward pedaling to determine which rehabilitation exercise produced lower forces between the patella and the femur, a variable that cannot be measured in human subjects.¹¹ Their results showed that backward pedaling produces greater forces between the patella and femur, suggesting that it not be recommended for rehabilitation of patients with patellofemoral pain.

Several research groups have developed simulations to study the causes of stiff-knee gait.^{12,13} This movement abnormality is often attributed to the knee-extending action of the rectus femoris muscle, which shows prolonged and increased activation in people with stiff-knee gait. As a result, surgery is frequently performed to reduce the knee extension moment this muscle produces. Pizazz and Delp developed a dynamic simulation to examine how abnormal activation of the rectus femoris affects knee flexion.¹² The simulation calculates joint motions from muscle activation patterns derived from recordings of muscle activity in normal walking.¹⁴ To clarify the role of the rectus femoris muscle, they performed simulations with an exaggerated activation input to this muscle. The simulations confirmed that stiff-knee gait may be caused by overactivity of the rectus femoris. The simulations also suggested that weakened hip flexors and other factors that determine the angular velocity of the knee at toe-off may be responsible for decreased knee flexion during swing phase. Thus, when attempting to correct stiff-knee gait, surgeons should consider these factors along with rectus femoris activity before operating on the rectus femoris muscle.

Limitations

SIMM has several important limitations. The software lets users define each muscle-tendon path as a series of line segments. This is reason-

able for muscles with small areas of attachment. However, it might be more realistic to model muscles with large areas of attachment, multiple origins, curved paths, or complex architecture as volumetric objects. As a compromise, users can split muscles with large or multiple attachment areas—such as the pectoralis in Figure 2—into any number of compartments.

Our method of computing muscle forces is based on a dimensionless model that can be scaled to represent a wide range of muscle architectures.⁴ However, the model assumes that all fibers within a muscle are at the same length for a given muscle–tendon length. This assumption may result in an underestimation of the range of joint angle over which a muscle can produce active force.¹⁵ The model also assumes that the force–length and force–velocity relations are independent, and it does not characterize muscle yielding or force enhancement after stretch. These limitations are intrinsic to the dimensionless model of muscle we used. Cross-bridge models, which represent the molecular mechanisms of force production,¹⁶ may be able to represent these complexities of muscle contraction. However, cross-bridge models have many more parameters and are impractical for simulating systems with many muscles.

SIMM's joint modeling technique lets users characterize the kinematics of any joint. Kinetic joint models, in which muscles, ligament, and articular contact forces govern joint motion, provide a more comprehensive representation of joint mechanics. Such kinetic models also compute joint contact forces, which are not directly available in SIMM models. Piazza and Delp implemented a rigid body contact model to explore motions of the knee during stair climbing.¹⁷ Integration of elastic contact models with multi-body dynamics is at the cutting edge of computational mechanics research and represents an important area for future development in biomechanical simulation.

Most of the simulations developed with SIMM run on inexpensive single-processor computers. However, performing neuromuscular simulations with many degrees of freedom is computationally expensive. For example, to compute the activation patterns of the muscles to produce a maximum height jump using dynamic optimization required nearly 800 hours on a single processor IBM RS/6000.¹⁸ The same optimization algorithm converged in 23 hours on an IBM SP2 when 128 parallel processors were used to calculate the derivatives needed for the opti-

mization. Simulations that incorporate sensory feedback and neural control of complex dynamic models are only practical given significant parallel computing resources.

The accuracy of a model developed with SIMM is limited by the accuracy of the biomechanical data on which the model parameters are based. If reliable data is not available, users must collect it before constructing a model. This can require extensive experiments prior to model development. Once a model is developed, users must test it extensively to identify the limits of its accuracy and application.

The example applications we presented earlier used generic models. These models are based on measurements of bone geometry, muscle–tendon paths, joint kinematics, muscle architecture, and muscle activations made on a relatively small number of subjects. The accuracy with which results from simulations using generic models can be applied to characterize the performance of individual subjects has not been widely tested. Future work is needed to determine how model parameters vary among subjects and to understand how these variations affect interpretation of the simulation results. The development of biomechanical models of individual subjects from medical image data is an area of intensive research that promises to address some of these issues.

Creating models with SIMM offers several advantages. It lets users build models that integrate the major steps involved in the production of voluntary movement—from neural signals to muscle forces to movement. SIMM provides a consistent framework for organizing model parameters. Users can increase model complexity one step at a time and critically evaluate the effect of each added complexity by comparison with experimental data. Tested models provide high-fidelity representations of many of the intrinsic complexities of the neuromusculoskeletal system and can be used to explore a wide range of scientific questions. Once users develop a model, they can easily distribute it to colleagues or investigators at other institutions. Our ultimate goal with SIMM is to provide a framework that lets investigators create a library of musculoskeletal models that can be

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exchanged, tested, and improved through multi-institutional collaboration. The first models of this library are now available to investigators around the world; you can see them at www.musculographics.com/gallery.htm and www.stanford.edu/group/nmbl. 

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