

VIEWING A MUSCULOSKELETAL MODEL

This tutorial will show you how to change the view of a musculoskeletal model, move the joints in it, and change the display properties of the bones. The Demo Leg Model in this tutorial represents an adult subject with a height of about 1.8 meters and a mass of about 75 kg. The model consists of 7 rigid body segments (pelvis, femur, patella, tibia/fibula, talus, foot, and toes) and includes the lines of action of 7 muscles and the patellar ligament. There are ten generalized coordinates (degrees of freedom) in this model (pelvis_rx, pelvis_ry, pelvis_rz, hip_adduction, hip_rotation, hip_flexion, knee_angle, ankle_angle, subt_angle, and mtp_angle).

When the Demo Leg Model is first loaded into SIMM, all of the joint angles are set to zero, and the model is displayed in the Demo Leg Model window with a sagittal view. The following steps will show you how to change the view and manipulate the model's joints.

1. Open the Model Viewer window by clicking the left mouse button on its name in the menu bar. There is a command menu on the left side of the window with various viewing commands. In the middle of the window is a list of the generalized coordinates (gencoords) in the Demo Leg Model. Next to each name is a number field which shows the current value of that gencoord. To the right of each field is a slider that you can use to change the value, or you can type in an exact value into the field.
2. Flex the hip by pressing the left mouse button on the thumb of the hip_flexion slider and moving it back and forth. Do the same for some of the other gencoords. If you want, you can click the left mouse button on the field for a certain gencoord and type in the value. Hit Enter when you are done typing in the number.
3. Click the left mouse button on *restore gc values* to reset the gencoords back to their starting values.
4. The last two items in the list of gencoords are not true gencoords, but rather are motions that were loaded with this model. Whenever you load a motion into SIMM and attach it to a model, another field and slider appear in the gencoord list so that you can apply the motion as if it were a gencoord. Press the left mouse button on the *normal_gait* slider and move it back and forth. The leg model will animate according to the motion data that was loaded in from the *normal_gait* data file. A second motion file, *crouch_gait* was also loaded with this model. You can animate the model according to this gait pattern as well by pressing the left mouse button on its slider. The *Gait Analysis* tutorial will show you some additional capabilities of animating and analyzing motions such as *normal gait* and *crouch gait*.
5. In addition to using the sliders in the Model Viewer, you can also move the joints in your model using keyboard commands. Click the left mouse button in the Demo Leg Model window (to make it the active window) and press the K key. As you move the cursor horizontally in the window, the knee will flex and extend. If you move the cursor to the left side of the window, the joint angle will decrease, thereby flexing the knee. If you move the cursor to the right, the joint angle will increase, thus extending the knee.
6. To flex and extend the hip, press the H key as well as the left mouse button, and move the cursor horizontally. Each of the ten gencoords can be changed using one or two keyboard keys that were specified in the joint file. To see the list of these keys, open the Model Viewer help and look under the heading *Model Window Viewing Commands*.

7. There are two methods of changing the view of the model using keyboard commands within the model window. The first method operates when the *trackball* checkbox is turned on in the Model Viewer window. Pressing the Control key and the left mouse button will pan the view within the model window. As you move the cursor in any direction, the model will follow. Pressing the Control key and the middle mouse button lets you zoom in and out of the model (for users with two-button mice, the F3 key can be used in place of the middle mouse button). Moving the cursor to the right will zoom in, and moving it left will zoom out. The zooming effect will be centered on the point under the cursor when you first press the two keys. Press the Control key and the right mouse button to rotate the model with the trackball method. Imagine a trackball superimposed on the model window, and you can move it using the cursor. Moving the cursor in some direction will rotate the model about an axis perpendicular to that direction. Try these three commands to pan, zoom, and rotate the model into some new view.
8. The second method of changing the view operates when the *trackball* checkbox is turned off. In this case, the Control key and mouse buttons function as follows. To rotate the model around the X-axis of the world frame, which always points horizontally to the right, press the Control key and the left mouse button. The direction and speed of rotation are determined by the position of the cursor in the model window. If the cursor is at the far right edge of the window, the model will rotate quickly in the positive direction around the X-axis. As you move the cursor left, towards the center of the window, the rate of rotation slows down. If the cursor is in the middle of the window, the rotation rate is zero. As you move the cursor further left, the rotation rate increase, but in the negative direction. In a similar fashion, pressing the Control key and the middle mouse button rotates the entire model around the Y-axis, which always points up (for users with two-button mice, the F3 key can be used in place of the middle mouse button). Pressing the Control key and the right mouse button rotates the model around the Z-axis, which points out of the screen towards you. Experiment with these viewing commands by clicking the left mouse button on the *trackball* checkbox to turn it off, and then moving the cursor back into the Demo Leg Model window and pressing the Control key and mouse buttons as described.
9. The other keyboard keys that you can use to change the model view are the I, O, L, R, U, and D keys. Pressing these keys in the model window will move the model in, out, left, right, up, and down, respectively.
10. Click the left mouse button on *restore camera* and choose *view 1* to restore the original view of the model.
11. Press the left mouse button on *muscles* to bring up a list of the muscle groups. Muscles are organized into functional groups to make it easier to turn them on and off and to plot their length and force properties. Select *all* from this menu to display a menu of all of the muscles in the Model Viewer window. The menu is displayed below the *trackball* checkbox, so you will probably need to make the Model Viewer window taller in order to see it.
12. Click the left mouse button on some of the muscle names and notice that they are removed from the display of the model in the model window. When you are done familiarizing yourself with the muscles, click on the muscle menu's title bar (labeled *all*) to turn all of the muscles back on. To put the muscle menu away, click the left mouse button on *<<done>>*.
13. You can change the display properties of any of the body segments using the *draw mode* item. Press the left mouse button on this item to bring up a list of objects whose drawing modes you can change. Move down to *all body segments* and then select *wireframe* from the submenu. In the model window you will notice that all of the bones are drawn in wireframe mode. Zoom in on one of the bones to see the individual polygons that comprise it. You can load bone files with any number and size of polygons

describing the bone surfaces. The bone files in the Demo Leg Model are relatively crude so that they can be drawn quickly without a 3D accelerator graphics card. When you are done viewing the wireframe bones, set their drawmode back to *gouraud shaded*, which is the default drawing mode.

14. Click the left mouse button in the Demo Leg Model window and position the cursor over the knee. Press the I key to zoom in until the knee nearly fills the model window.
15. Click the left mouse button on *muscle points* in the Model Viewer window to turn on the display of the muscle attachment points.
16. Using the *knee_angle* slider, flex the knee and watch how the path of the vastus lateralis muscle (the knee extensor that is called *vas_lat* in the muscle menu) changes as you flex past -60 degrees. For small knee flexion angles, the path of this muscle is defined by three attachment points: two on the shaft of the femur, and one on the patella. At about -70 degrees, a fourth point is introduced to prevent the path from passing through the distal femur. The coordinates of this via, or wrapping, point, and the joint angles at which it is active, are defined in the muscle file. At -110 degrees, a fifth point is introduced to further constrain the muscle path. For more information about specifying and editing muscle attachment and wrapping points, read Section 3.4 of the SIMM manual.
17. When you are done viewing how vastus lateralis wraps over the femur, click the left mouse button on *restore camera* and choose *view 1* to restore the view, and click on the *muscle points* checkbox to turn off the display of the muscle points.

PLOTTING MUSCLE PROPERTIES

This tutorial will show you how to plot properties of the muscle-tendon actuators in the Demo Leg Model. Since musculotendon force depends on musculotendon length, and since joint moment depends on both musculotendon force and moment arm, accurate specification of musculoskeletal geometry is essential if muscle forces and joint moments are to be estimated accurately. Further, because musculotendon lengths and moment arms depend upon limb position, muscle forces and joint moments also depend on limb position, but in a much more complex manner. Thus, studying the relationships between joint angles, muscle lengths, and moment arms may provide insight into the behavior of muscle forces and joint moments as well.

The Plot Maker tool allows you to plot muscle-tendon properties such as length, moment arm, force, and joint moment as a function of any joint angle or motion variable. Follow these steps to generate a plot of muscle fiber length vs. knee angle for the vastus lateralis muscle.

1. If it is not already open, open the Model Viewer window by clicking the left mouse button on its name in the menu bar.
2. Reset the joint angles of the Demo Leg Model by clicking the left mouse button on *restore gc values*. Reset the view by clicking the left mouse button on *restore camera* and choosing *view 1*.
3. Close the Model Viewer window by clicking the left mouse button on its close box.
4. Open the Plot Maker window by clicking the left mouse button on its name in the menu bar.
5. Press the left mouse button on *muscles* to bring up the menu of muscle groups. Select *all* at the bottom of the menu. SIMM will display a menu containing all of the muscles. You may need to scroll down within the Plot Maker window or make the window bigger to see the menu. It is displayed below the checkboxes (e.g., sum, rectify).
6. You can turn on any number of muscles in this menu to generate plot curves of their properties. In this case, select the semimembranosus and vastus lateralis muscles by clicking on *semimem* and *vas_lat* with the left mouse button.
7. To plot the fiber lengths of these two muscles as a function of knee angle, you now need to choose the appropriate Y and X variables in the Plot Maker. Click the left mouse button on *y variable* and select *fiber length*. Then click on *x variable* and choose *knee_angle*.
8. Click the left mouse button on *make curves* to generate the fiber length curves. A plot window will appear showing the fiber length vs. knee angle curves for the selected muscles. The units in all plots are meters (length), Newtons (force), and Newton-meters (moment).
9. Notice that the fiber length curve for semimembranosus decreases as you flex the knee (right to left in the plot window), and the curve for vastus lateralis increases. This is because the two muscles are on opposite sides of the joint. Also notice that the curve for semimembranosus "bottoms out" at about -80 degrees. For knee flexion angles greater than this, the semimembranosus muscle fibers do not shorten any further. This is because the total musculotendon length has dropped below the resting tendon length. When this happens the muscle is too short to develop force, so SIMM sets its tendon length to its resting length and its fiber length to the optimal fiber length times the sine of the pennation angle (which is a constant). For more information on the parameters used to define a mathematical model of a muscle, read Chapter 4.4 of the SIMM manual.

10. Now flex the hip by clicking the left mouse button in the Demo Leg Model window (to make it the active window) and pressing the H key and the left mouse button. While pressing the keys, move the cursor left to extend and right to flex the hip until the flexion angle is about 60 degrees.
11. Click the left mouse button on *make curves* again to recalculate the fiber length curves. Notice that the curve for vastus lateralis did not change (the magenta curve completely covers the green one). However, the curve for semimembranosus increased significantly. This is because the semimembranosus muscle crosses the hip as well as the knee, so when you flexed the hip, the muscle lengthened. Vastus lateralis, however, does not cross the hip, so its length did not change.
12. Delete this plot by clicking the left mouse button on its close box.
13. Open the Model Viewer and click the left mouse button on *restore gc values* to reset the gencoords to their initial values. Close the Model Viewer window when you are done.
14. Back in the Plot Maker window, press the left mouse button on *y variable* and choose *force* as the Y variable.
15. Click the left mouse button on *make curves* to plot muscle force vs. knee angle for the two muscles. Notice that the force for semimembranosus is zero for all knee angle values less than -50 degrees. As mentioned above, this is because the muscle is very short in this range of motion.
16. Now flex the hip by clicking the left mouse button in the Demo Leg Model window (to make it the active window) and pressing the H key and the left mouse button. While pressing the keys, move the cursor left to extend and right to flex the hip until the flexion angle is about 60 degrees.
17. Click the left mouse button on *make curves* again to recalculate the force curves. Notice that the curve for semimembranosus changes, while the curve for vastus lateralis does not, for the same reasons mentioned above for the fiber length plot.
18. Now click on the *act override* checkbox to turn it on. Then click the left mouse button on the *activation* field and type in a value of 0.5. Hit return when you are done entering the number. You have now set the activation level of both muscles to 0.5 (half of the maximum value of 1.0).
19. Click the left mouse button on *make curves* to calculate the force curves again. Notice that the two curves are lower than before, but not exactly half of their previous levels. This is because you are plotting the total isometric force in each muscle (active plus passive). By setting the activation to 0.5, you are halving the active force, but the passive force is relatively unchanged (it changes a little because the fiber length changes slightly). Thus the curves for total force at an activation of 0.5 are only approximately half of their values at an activation of 1.0.
20. Continue to experiment with the different Y variables, X variables, and plotting options (like *sum*, *active*, and *passive*). The inter-dependence of muscle fiber length and force is quite complex, and is made more so by activation levels, active and passive force components, and muscle paths that span more than one joint. Using the Plot Maker, however, it is quick and easy to plot many different muscle properties and begin to gain insight into how muscles function, as represented by their models in SIMM.

JOINT EDITING

This tutorial will show you how to change the properties of one of the joints in the Demo Leg model. You will be editing the kinematic properties of the femoral-tibial joint, which is the joint in the knee that describes the motion between the femur and the tibia (the other part of the knee is the tibial-patellar joint). You will change the joint from a moving pin joint to a fixed pin joint, and will determine the effect this change has on the moment arm of one of the hamstrings muscles.

1. If it is not already open, open the Model Viewer window by clicking the left mouse button on its name in the menu bar.
2. Reset the joint angles of the Demo Leg model by clicking the left mouse button on *restore gc values*.
3. Close the Model Viewer window by clicking the left mouse button on its close box, and then click the left mouse button in the Demo Leg Model window to make it the active window.
4. Zoom in on the knee joint by putting the cursor over the knee and pressing the I key. Zoom in enough so that you can clearly see the bones and the spaces between them.
5. Press the K key to flex the knee. Move the cursor to the left to flex the knee, and to the right to extend the knee. Notice how the bones move in relation to each other.
6. Open the Joint Editor by clicking the left mouse button on its name in the menu bar.
7. Select the femoral-tibial joint by pressing the left mouse button on the *select joint* button and selecting *femoral-tibial* from the joint menu.
8. Notice the values in the six degree-of-freedom boxes in the lower left corner of the tool window. Three of them ($r1$, $r2$, tz) are zero, and the other three are each functions of *knee_angle*. *Knee_angle* is the generalized coordinate in this joint definition, meaning that it is the independent variable (or true degree of freedom), and $r3$, tx , and ty are dependent functions of *knee_angle*. This joint is called a "moving pin" joint because it involves a single axis of rotation ($r3$, rotation about the Z axis), but the center of rotation moves in X and Y, rather than remaining fixed.
9. Select tx by clicking the left mouse button in its box. The kinematic function for tx is displayed in the gray box to the right. The yellow circles are control points for the function (specified in the joint file) and the white line is a cubic-spline fit to those control points. Press the left mouse button on one of the yellow points and drag it to a new position. When you release the mouse button, the kinematic properties for the femoral-tibial joint will be updated. Click the left mouse button in the Demo Leg Model window and press the K key to flex the knee and observe the changes. If you want to undo your change you can click the left mouse button on *restore* to restore the entire joint to its original state.
10. Press the left mouse button on *dof type*, move down to tx in the *dof* menu, and then select *constant* from the *dof type* submenu. This changes the tx component of the joint from a function to a constant. SIMM averages all of the values of the control points in the original function to calculate the value of the constant.
11. Make the same change to ty . Press the left mouse button on *dof type*, move down to ty in the *dof* menu, and then select *constant* from the *dof type* submenu. The femoral-tibial joint is now a fixed pin, with rotation about the Z axis. The rotation, $r3$, is about axis3, as specified in the joint file. In the Demo Leg Model, axis3 is defined to be the Z axis.

12. Click the left mouse button in the Demo Leg Model window and press the K key to flex the knee again. Notice the difference between the original joint and the fixed pin version. The spacing between the femur and tibia now changes dramatically when you flex the knee. Also, the kinematics for the patella need to be changed because the patella passes through the femur during flexion. Also notice that the muscle path for the vastus lateralis muscle (one of the quadriceps) is now inappropriately specified. The wrapping points for this muscle were carefully specified for the original knee kinematics. Now that the joint has changed, the wrapping points should be moved so that the muscle wraps smoothly over the distal femur as the knee flexes. This exercise is left to the reader, since the purpose of this tutorial is to briefly show you how to change the kinematics for a joint and to plot its effects.
13. Close the Joint Editor window by clicking the left mouse button on its close box. Open the Plot Maker window by clicking the left mouse button on its name in the menu bar.
14. If the *all* muscle menu is not already displayed, press the left mouse button on *muscles* and select *all* from the muscle group menu. Make the Plot Maker window taller by clicking on its bottom edge and dragging down until you can see the entire muscle menu.
15. Click the left mouse button on *semimem* to turn on plotting for semimembranosus (and make sure that no other muscles are on).
16. If you have already made one or more plots, press the left mouse button on *plot* at the top of the Plot Maker window, and choose *new plot* from the menu. This tells SIMM to open a new plot window next time it makes a plot curve.
17. Now it is time to choose which properties of semimembranosus you want to plot. In this tutorial, we will be plotting the muscle's moment arm about the knee, over the entire range of the knee joint. More specifically, SIMM will be calculating, for each value of *knee_angle* in the range 0.0 to -120.0, the moment arm of semimembranosus with respect to the *knee_angle* gencoord. In SIMM, you always calculate muscle moment arms and moments with respect to generalized coordinates, rather than with respect to joints or DOFs (*r1*, *r2*, *r3*, *tx*, *ty*, *tz*). To plot the moment arm for semimembranosus about the knee, you need to select *knee_angle* moment arm as the Y-variable for plotting. Click the left mouse button on *y variable*, move down to *moment arm*, and select *knee_angle* from the *Gencoords* menu.
18. To select *knee_angle* as the X-variable, press the left mouse button on *x variable* and select *knee_angle* from the menu.
19. Press the left mouse button on *make curves*. SIMM will calculate the moment arm curve for semimembranosus and open a new plot window in which to display it. This first curve represents the moment arm using the new fixed pin knee joint that you just made.
20. Open the Joint Editor window again and click the left mouse button on *restore* to reset the femoral-tibial joint to its original state.
21. Back in the Plot Maker window, click the left mouse button on *make curves* again to calculate semimembranosus moment arm a second time. This green curve represents the moment arm using the original moving pin knee joint. Notice that the moment arms differ by as much as 15 mm (the units in the plot window are meters). If you wanted to decrease this difference and improve the realism of the fixed pin knee, you could edit the joint parameters and re-plot the curve until you matched the moving pin characteristics as best you could.

GAIT ANALYSIS

SIMM contains many features that can help you analyze movement data that is collected in gait labs and other motion analysis facilities. The SIMM motion file format has support not only for joint angle data, but also ground-reaction force information and EMG data. SIMM is a very powerful motion analysis tool because it can playback your recorded animations complete with display of ground-reaction forces and EMG levels, plus it can calculate muscle lengths and other properties during the recorded motion. A description of all of the SIMM features that can be used to analyze a recorded gait cycle is beyond the scope of this tutorial. In this tutorial we will briefly compare two gait patterns, one normal and one with "crouch" gait, and investigate one of the issues that surgeons deal with when diagnosing the patient with crouch gait. This tutorial does not introduce you to the features in the Gait Module, which is an optional component of SIMM that converts GCD motion files into SIMM models scaled to match the size of the subject. For information on the Gait Module, consult the tutorial called *Gait Module Demo*.

Crouch gait is one of the most common walking abnormalities among persons with cerebral palsy. It is characterized by excessive flexion of the knee during the stance phase, which is often accompanied by exaggerated flexion, adduction, and internal rotation of the hip. One possible cause of crouch gait is short hamstrings, and orthopaedic surgeons will sometimes lengthen the hamstrings of such patients in an attempt to improve their posture and/or gait. But, other causes of excessive knee flexion are possible (e.g., inadequate plantar flexion strength, short hip flexors), and lengthening the hamstrings can compromise the muscles' capacity to generate forces and joint moments, leaving some patients with weak or dysfunctional limbs. How can one determine whether a hamstrings lengthening procedure is warranted?

One way to judge whether a patient's hamstrings are shorter than "normal" is to develop a musculoskeletal model and compare the length of the hamstrings over the patient's crouch gait cycle to the length of the hamstrings over a normal gait cycle. In this tutorial we will animate the Demo Leg Model according to a normal gait pattern as well as crouch gait, and make plots of the length of one of the hamstrings muscles during each gait pattern.

1. First, familiarize yourself with the two gait patterns by animating the model according to each one. Open the Model Viewer and press the left mouse button on *start/stop* to bring up the menu of motions linked to this model. Select *normal gait* from the menu, and watch the leg in the Demo Leg Model "walk." The pelvis rotates as it would during normal gait, but the center of it remains fixed in the model window. To speed up or slow down the animation, press the left mouse button on the *gear* slider below the *model name* field and drag the thumb to the left or right.
2. Click the left mouse button on the *start/stop* item to stop the animation. Now press on the left mouse button on the item again to bring up the menu of motions. This time choose *crouch_gait* from the menu and watch the leg model walk with an exaggerated knee flexion pattern.
3. Click the left mouse button on *start/stop* to stop the animation.
4. To compare these two gait patterns functionally, we will use the Plot Maker. Click the left mouse button on the close box of the Model Viewer to put it away. Then open the Plot Maker by clicking the left mouse button on its name in the menu bar.
5. If you have any plots open, close them by clicking the left mouse button on their close boxes.
6. Press the left mouse button on *motion curve* to bring up the menu of motions linked to this model. Move down to *normal_gait*, then down to *Generalized Coordinates*, and then select *knee_angle* from the

Generalized Coordinates submenu. SIMM will open a new plot window and display a curve representing the knee angle over the entire range of the normal gait cycle. The horizontal axis of the plot ranges from 0.0 to 100.0, or percentage of gait cycle. Notice the two magenta lines on the plot. The first, at an X value of 0.0, shows when heel strike occurs. This is the time in the gait cycle when the right heel first contacts the ground. The second line, at an X value of about 62.0, is when the right foot (toe) leaves the ground at the end of stance phase.

7. Now press the left mouse button on *motion curve* again to bring up the menu of motions. Move down to *crouch_gait*, then down to *Generalized Coordinates*, and then select *knee_angle*. SIMM will make a second curve in the plot window, this one representing the knee angle during the crouch gait cycle. Notice that the knee is much more flexed during crouch gait than during normal gait, and it never approaches full extension.
8. Animate the model according to the two gait patterns again, and watch as a yellow line moves along the plot to indicate the current position. To animate the model without opening the Model Viewer, click the left mouse button in the Demo Leg Model window and press the G key to animate the normal gait pattern. As you move the cursor horizontally, you can control the speed and direction of the animation. To animate the crouch gait pattern, press the C key.
9. Delete the knee angle plot by clicking the left mouse button on its close box.
10. If it is not already displayed in the Plot Maker, display the *all* muscle menu by pressing the left mouse button on *muscles* and selecting *all*. Click the left mouse button on *semimem* in this menu so that you can plot the length of the semimembranosus muscle during the two gait patterns.
11. Press the left mouse button on *y variable* and select *musculotendon length* from the y variable menu.
12. Press the left mouse button on *x variable* and select *normal_gait* from the x variable menu.
13. Click the left mouse button on *make curves*. SIMM will open a new plot window with a curve representing the length of the semimembranosus muscle during the normal gait pattern.
14. Press the left mouse button on *x variable* and select *crouch_gait* from the x variable menu.
15. Click the left mouse button on *make curves* again. SIMM will add a second curve to the plot, this one representing the length of semimembranosus during crouch gait. Notice that the curves are fairly similar. They are rarely more than one centimeter apart, and they have approximately the same minimum and maximum values. This plot suggests that the hamstrings muscle is not too tight during gait in this particular patient because its length is nearly the same as its length during "normal" gait. To see why this is so, you can make one more plot; this time of hip flexion angle during gait.
16. Press the left mouse button on *plot* near the top of the Plot Maker window and select *new plot* from the plot menu.
17. Press the left mouse button on *motion curve*, move down to *normal_gait*, then down to *Generalized Coordinates*, and then select *hip_flexion* from the Generalized Coordinates submenu. SIMM will open a new plot window with a curve representing the hip flexion angle during normal gait. Now plot the hip flexion angle for crouch gait in a similar manner. Notice that the hip flexion angle is greater during crouch gait for most of the gait cycle. This suggests that while the knee is more flexed during crouch (thus shortening the hamstrings), the hip is more flexed as well, which results in the hamstrings being lengthened. In this example, the two effects nearly cancel each other out, resulting in similar hamstrings length plots for normal and crouch gait.

GAIT MODULE DEMO

The contents of this tutorial are also available in Adobe Acrobat™ format in the file *Tutorials.pdf*. We recommend you open or print this tutorial using Acrobat before proceeding. This will make it easier for you to make selections in the SIMM Gait Options dialog box while reading the tutorial text.

The Gait Module is an optional component of SIMM that enables you to easily animate and analyze three-dimensional motion data. To visualize the relationships between external forces, muscle activity, and the resulting body motion, the software displays ground-reaction force vectors superimposed on the skeleton and changes muscle colors to reflect their activation levels. This provides an environment to better interpret the causes of complex movement patterns. The major features of the Gait Module are its ability to:

- * translate GCD (gait cycle data) files into SIMM joint, muscle, and motion files,
- * show the timing of gait events, such as heel strike, in plots of gait data,
- * display 3D muscle shapes for more realistic animations,
- * display ground-reaction force vectors with the skeletal model,
- * vary the sizes and colors of muscles to show their activation levels during the motion, and
- * display standard deviations of gait variables in the plot windows.

This tutorial includes one GCD file with motion data for a normal gait pattern. The file contains kinematic and force-plate data for both legs, and EMG data for one of the muscles in the right leg. In this tutorial you will make several SIMM models from this GCD file and explore some of the features of each model.

1. Click on File... in the SIMM menu bar and choose *Open Sample Gait...* SIMM will open the sample GCD file and display the Gait Options dialog box. This dialog box lets you select several options for converting the GCD file into a SIMM model.
2. In the dialog box, notice the three choices for *models*, labeled *raw data*, *scaled*, and *unscaled*. These are the three types of SIMM models that you can create from a GCD file. Each has certain advantages, so in this tutorial we will create a model of each type to show its unique features. Select the *raw data* model by clicking the left mouse button on its radio button. This model is the simplest model that the Gait Module can create. It contains no joint or muscle modeling; each limb segment is scaled to match the anatomical data in the GCD file, and can move independently of the others, with a full six degrees of freedom. This model is useful for checking errors in the motion-tracking hardware and software because the motions of the limb segments precisely follow the marker data. There are no muscles in this model because computation of muscle lengths and forces is not appropriate for a model with scaled limb segments and no joints.
3. Now look at the two *limbs* checkboxes, labeled *left* and *right*. The demo GCD file contains bilateral motion data, so you can choose whether you want to create a model of the left leg, right leg, or both legs. For other GCD files, SIMM will pre-scan the file to determine if motion data for each limb is present, and then enable or disable the checkboxes as appropriate. Leave both checkboxes turned on so that a bilateral model is created.
4. The *model name* field holds the name that will be given to the musculoskeletal model that you are about to create from the GCD file. The default name is made from the base of the GCD filename. The Gait Module creates other names from the \$REFERENCE and \$NAME fields in the GCD file, or you can type in your own. For now, leave the name set to *Demo_Gait*.

5. The *save intermediate files* checkbox controls whether or not you want to save copies of the joint, muscle, and motion files that the Gait Module creates from the GCD file. If you save them, then you can load them into SIMM at a later time without using the Gait Module or referring back to the GCD file. For now, leave the option turned off since we will not need the files after we have loaded the model.
6. Click the left mouse button on *OK* to confirm your choices. The Gait Module will convert the GCD file into a SIMM model and display it in a new model window. When the model is first displayed, it is configured according to the first frame of motion data. Notice the blue squares below the feet. These represent the force plates in the motion lab. Since the coordinates of the corners of each force plate are in the GCD file, SIMM can display them under the feet in the appropriate positions.
7. Click the left mouse button in the *Demo_Gait* model window and then press the G key. The model will walk over the force plates, and its speed and direction are controlled by the position of the cursor in the window. If the cursor is on the right side of the window, the model will walk forwards, with increasing speed as you move the cursor closer to the right edge of the window. If the cursor is on the left side of the window, the model will walk backwards.
8. As the *Demo_Gait* model walks, notice the green vectors under the force plates (you may want to press the O key to move the model out for a better view). These represent the ground-reaction forces as measured by the force plates. Also, if you look closely you can see that just after heel strike for each leg, the joint spacing in the ankle and knee joints decreases. This artifact in the motion data is most likely caused by the markers moving with respect to the bones when the heel strikes the floor. There is probably some actual compression of the joints during stance (due to the higher loads on the joints), but this effect is amplified by marker movement. This raw data model is good for showing motion artifacts and errors because the data is not masked by joint modeling. When using the Gait Module for animating GCD files, it is a good idea to occasionally create a raw data model to check the accuracy of the marker data.
9. Since the raw data model does not have models of the joints or muscles, however, it is of limited use in a detailed analysis of the gait data. We will now make a SIMM model that does have a more realistic kinematic model of the limbs. But first delete the *Demo_Gait* model by clicking the left mouse button on its close box.
10. Click on *File...* in the SIMM menu bar and choose *Open Sample Gait...* again. SIMM will display the Gait Options dialog box with the same options as before. This time, do not change the default model type, but rather leave it set to *scaled*. This model type contains over forty muscle-tendon actuators for each limb, and is scaled to match the size of the patient (in this tutorial there are only 7 muscles). The hips and ankles are modeled as ball-and-socket joints, and the knees are three-degree-of-freedom joints with sliding and rolling of the tibia and femur. These joints allow for abnormal motion (e.g. excessive varus/valgus knee motion), but do not allow the bones to disarticulate. The limb segments have been scaled to match the limb lengths calculated from the GCD file. Because this model contains muscles and lax joints, it is useful for making a detailed analysis of the patient data. Muscle-tendon lengths can be plotted, and abnormal joint motions can be viewed. Muscle forces and moments cannot be plotted, however, because the force-generating parameters (e.g., optimal fiber length) are not scaled with the limb segments.
11. Click the left mouse button on *OK* to confirm your choices. The Gait Module will convert the GCD file into a scaled model and display it in a new model window. Click the left mouse button on the model

window and then press the G key to animate the model. The position of the cursor within the model window controls the speed and direction of the walking as described above.

12. Open the Model Viewer by clicking the left mouse button on its name in the menu bar. Notice the list of gencoords for this model. The first six allow the entire model to rotate and translate with respect to ground. The other 16 (eight for each leg) are used in the hip, knee, and ankle joints. At the bottom of this list is the name of the motion variable, *Demo_Gait_motion* (there may be a number in parentheses after the name).
13. Close the Model Viewer window and open the Plot Maker by clicking the left mouse button on its name in the menu bar. If you created some plots before beginning this tutorial, then choose *new* from the Plot menu at the top of the Plot Maker window. Then press the left mouse button on the *motion curves* button and choose *Demo_Gait_motion > Generalized Coordinates > RtKneeFlexExt* from the submenu. SIMM will create a plot window with one curve of data- the right knee angle during the *Demo_Gait* motion.
14. Notice the magenta vertical lines on the plot. These lines represent gait events that were recorded in the GCD file. Each line has a label at the bottom describing the event. *rfo* stands for "right foot off," the time at which the right foot left the ground. *rfc* stands for "right foot contact," *lfo* stands for "left foot off," and *lfc* stands for "left foot contact." Also notice that the red plot curve has a darker-red region behind it, with varying thickness. This is the standard deviation data that was present in the GCD file. If a GCD file is made by averaging several gait cycles, and the resulting standard deviation data is recorded in the GCD file, SIMM will display it whenever you plot the corresponding data curve.
15. Click the left mouse button in the *Demo_Gait* model window and then press the G key to animate the model. Notice that as the limbs move, a yellow bar moves across the plot you just created, to show you where in the plot data the model animation currently is.
16. When you are done animating the model and examining the plot, delete the plot by clicking the left mouse button on its close box.
17. Because the scaled model contains muscle-tendon actuators for each limb, you can plot their lengths during the gait cycle. Plots of muscle lengths during gait can be very useful in helping diagnose gait pathologies, such as crouch gait in children with cerebral palsy. This is one of the most powerful features of SIMM because it cannot be done with traditional motion capture systems.
18. In the Plot Maker window, press the left mouse button on the *muscles* button and choose *RtKneeFlex* from the muscle group menu. A menu of the right knee flexor muscles will appear below the plot option check boxes (you may need to make the Plot Maker window taller to see the menu). Select both muscles, *RtSemiMem* and *RtLatGas*, by clicking the left mouse button on their names.
19. Press the left mouse button on the *y variable* button and choose *musculotendon length* from the pop-up menu. Now click on the *x variable* button and choose *Demo_Gait_motion* from the bottom of the pop-up menu.
20. Click the left mouse button on *make curves* to generate the plot. The Plot Maker will calculate the musculotendon length (y variable) as a function of the gait cycle (x variable) for the two muscles you have selected. As with the previous plot you made, you can animate the model by pressing the G key in the model window and the yellow bar will follow along in the plot. If this gait cycle were abnormal and you

were attempting to determine why, you might want to compare this plot of muscle lengths to a plot of muscle lengths during a normal gait cycle. This type of analysis is described in more detail in another SIMM tutorial, *Gait Analysis*.

21. After examining the plot, delete it by clicking the left mouse button on its close box. Close the Plot Maker window as well, and delete the Demo_Gait model by clicking on its close box.
22. Click on File... in the SIMM menu bar and select *Open Sample Gait...* again. This time, click on the *unscaled* model type. This model contains over forty muscle-tendon actuators for each limb (there are only seven in this tutorial), but is not scaled to match the size of the patient. The hip is modeled as a ball-and-socket joint, the knee is modeled as a one-degree-of-freedom joint (that includes sliding and rolling of the femur, tibia, and patella), and the ankle is modeled as a pin joint. The limb segments have not been scaled to match the limb lengths calculated from the GCD file, but instead represent the limb lengths in an average adult male. If the individual's limb lengths do not match this nominal model, you will notice some anomalies in the animation. For example, the foot will slip on the floor during stance, and the ground-reaction forces will not remain under the foot. This model is useful, however, if you want to estimate the forces and moments that the muscles are capable of generating during the recorded motion. If you record EMG data as well, this information can be saved in the motion file for a better estimate of the muscle forces. How accurate these estimates are depends on several factors, such as the individual's limb lengths and his or her muscle strengths. This model is not meant to be an accurate representation of a specific individual's muscle forces, but can be used to compare muscle force-generating capabilities of a nominal model for different gait patterns.
23. Click on the *OK* button to make the model. Notice that this unscaled model has no force plates under the feet. Because the limbs are not scaled to match the subject, the height and positions of the force plates do not line up with these limbs. Also, the feet will appear to slip during stance phase when they should be stationary. Thus SIMM does not display the floor at all, to indicate that the foot-floor interaction is not realistic with this unscaled model. The ground-reaction force vectors will not line up under the feet either, but they are displayed when you animate the model to give you some sense of where the foot is contacting the ground and with how much force. As with the previous models, you can press the G key in the model window to make the model walk.
24. Open the Plot Maker window and press the left mouse button on the *muscles* button. Choose the *RtKneeExt* muscle group and then click on *RtVastLat* in this menu to turn on vastus lateralis.
25. Click on the *y variable* button and choose *force*, and click on the *x variable* button and choose *Demo_Gait_motion* from the bottom of the pop-up menu.
26. Click on *make curves* to make the plot. SIMM will calculate the force in *RtVastLat* during the gait cycle and display the curve in a new plot. To calculate the force, SIMM first calculates the length of the muscle at each timestep in the gait cycle. It then computes the isometric force in the muscle (assuming full activation), and then scales this force by the activation level for *RtVastLat* specified in the motion file for that timestep.
27. Now click the left mouse button on the *act override* checkbox. This tells SIMM to ignore the muscle activation levels specified in the motion file and instead use the value in the *activation* field in the Plot Maker options (which is set to 1.0). Click on *make curves* again to generate this plot. SIMM will calculate and display a curve of the isometric force in *RtVastLat* during the gait cycle assuming that the muscle is fully activated the whole time. You can compare the two curves to see if the subject was using

the muscle "efficiently" (i.e., during the periods when it could develop the most isometric force). You can also have SIMM estimate the dynamic force in RtVastLat by taking into account the contraction velocity of the muscle fibers. This calculation may be the best estimate of the actual force that the subject's RtVastLat muscle developed during this recorded gait cycle. See the Plot Maker section of the SIMM manual for details on how to calculate dynamic force and the assumptions involved in this calculation.

28. When you are done examining the plot, delete both the model and the plot by clicking the left mouse button on their close boxes, and close the Plot Maker window as well.
29. The last model we will make from the sample GCD file contains 3D descriptions of the shapes of some of the leg muscles, to make gait animations look more realistic. Click on File... in the SIMM menu bar and choose *Open Sample Gait...* Click on the *unscaled* model type again, but this time also click on the *3D muscles* checkbox to turn it on. Click *OK* to confirm your choices and SIMM will create another unscaled model from the GCD file (it may take a few seconds to make this model). This model includes 3D surface descriptions of 8 muscles on each leg. The colors of the muscle surfaces will change to reflect their activation levels while you animate the gait cycle, as long as there is EMG information for those muscles stored in the GCD file (in this sample file there is EMG data only for RtVastLat). You cannot calculate muscle lengths or forces with this model, but it can be useful if you want to display a more realistic limb model to animate the gait cycle. Once the model is loaded, you can click on its window and press the G key to make the model walk.
30. You have now loaded each type of musculoskeletal model that the Gait module can create from a GCD file, and have learned a little about the benefits of each one. If you want, you can re-load several of the models at once to better compare their features, and can make plots of joint angles, muscle lengths, and muscle forces to do an even more detailed comparison. The Plot Maker contains many plotting options that will help you analyze gait and compare different models and motion files. Consult the Plot Maker section of the SIMM manual, as well as the *Gait Analysis* tutorial, for more information.

DYNAMICS PIPELINE DEMO

The Dynamics Pipeline is a suite of software tools that enables you to perform forward and inverse dynamic simulations on SIMM musculoskeletal models. The Pipeline connects SIMM to SD/FAST (Symbolic Dynamics, Mountain View, CA, <http://www.symdyn.com>), which simulates the dynamics of rigid-body systems.

For forward dynamics, you specify the on/off times of the muscles, and the Pipeline will compute the resulting motions of the body segments. The Pipeline has built into it several models for computing the dynamic forces in muscles. You can choose among them when you start a simulation, based on your accuracy and computation needs. For inverse dynamics, you specify the time histories of the joint angles during some activity, and the Pipeline will calculate the torques required to generate that motion.

This tutorial demonstrates some of the capabilities of a forward dynamics simulation built using the Dynamics Pipeline. This demo contains a model of the leg with a forward simulation that allows you to specify the excitation patterns of the muscles. The simulation solves for the motions of the body segments due to the muscle activity, and writes out a motion file that you can load back into SIMM for playback and analysis. The code and input files for this simulation are located in the PipelineDemo folder. This tutorial will show you how to edit some of these files and create a new forward simulation.

1. Load the precomputed motion file that comes in the PipelineDemo folder. From the SIMM File menu, choose Open... and select the file PipelineDemo\forward.mot. This motion file contains the gencoord values and muscle activation patterns that were output when the forward simulation was last run. Each time you run the simulation, it creates a new file forward.mot with the results of the simulation.
2. Open the Model Viewer by clicking the left mouse button on its name in the menu bar. Notice the name *sd_motion* at the bottom of the list of gencoords. *sd_motion* is the name of the motion that is in the file forward.mot. There is a number field to the right of the name, and a slider bar further to the right. You can use either to change the value of the motion variable.
3. Click the left mouse button on the thumb of the *sd_motion* slider (keep its value at 0.0). Notice that the muscles on the model have all gotten darker and thinner. The color and thickness of the muscles corresponds to their activation levels. At the beginning of the demo simulation, all of the muscles are turned off, hence they are displayed with thin, dark red lines.
4. Click the left mouse button in the model window and then press the O key to move the model back away from you. Keep the O key pressed until the leg is about half the size it used to be. This will allow you to see the entire leg as it is animated according to *sd_motion*.
5. Press the left mouse button on the right arrow of the *sd_motion* slider and keep it pressed as the leg moves through the entire motion. Notice how the muscles change color and thickness during the simulation. When you are done, reset *sd_motion* back to 0.0.
6. Now turn off clamping of all of the gencoords. The clamp/unclamp box for each gencoord is located between its number field and slider bar under the column heading "C". Click the left mouse button on each one so that they are all off. When a gencoord is unclamped, it is allowed to go beyond its normal range of motion when you type an out-of-range number in the number field or if the motion file contains out-of-range gencoord values.

7. Replay *sd_motion* by pressing the left mouse button on the right arrow of its slider bar. Notice how the names and values of some of the gencoords turn red when they go beyond their normal range of motion. In a Dynamics Pipeline simulation, joints (more specifically, gencoords) are kept within normal physiological ranges by the use of restraint torques. These torques are user-defined functions that apply torques or forces to a gencoord when it goes beyond its range of motion. Because the torques do not come on until the gencoord is already out of range, it may continue to go out of range for several degrees, depending on how strong the restraint torque is.
8. You are now going to change some input parameters to the dynamic simulation and perform another forward simulation. Minimize the main SIMM application window and bring up a display of the contents of the PipelineDemo folder. Open the file forparams.txt. This file contains the names of all of the input and output files used in a simulation. The change you will make is to add the name of a file that contains an external force applied to the femur. Add the line "kinetics_file forces.ktx" anywhere in the file and then save the file. If you would like to look at the format of this kinetics file, you can open and view it as well.
9. Double click on sdfor.exe to run a new dynamic simulation. This program opens the file forparams.txt to get the list of input and output files, and then sets up and runs a simulation based on the data in the input file. The simulation time is 1.1 seconds, and you can watch its progress in the shell window. The simulation takes a minute or two to run, and as it proceeds it writes the results to the file forward.mot.
10. When the simulation is complete, the shell window will disappear. Go back to SIMM and load the newly created motion file, forward.mot.
11. In the Model Viewer window, notice the new motion, called *sd_motion (4)* below *sd_motion*. Press the left mouse button on the right arrow of the motion slider to animate the model according to the data in this new motion file. Notice that at 0.5 seconds (simulation time) a green vector appears, pointing at the middle of the femur. This vector represents the external force that is being applied to the femur. Keep animating the motion and watch the vector get bigger and push the leg higher than in the previous simulation.
12. Minimize the SIMM application window again and go back to the display of the PipelineDemo folder. Open the file demoModel.msl and scroll down to the definition of the *semimem* muscle. At the bottom of the definition of this muscle there are pairs of numbers specified between the keywords beginexcitation and endexcitation. The first number in each pair specifies a time, in seconds, and the second number is the muscle excitation level (from 0.0 to 1.0) at that time. The simulation code reads these time/excitation pairs and fits a function to them (you can specify whether you want a spline fit or a step function) in order to determine the excitation level of each muscle during the simulation. The excitation pattern for *semimem* starts at its maximum, 1.0, and then drops to 0.0 at 0.6 seconds. Change the 1.0 to 0.0 so that the muscle is always off during this simulation. If you would like to change the excitation patterns of other muscles, change the numbers in their definitions accordingly.
13. Double click on sdfor.exe to run the simulation again.
14. When the simulation is complete, go back to SIMM and load the new results, which are stored in forward.mot.

15. In the Model Viewer, the new motion is called *sd_motion (5)* and is put at the bottom of the gencoord and motion list. Use its slider bar to replay the motion and compare it to the previous simulations. One of the differences compared to *sd_motion (4)* is that the knee does not flex as much. This is because semimem is a knee flexor (as well as hip extensor), so without it (you set its excitation to 0.0 in demoModel.msl) there is not as much knee flexion moment as before.
16. To quantify the differences in knee flexion between these two simulations, open the Plot Maker window and plot two motion curves. Click the left mouse button on *motion curve* and roll off to *sd_motion (4)* and then *Generalized Coordinates* and then choose *knee_angle*. SIMM will open a new plot window with a curve representing the *knee_angle* values for that motion. Now click on *motion curves* again and choose *sd_motion (5)* --> *Generalized Coordinates* --> *knee_angle*. The plot window now contains the *knee_angle* curves from the last two simulations you performed. The green curve (from *sd_motion (5)*) shows less knee flexion than the red curve because of the missing semimem flexion moment. Also notice that there is a small "bounce" in the green curve at about 0.5 seconds, as *knee_angle* approaches 0.0. This bounce is due to the restraint torque at the knee. *Knee_angle* briefly goes beyond 0.0 (the upper end of its range of motion), so the restraint torque kicks in and pushes the knee back into range. This does not happen in *sd_motion (4)* because the knee never extends that far.
17. If you would like, you can plot other motion curves to further compare the results of the two simulations. You can also plot various muscle properties, such as length, force, and moment, to see how they differ as well. See the Plot Maker section of the SIMM User Guide for details on the plotting options that can help you analyze a dynamic simulation.
18. It's now time to look at some of the dynamic simulation source code. One source file, *formain.c*, is provided with this demo so that you can examine it, learn how it is structured, and make changes to it. A precompiled library of the remaining source files in a forward simulation is included in the PipelineDemo folder so that you can edit *formain.c*, compile the results, and run your customized simulation.
19. Minimize the SIMM application window and go back to the PipelineDemo folder. Open the file *formain.c* and look at how it is laid out. Some of the high-level simulation parameters are declared and initialized near the top of *main()*. *Nstep* is the number of timesteps in the simulation, and *dt* is the length, in seconds, of each timestep. The main simulation loop, which loops once for each timestep, begins right after the call to *init_muscle_states()*. If you would like to make changes to the code and run a simulation, you can use one of the project files located in the folders within PipelineDemo. There are project files for Microsoft Visual C++ 5.0 (MSVisualC++\PipeDemo.dsw) and Metrowerks CodeWarrior Pro 3.0 (CodeWarrior\PipeDemo.mcp). There is also a Makefile provided which you can use as a reference if you want to use a different compiler.