Simulation Lab #3:
Kinematic and Geometric Modeling of the Hip, Knee, and Associated Muscles

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Mechanics of the Human Locomotor System
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I. Introduction

Quantitative descriptions of musculoskeletal geometry are an essential building block for developing muscle-actuated, forward dynamic simulations of movement. The path geometry of a muscle determines its moment arms, and therefore, its moment-generating capacity for a given level of muscle force. The force that a muscle can produce also depends on its moment arm — the moment arm determines the length change of the muscle with joint rotation, and the muscle's force-generating capacity depends on its shortening velocity and length. Hence, if descriptions of the musculoskeletal geometry are not sufficiently representative, analyses based on dynamic simulations may be misleading (or perhaps totally bogus…). In this lab, you will gain experience building and evaluating models of musculoskeletal geometry.

II. Objectives

In this simulation exercise you will use SIMM (Software for Interactive Musculoskeletal Modeling, Delp and Loan, 1995) to:

- Visualize the three-dimensional (3D) surface geometry of the pelvis, femur, tibia, fibula, and selected lower limb muscles
- Implement a simple kinematic description of the hip joint
- Implement simple and complex kinematic descriptions of the knee joint
- Represent lines of action of the semitendinosus muscle over a range of hip and knee joint angles using via points and wrapping surfaces
- Assess the accuracy of your musculoskeletal model by comparing hip and knee flexion moment arms computed with the model to the muscle moment arms determined experimentally from tendon excursion measurements

III. Deliverables

At the completion of this lab, you will need to turn in computer files from your modeling work.

Please turn in:

1. A written report
   A Microsoft Word template for the report called `Simulation_Lab3_Report.doc` is available on the course web site.
2. A printout of your well-commented joint file `lab3.jnt`.
3. A printout of your well-commented muscle file `lab3.msl`.

IV. Input Files

All necessary input files for the lab will be provided in a single zip file on the course web site.

1. SIMM Muscle and Joint Files

`visualize_anatomy.jnt`
A joint file that displays the 3D surface representations of bones and muscles obtained from MR images of a lower extremity cadaver specimen

`no_musc.msl`
A muscle file (without muscles) to load with `visualize_anatomy.jnt` to avoid error messages in SIMM

`lab3.jnt`
A joint file you will edit to create your lower extremity model

`lab3.msl`
A muscle file you will edit to create your lower extremity model

`bonefiles/*.seg`
`bonefiles/*.base`
SIMM bone files that represent the 3D bone and muscle surfaces as polygon meshes

2. SIMM Sample Muscle and Joint Files

`arm.jnt`
A sample joint file that describes a kinematic model of an arm

`arm.msl`
A sample muscle file that describes muscle paths for the arm model

3. SIMM Bone Reference Frames

`femur_landmarks.msl`
A muscle file that describes anatomical landmarks used for establishing the femur reference frame

`get_rpy.m`

A MATLAB m-file that calculates roll, pitch, yaw angles from a transformation matrix

4. **SIMM Plot Files**

   `plotfiles/*.plt`
   SIMM plot files that describe muscle moment arms determined experimentally on the cadaver specimen

   `st_hipflexion.plt`
   semitendinosus hip extension moment arms vs. hip flexion angle

   `st_kneeflexion.plt`
   semitendinosus knee flexion arms vs. knee flexion angle

V. Getting Started

If you have not already done so, you should complete the first two SIMM tutorials. In addition, you may want to reference the SIMM manual while you are doing this assignment. A PDF version of the manual is posted on the course web site. Also, the SIMM help menus are very useful. From the class website, download `Lab3.zip` to the directory where you are working and unzip the file.

VI. Examine a Sample Kinematic Model of the Arm

In this section, you will load a sample kinematic model of the arm (Murray et al., 1995) and study the corresponding joint and muscle files.

- Start SIMM from the Programs Menu in Windows.
- Load the arm model `arm.jnt` from the File pull down menu.
- Open the joint file `arm.jnt` and the muscle file `arm.msl` in a text editor.

Feel free to examine the model and the corresponding joint and muscle files. You will construct a similar model of the lower extremity, so you may want to use the arm model as a reference while you work through the assignment. SIMM joint and muscle files are reviewed in the paper by Delp and Loan (1995) and are described in detail in the SIMM manual.

When you are done, exit SIMM by pressing the exit button in the upper right hand corner or exit from the File Menu.

VII. Create a Kinematic Model of the Lower Extremity

You will create a kinematic musculoskeletal model that can estimate the lengths and moment arms of the semitendinosus muscle (one of the medial hamstrings) through a range of hip and knee joint angles based on MR images of a cadaver specimen at one body position (the “scanned” position). To do this, you will define reference frames for the pelvis, femur, and tibia, implement kinematic representations of the hip and knee joints, specify attachments of the semitendinosus muscle, and prescribe wrapping surfaces and via points that simulate interactions between the muscle and surrounding structures.

VII-A. Visualize Lower Limb Muscle and Bone Surface Geometry

In this section, you will visualize the 3D surfaces of the pelvis, femur, tibia, fibula, and selected muscles that you will use to build your kinematic model. We obtained the 3D surface data by (1) acquiring five series of axial and sagittal MR images, (2) identifying and outlining the structures of interest on each 2D image, (3) generating 3D surfaces of each structure based on the 2D outlines, and (4) registering the surfaces from an adjacent series of images (see Arnold et al., 2000 for details). We have made a simple SIMM joint file called `visualize_anatomy.jnt` that displays the 3D bone and muscle surfaces.

- Start SIMM from the Programs Menu in Windows.
- Load the model `visualize_anatomy.jnt` from the File pull down menu.
- Open the joint file `visualize_anatomy.jnt` in a text editor.

VII-A.1. Examine the 3D anatomy of your lower limb specimen.

Use the `model viewer` tool to identify and examine the pelvis, femur, tibia, and fibula bones, and the medial hamstrings (semimembranosus and semitendinosus) muscles. You will base your model on these surfaces.

Display the medial hamstrings in `wireframe` mode by:
- changing the `drawmode` of the `muscles` group to `none`.
- changing the `drawmode` of the `medial_hams` group to `wireframe`.

NOTE: You can also change the properties by putting the mouse pointer over the object of interest and clicking the right mouse button. A pop-up menu will appear with the available properties.

The surface geometry of the muscles and bones are represented as polygonal meshes. The vertices of the polygons are defined with respect to a cartesian coordinate system.

NOTE: In SIMM the polygonal meshes are stored in “bone files” even though they may represent structures other than bones. Later in the lab you will create muscle paths from these surfaces, which will be defined in a “muscle file.”

VII-A.2. Visualize and understand how segments are related by joints.

FIRST: Examine the joint file `visualize_anatomy.jnt`.

Locate the definitions of the segments, joints, generalized coordinates, and kinematic functions in the joint file `visualize_anatomy.jnt`. You will be editing a similar joint file when you build your model.

In this model, the `grnd_pelvis` joint specifies the transformation from the ground segment to the pelvis segment, and allows the model to be reoriented using the slider bars in the model window. All of the other structures are "jointed" to the pelvis using a special joint called a `STATIC_JOINT`, which is defined at the top of the joint file to have rotations and translations of zero (i.e., the segment reference frames are coincident). In this model, the muscle structures are not true muscles; they are 3D objects to help you visualize the anatomy. Refer to Chapter 3.3 in the SIMM manual for more information about joint files.

<u>SECOND</u>: Use the joint editor tool to manipulate the kinematics of a joint.

Find the `axes 0.2` parameter for the `pelvis` segment in the joint file. This command displays the reference frame of the segment in the model window, with each axis 0.2 units long. The units for the `visualize_anatomy.jnt` model are meters.

- Add an `axes 0.1` parameter to the `femur` segment in the joint file and save the file.
- Close your previous model in SIMM by putting the cursor in the `model window` and hitting the `backspace` key.
- Reload `visualize_anatomy.jnt` with your changes.

Notice that the femur reference frame is coincident with the pelvis reference frame.

- Open the `Joint Editor` tool.

The joint editor enables you to interactively manipulate the kinematics of a joint.

- From the `Select Joint` menu, select the `pelvis_femur` joint.
- Change values of `tx, ty, tz` to reposition the femur relative to the pelvis.
- Change values of `rx, ry, rz` to reorient the femur relative to the pelvis.

Each bone is defined relative to its segment reference frame, and the transformation between two segment reference frames is defined by a joint. In the next section of the lab, you will implement a model of the hip joint by redefining the femur reference frame, specifying the translations between the pelvis and the hip center, and describing the rotations between the pelvis and the femur as functions of hip flexion, abduction, and rotation angles.

VII-B. Implement a Kinematic Description of the Hip Joint

Now you are ready to start building your own model!

- Close the `Visualize 3D Anatomy` model by clicking on the exit button in the upper right-hand corner.

- Load the joint file `lab3.jnt` (NOTE: SIMM will automatically open the muscle file `femur_landmarks.msl`, since it is defined in the joints file as the corresponding muscle file.
- Open the joint file `lab3.jnt` and the muscle file `femur_landmarks.msl` in your favorite text editor.

Your task in this section is to implement a kinematic description of the hip joint in the file `lab3.jnt`.

Your hip should:

- have three degrees of freedom (i.e., ball-and-socket joint)
- rotate about the center of femoral head about axes that correspond to flexion/extension, abduction/adduction, and internal/external rotation (i.e., angles that are meaningful to biomechanists and clinicians).

There are several ways to achieve this in SIMM. One way is outlined below.

VII-B.1. Establish a new reference frame for the femur.

Implementation of the hip joint kinematics in SIMM will be greatly simplified if the origin of the femur segment reference frame is located at the desired center of rotation and the axes of the femur segment reference frame are aligned with the desired axes of rotation. In particular, it will be advantageous if the femur reference frame is defined similar to the coordinate system shown in Fig. 1. Please use this coordinate system so that everyone is consistent.

The **origin** of the desired femur segment reference frame (hip center) is the center of the femoral head.

The **Y axis** (superior-inferior) is the vector joining the hip center and the midpoint between the lateral epicondyle and medial epicondyle.

The **X axis** (anterior-posterior) is the vector normal to the plane defined by the hip center, the medial epicondyle and the lateral epicondyle.

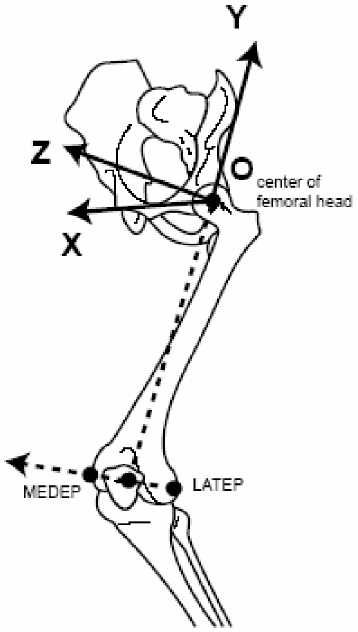


Fig. 1. Landmarks that define the femur segment coordinate system. **O** is the center of the femoral head, **MEDEP** is the medial epicondyle, and **LATEP** is the lateral epicondyle.

The **Z axis** (medial-lateral) is orthogonal to both the Y and X axes. Establishing a new reference frame for a segment involves three main steps. The notation for describing transformation matrices that is used throughout this document was adopted from Craig (1989).

FIRST: Determine the 4x4 transformation matrix ${}^{base}_{femur}T$ that describes the desired femur reference frame (femur) relative to the current frame (base):

$$ {}^{base}_{femur}T = \begin{bmatrix} {}^{base}_{femur}R & {}^{base}_{femur}P_O \\ 0 & 1 \end{bmatrix} = \begin{bmatrix} {}^{base}_{femur}X & {}^{base}_{femur}Y & {}^{base}_{femur}Z & {}^{base}_{femur}P_O \\ 0 & 0 & 0 & 1 \end{bmatrix} $$

where ${}^{base}_{femur}R$ is a 3x3 rotation matrix that describes the orientation of the desired femur reference frame relative to the current base reference frame, ${}^{base}_{femur}X$, ${}^{base}_{femur}Y$, ${}^{base}_{femur}Z$ are 3x1 unit vectors representing the X, Y, and Z axes of the desired femur reference frame relative to the current base reference frame, respectively, and ${}^{base}_{femur}P_O$ is a 3x1 vector that describes the position of the desired femur reference frame origin relative to the current base reference frame.

To help you out, we've marked the landmarks with muscle points in the muscle file `femur_landmarks.msl`, which you have already loaded.

Use the `Muscle Editor` tool (use the SIMM help menu if needed) to get the X, Y, Z coordinates of the hip center, the medial epicondyle, and the lateral epicondyle with respect to the current base reference frame, and write these in your report (Table 1).

Use these coordinates to establish the transformation matrix, ${}^{base}_{femur}T$, and write this 4x4 matrix in your report (Table 2). Make sure that the X, Y, Z vectors are unit vectors that define a right-handed coordinate system.

SECOND: Determine the 4x4 transformation matrix ${}^{femur}_{base}T$ that describes the current (base) reference frame relative to the desired femur reference frame (femur).

To establish your new reference frame for the femur, you need to determine the coordinates of the femur bone vertices with respect to the desired frame.

The transformation matrix obtained in the first step (${}^{base}_{femur}T$) would transform a bone defined in the desired femur frame (femur) to a bone defined in the current base frame (base):

$$ {}^{base}V = {}^{base}_{femur}T \cdot {}^{femur}V $$

where ${}^{base}V$ denotes the matrix of the femur bone vertices defined in the current base frame, and ${}^{femur}V$ denotes the matrix of the femur bone vertices defined in the desired femur frame. However, you want to transform the existing femur bone (defined in the current base frame) to a bone defined in the desired femur frame:

$$ {}^{\text{femur}}V = {}^{\text{femur}}_{\text{base}}T \cdot {}^{\text{base}}V $$

The transformation matrix that does this is the inverse of ${}^{\text{base}}_{\text{femur}}T$:

$$ {}^{\text{femur}}_{\text{base}}T = \left({}^{\text{base}}_{\text{femur}}T\right)^{-1} $$

Calculate ${}^{\text{femur}}_{\text{base}}T$ and write the matrix in your report (Table 3).

THIRD: Parameterize the transformation matrix ${}^{\text{femur}}_{\text{base}}T$ by a set of three rotations ϕ, θ, and φ and three translations p_x, p_y, and p_z:

$$ {}^{\text{femur}}_{\text{base}}T = \begin{bmatrix} 1 & 0 & 0 & p_x \\ 0 & 1 & 0 & p_y \\ 0 & 0 & 1 & p_z \\ 0 & 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} & & & 0 \\ & \text{Rot}(z,\phi) & & 0 \\ & & & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} & & & 0 \\ & \text{Rot}(y,\theta) & & 0 \\ & & & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} \cdot \begin{bmatrix} & & & 0 \\ & \text{Rot}(x,\varphi) & & 0 \\ & & & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix} $$

where Rot(z, ϕ) is a 3x3 rotation matrix that represents a rotation about the Z axis by ϕ degrees, Rot(y, θ) represents a rotation about the Y axis by θ degrees, and Rot(x, φ) represents a rotation about the X axis by φ degrees. You are welcome to write your own code that extracts ϕ,θ, and φ. from ${}^{\text{femur}}_{\text{base}}T$ or you may use MATLAB to call the function, `get_rpy.m`, which we have provided. The function `get_rpy.m` reads a 4x4 transformation matrix and outputs ϕ,θ, and φ. See the code for more details.

Write the values of ϕ, θ, and φ and the translations, p_x, p_y, and p_z, in your report (Table 4).

FOURTH: Transform the existing femur bone using the SIMM utility program `norm` (See Chapter 4 in the SIMM manual for details about `norm`). Copy `norm.exe` from the `C:\ProgramFiles\Musculographics\SIMM3.3` directory into your current directory.

From the DOS prompt in your current directory, type:

```
norm s1_femur.base lab3_femur.seg –rx φ -ry θ -rz ϕ -tx px –ty py –tz pz
```

The transformations will be performed in the order in which they are entered in the command line. The vertices of your “normed” bone will be defined in your desired femur reference frame.

FIFTH: Check out your new femur!

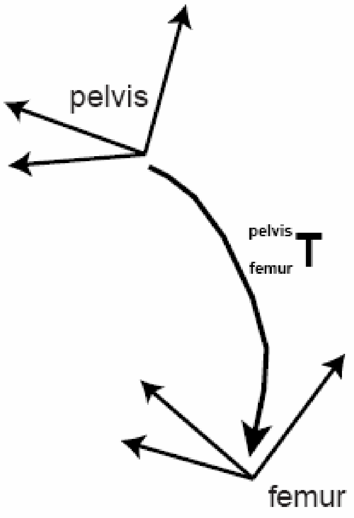
- To display your new femur bone, add a `segment` called `lab3femur` to the joint file `lab3.jnt`. Make sure your new bone `lab3_femur.seg` is in your `bones` folder. You may want to use the `axes` command to display its reference frame, and the `material` command to assign it a color. (See the `visualize_anatomy.jnt` joint file for sample material properties.)

- Add a normal joint (e.g., see next section) to `lab3.jnt` that connects the `lab3femur` segment to the `pelvis` segment. The translation from the pelvis reference frame to the hip joint center should be tx = -0.0522, ty = -0.0744 and tz= -0.0934.
- Reload the `lab3.jnt` model and visually inspect the `lab3femur.seg` bone. Is the center of the femoral head at the origin of the `lab3femur` segment reference frame? Do the axes for the `lab3femur` segment correspond to Fig. 1? Where is `lab3femur`'s reference frame relative to the `pelvis`? Your next job is to restore the position of the femoral head in the acetabulum and add degrees of freedom at the hip.

VII-B.2. Implement the hip kinematics in lab3.jnt.

In SIMM, joint kinematics are specified as a series of body-fixed translations and rotations that relate the position and orientation of one body segment to another. The transformations are performed in a user-defined order, and consist of three orthogonal translations and three rotations around user-defined axes. Each translation and rotation may be defined as a constant or as a function of a generalized coordinate.

The hip joint in your model will specify the transformation, ${}^{\text{pelvis}}_{\text{femur}}T$, from the `pelvis` segment (pelvis) to the `lab3femur` segment (femur) as a function of the three generalized coordinates hip flexion, hip adduction, and hip rotation (Fig. 2).



$$[\text{pelvis}] = {}^{\text{pelvis}}_{\text{femur}}T \cdot [\text{lab1femur}]$$

Fig. 2. Schematic of the transformation that defines the hip joint.

Add a new joint with the following syntax:

```
beginjoint my_hip
segments pelvis lab3femur
order t r3 r1 r2
```

```
tx constant tx_value
ty constant ty_value
tz constant tz_value
axis1 1.0 0.0 0.0
axis2 0.0 1.0 0.0
axis3 0.0 0.0 1.0
r1 function f1(hip_adduction)
r2 function f2(hip_rotation)
r3 function f3(hip_flexion)
endjoint
```

This joint specifies the body-fixed transformations between the `pelvis` segment and the `lab3femur` segment in the order: translations (`tx`, `ty`, `tz`), then hip flexion (`r3`), then hip adduction (`r1`), then hip rotation (`r2`).

$$\xrightarrow{\textit{body fixed}}$$

$$[pelvis] = Trans(tx,ty,tz)\cdot Rot(z,hip\_flexion)\cdot Rot(x,hip\_adduction)\cdot Rot(y,hip\_rotation)\cdot[lab3\,femur]$$

Your task is to define the kinematic functions, `f1`, `f2`, and `f3` such that hip flexion, adduction, and internal rotation are positive. Make sure that when the hip flexion, adduction, and rotation angles are all equal to zero degrees, the limb is in the upright, standing position.

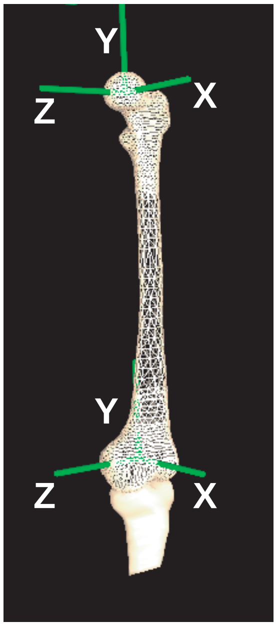


Fig. 3. Reference frames for the femur and tibia bones in full knee extension.

To check your hip joint, your `lab3femur` bone should align with the `femur` bone at the following joint angles, which define the scanned limb position:
`hip_flexion = 24.6` degrees
`hip_adduction = -5.45` degrees
`hip_rotation = 16.0` degrees.

VII-C. Implement Kinematic Descriptions of the Knee Joint

Now that your model has a functional hip joint, your next step is to specify the kinematics of the knee. In particular, you will define the motions between the femur and tibia (the tibiofemoral joint). As you may already know, the tibiofemoral kinematics are more complex than the hip kinematics. To accurately describe the rolling and sliding motion of the tibia relative to the femur, 3D rotations and translations are needed. You might wonder, can’t I just represent the knee as a simple hinge joint in the sagittal plane? When is it important to represent the relative translations between the bones (rolling and sliding) and the 3D rotations between the bones (the screw-home mechanism)? Do differences in the knee kinematics really affect the muscle moment arms enough to matter? Let’s investigate these issues?

You will implement two descriptions of tibiofemoral kinematics, each with a different degree of complexity:

Knee Joint #1: hinge joint about an axis through the epicondyles.
Knee Joint #2: joint with relative translations and 3D rotations between the femur and tibia.

VII-C.1. Create Knee Joint #1.

The tibia and fibula bones that comprise the `tibia` segment in `lab3.jnt` (`s1_tibia.base` and `s1_fibula.base`) are defined relative to the base reference frame in the scanned position. We have "normed" copies of these bones for you so that (1) the reference frame origin is coincident with the midpoint between the medial and lateral epicondyles, and (2) the reference frame axes are aligned with the `lab3_femur` segment axes when the knee is at full extension (Fig. 3). The normed copies of the bones are called `tibia_knee1.seg` and `fibula_knee1.seg`.

To create Knee Joint #1 (a hinge joint about an axis through the epicondyles):

<u>FIRST</u>: Add a segment called `lab3tibia1` to your joint file `lab3.jnt` that displays the bone files `tibia_knee1.seg` and `fibula_knee1.seg`.

<u>SECOND</u>: Define a joint between the `lab3femur` and `lab3tibia1` segments with the following syntax:

```
beginjoint my_firstknee
segments lab3femur lab3tibia1
order t r1 r2 r3
tx constant tx_value
ty constant ty_value
tz constant tz_value
axis1 1.0 0.0 0.0
axis2 0.0 1.0 0.0
axis3 0.0 0.0 1.0
r1 constant 0.00
r2 constant 0.00
r3 function f4(knee_flexion)
endjoint
```

Your joint should:

- define `tx_value`, `ty_value`, and `tz_value` to locate the `lab3tibia1` reference frame at the midpoint between the medial and lateral epicondyles.
- define the kinematic function `f4` such that the `lab3tibia1` segment rotates about its mediallateral (z) axis with knee flexion defined as positive.

<u>THIRD</u>: Check Knee Joint #1.

To check your knee joint, your `lab3tibia1` bone should align with the `tibia` bone when the limb is at the following joint angles, which define the scanned limb position:
`hip_flexion = 24.6` degrees
`hip_adduction = -5.45` degrees
`hip_rotation = 16.0` degrees
`knee_flexion = 22.0` degrees

Inspect how the tibia moves about the femur for different angles. Does the tibia have rolling and sliding motion? Does it exhibit any gapping between the tibial plateau and the femoral condyles?

VII-C.2. Create Knee Joint #2.

Let's take advantage of published experimental measurements of tibiofemoral kinematics. Fortunately there are researchers that devote their lives to studying the motions of the tibia and femur during knee flexion. You will base Knee Joint #2 (joint with relative translations and 3D rotations between the femur and tibia) on a reliable set of experimental data reported by Walker et al. (1988). Walker et al. measured tibiofemoral kinematics in 23 knee specimens. They tracked the motions of landmarks on the femur and tibia with radiographs while flexing and extending the knees by attaching a motor to the quadriceps tendon. The landmarks for each specimen were scaled to an average-sized knee and were used to determine the translations and rotations of the femur relative to the tibia through a range of knee flexion. The translations and rotations, averaged for the 23 specimens, were fit to polynomial equations as a function of knee flexion angle.

The polynomial equations reported by Walker et al. (1988) describe the varus rotation (VARUS), internal rotation (INTROT), superior translation (yDIS), and anterior translation (zDIS) of the femur relative to the tibia as functions of knee flexion angle (F). Here we've adopted the notation of Walker et al.; please see the paper for details. Walker et al.'s reference frames for the femur and tibia are defined as follows when the knee is in full extension (see Figs. 4 and below):

The **origin** is located at the midpoint between centers of spheres fit to the medial femoral condyle (MC) and lateral femoral condyle (LC).

The **X axis** (medial-lateral) is the vector that joins MC and LC.

The **Y axis** (superior-inferior) is the cross product of the vector parallel to the medial tibial plateau (Ant- Post) and the X axis, defined with the knee in full extension.

The **Z axis** (anterior posterior) is orthogonal to both the Y and X axes.

Your objective in this section is to implement Walker et al.'s description of tibiofemoral kinematics in your lower extremity model. To achieve this, use the polynomial equations in the Walker article to generate the `f5-f6` in the joint description `my_secondknee` below. The equations are as follows:

```
tx = ((-0.1283*F)+(4.796e-4)*F*F+7.5)*0.001
```

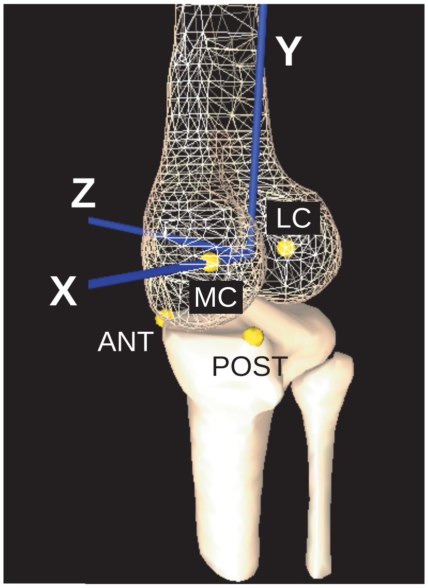


Fig. 4. Landmarks that define Walker et al's femur and tibia segment reference frames for a right limb specimen. Reference frames for the femur and tibia are coincident at full knee extension. **MC** is the center of a sphere fit to the medial posterior femoral condyle, **LC** is the center of a sphere fit to the lateral posterior femoral condyle, **ANT** is an anterior point on the medial tibial plateau, and **POST** is a posterior point on the medial tibial plateau.

```
ty = ((-0.0683*F+(8.804e-4)*F*F-(3.75e-6)*F*F*F )- 382.6)*0.001
```

NOTE: The equations are slightly different than the Walker article and we added an offset in the z-directions due to slight differences in the bone geometry. Then add two additional degrees-of-freedom for the knee rotations `knee_varus` and `knee_rotation`.

Add a segment to `lab3.jnt` using the segments `tibia_knee2.seg` and `fibula_knee2.seg`. Be very careful to account for differences in reference frames and sign conventions. Add the joint below to your joint file `lab3.jnt`.

```
beginjoint my_secondknee
segments lab3femur lab3tibia2
order t r1 r2 r3
tx constant f5(knee_flexion)
ty constant f6(knee_flexion)
tz constant 0.005
axis1 1.0 0.0 0.0
axis2 0.0 1.0 0.0
axis3 0.0 0.0 1.0
r1 constant f7(knee_varus)
r2 constant f8(knee_rotation)
r3 function f9(knee_flexion)
endjoint
```

Your kinematic functions should define yDIS, zDIS, INTROT, VARUS, and F over a 0 to 120 degree range of the generalized coordinate `knee_flexion`. Make sure that the signs of the rotations and translations are consistent with your model.

Now, reload your model and check Knee Joint #2.

To check your knee joint, your `lab3tibia2` bone should align with the `tibia` bone when the `knee_flexion` angle is 22.0 degrees.

Inspect how the tibia moves about the femur. Does the tibia have rolling and sliding motion? Does it exhibit any gapping between the tibial plateau and the femoral condyles? How does motion if Knee Joint #2 differ from the motion of Knee Joint #1? Does Knee Joint #2 look better than the hinge knee? Briefly answer these questions in your written report.

VII-D. Specify Muscle-Tendon Paths for the Semitendinosus

You have now completed the most rigorous part of the lab. In this section, you will represent the path geometry of the semitendinosus muscle in SIMM using a series of line segments. Your goal is to develop and implement a method to locate the muscle attachments and to specify wrapping surfaces and via points as needed to accurately characterize the muscle path over a range of motion. The hip and knee flexion moment arms computed with your model of the specimen should compare well with the muscle moment arms determined experimentally on the same specimen. Your method should be repeatable; that is, based on a written description of your method, someone else should be able to reproduce your muscle path geometry.

You might wonder, can't I just represent the muscle as a straight line from origin to insertion? When is it important to introduce via points and wrapping surfaces to simulate interactions between the muscle and surrounding structures? Do differences in the knee kinematics really affect the muscle moment arms enough to matter? Let's investigate these issues.

You will define three representations of the semitendinosus muscle path:

Muscle Path #1: straight line from origin to insertion, attached to the `lab3tibia2` segment
Muscle Path #2: series of straight lines constrained by via points and/or wrapping surfaces, attached to the `lab3tibia2` segment
Muscle Path #3: series of straight lines constrained by via points and/or wrapping surfaces, attached to the `lab3tibia1` segment

NOTE: If you combine via points with wrapping objects, SIMM first checks to see if there are any via points and implements them first, then checks to see if there are any wrapping objects. Therefore, when you use wrapping objects, you may want to remove all via points.

VII-D.1. Create and Evaluate Muscle Path #1.

<u>VII-D.1.1. Represent the semitendinosus as a straight line from origin to insertion.</u>

<u>FIRST</u>: Approximate the origin and insertion sites of the semitendinosus.

- Load `lab3.jnt` and `no_musc.msl`.
- Put the model in the scanned position:
  `hip_flexion = 24.6` degrees
  `hip_adduction = -5.45` degrees

`hip_rotation = 16.0` degrees
`knee_flexion = 22.0` degrees

Use the `Muscle Editor` tool to identify the coordinates of bone vertices that approximate the attachments of the semitendinosus on the pelvis and tibia. As a help, we have added `landmarks` to estimate the bone vertices of the origin and insertion points.

- Open the `Muscle Editor` tool. Make sure the `muscle points` is checked in the `Model Viewer`. Identify the 3D coordinates of a muscle attachment points of the semitendinosus origin and insertion. Write these coordinates in your report (Table 5).

SECOND: Define the semitendinosus attachments in the muscle file `lab3.msl`.

- Open `lab3.msl` in a text editor.
- Replace the first point in the `semiten_o2i` muscle definition with the semitendinosus origin that you found. Make sure that the point is attached to the `pelvis` segment.
- Replace the second point in the `semiten_o2i` muscle definition with the semitendinosus insertion that you found. Make sure that the point is attached to the `lab3tibia2` segment.

VII-D.1.2. Evaluate your straight-line semitendinosus path.

- Load `lab3.jnt` and `lab3.msl`.
- Visually inspect your muscle. Does it look anatomical? Does it penetrate any bones?

An important step in building a model is to evaluate its accuracy. It is critical to understand the limitations of your model. Through the process of testing a model, you can often identify ways to make the model more accurate.

In this section, you will evaluate the accuracy of the semitendinosus moment arms predicted by your model with the simple straight-line path. To do this, you will compare the moment arms calculated with your model to the moment arms determined experimentally. We measured the hip extension and knee flexion moment arms of the semitendinosus muscle (and other muscles) in your specimen. We determined the moment arms using the tendon displacement method (An et al., 1984). This experiment involved measuring the excursions of the muscle over a range of hip flexion and knee flexion angles. Moment arms (*ma*) were calculated as the partial derivative of muscle-tendon length ($\partial \ell$) with respect to joint angle (θ). That is,

$$ma = \frac{\partial \ell}{\partial \theta}$$

The hip flexion moment arms were determined with the specimen’s hip adduction, hip rotation, and knee flexion angles equal to zero. The knee flexion moment arms were determined with the specimen’s hip flexion, hip adduction, and hip rotation angles equal to zero. For more details on the experimental setup, see Arnold et al., 2000.

To compare the moment arms predicted by your model of the semitendinosus to the experimentally determined moment arms:

<u>FIRST</u>: Plot the hip flexion and knee flexion moment arms of your `semiten_o2i` muscle.

To plot the hip flexion moment arms versus hip flexion angle:

- Set the model's hip adduction, hip rotation, and knee flexion angles equal to zero.
- Open the `Plot Maker` tool.
- `Left mouse click` on `y variable > moment arm > hip_flexion`
- `Left mouse click` on `muscles > all`
- Click on `semiten_o2i`.
- `Left mouse click` on `make curves`.

To plot the knee flexion moment arms versus knee flexion angle:

- `Left mouse click` on `plot > new plot`
- Set the model's hip flexion, hip adduction, and hip rotation angles equal to zero.
- `Left mouse click` on `y variable > moment arm > knee_flexion`, `x variable > knee_flexion`.
- `Left mouse click` on `make curves`.

<u>SECOND</u>: Plot the experimental data superimposed on the corresponding curves.

From the `File` menu, open the following plot files corresponding to the experimental data (they are in the `Plotfiles` directory).

`st_hipflexion.plt`
semitendinosus hip extension moment arms vs. hip flexion angle

`st_kneeflexion.plt`
semitendinosus knee flexion arms vs. knee flexion angle

Make sure you superimpose the experimental data onto the appropriate plot.

<u>THIRD</u>: Write each plot to a file.

- From the `File` menu, select `Save Plot`.
- Select the plot format: `plot format >`
  `ASCII`: Writes the plot in ascii format. This does not write the curve corresponding to the experimental data. You can access the experimental data by opening the input plot files (in your `plotfiles` directory).
  `Postscript`: Writes the plot in postscript format. The curves corresponding to the experimental data will be included in the figure.

- Edit the `name` of the plot file as you like.

The plot file should be written to your `outfiles` directory. Include these plots in your written report, and comment on the validity of representing the semitendinosus path geometry as a straight line from origin to insertion.

VII-D.2. Create and Evaluate Muscle Path #2.

How well did your straight-line path match the experimental data? Here's your chance to develop an improved method for defining the muscle path over a range of motion. You have three options for refining the path geometry of a muscle in SIMM:

- Refine the attachments
- Add via points
- Introduce wrapping surfaces

VII-D.2.1. Refine your semitendinosus path by specifying via points and wrapping surfaces.

- In your muscle file `lab3.msl`, copy the muscle definition for `semiten_o2i` to a new muscle named `my_semiten`.
- Save `lab3.msl` and reload your model.

Refine the attachment sites for your new muscle `my_semiten`. Add a wrapping surface (see Section VII-D.2.3) and any necessary via points. Save your changes (see Section VII-D.2.2). Iterate until you are satisfied with the agreement between the hip and knee flexion moment arms calculated with your model and the moment arms obtained from the experiment.

When defining your muscle path, you should follow these rules:

- Attachments must lie within the 3D muscle surface and on the surface of the pelvis (origin) and tibia (insertion).
- Via points must lie within the 3D muscle surface when the limb is in the scanned position.
- Only one wrapping surface can be used.

The optimal muscle path will:

- not penetrate bones or other muscles over a -15 to 90 degree range of hip flexion and a 0 to 120 degree range of knee flexion
- predict hip and knee flexion moment arms that compare well with the moment arms determined experimentally (average error less than 10%)
- predict moment arms curves that are continuous and smooth

Once you have settled on your final semitendinosus muscle path, plot the hip and knee flexion moment arms compared to the experimental data. Include these plots in your report. Summarize your method for representing the muscle path geometry. How did you define the attachments? What was your rationale for locating the wrapping surface and/or via points? Which of these parameters are the moment arms most sensitive to? If you didn't have experimental data for reference, how confident would you be in the moment arms predicted by a kinematic musculoskeletal model?

VII-D.2.2. Learn some helpful (and slightly random) SIMM hints.

To SAVE changes to a model from within SIMM:

- Select the model of interest and from the `File` menu, select `Save Joints` or `Save Muscles`
- Edit the name of the `output joint file` or `output muscle file` as you like.
- `Click` on `Save` to write the joint or muscle file.
- You might want to save all your files to your `outfiles` directory.

NOTE: When a file is saved from within SIMM, it will not include any of the comments or special formats that were in the original file. Our recommendation is to never write over your original file. After you have saved the output file, open both your original file and the output file. Copy the changes in your output file to your current working version of the original file (and perhaps comment what you changed). This way you can more easily preserve the comments and formats in your original joint and muscle files.

To use a SIMM motion file to define the "scanned" position:

- Since the 3D muscle surface is defined in the scanned position, you will reference this limb position frequently when refining your semitendinosus path. If you want, you can create a motion file with only one entry—the scanned position—and load the motion file with your model. This way you can put the model in the scanned position by simply clicking on the slider bar that corresponds to the “motion.” Refer to the SIMM manual (Chapter 3) for how to create a SIMM motion file.

VII-D.2.3. Learn some SIMM hints for defining wrapping surfaces.

You can use the `Wrap Editor` tool to constrain a muscle’s path to wrap over a wrap object.

To add a new wrap object:

- `Click` on `wrap object > new wrap object`.
- Name the object in the `name` field.
- `Click` on `segment` > ___ to attach the object to a segment.
- `Click` on `muscles > all` and select `my_semiten`.

NOTE: Currently, SIMM only allows a muscle to wrap over one wrap object at a time.

To change the size and shape of your wrap object:

- Specify the geometric primitive: `sphere`, `cylinder`, or `ellipsoid`.

- Edit the values of the `radii` and/or `height` of your wrap object.

NOTE: For the purposes of this exercise, you probably do not need to worry about the wrapping `method` parameter and the `constrain to quadrant` parameter. If you would like more information about these parameters, please see the SIMM manual (Chapter 2).

To manipulate the position and orientation of your wrap object:

If the `trackball` check box in the wrap editor is checked:

- Press the `w key` and `left mouse button` to translate the object within the plane.
- Press the `w key` and `right mouse button` to rotate the object.
- Press the `w key` and click and drag the object around.

If the `trackball` check box in the wrap editor is NOT checked:

- Press the `w key` and `left` or `right mouse buttons` to rotate the object about the x, y, or z axes. If the `transform in local frame` radiobutton is selected, then the wrap object will rotate about its local x, y, and z axes. If the `transform in parent frame` radiobutton is selected, then the wrap object will rotate about its parent segment's x, y, and z axes.

To temporarily save your wrap object:

- `Click` on `save` to temporarily save your changes.
- `Click` on `restore` to revert to the last saved model.

NOTE: Clicking on `save` in the `wrap editor` tool does not save the wrap object to a file.

To save your wrap object to a file:

- Open the `File > Save Joints` and `Save Muscles`.
- Save both the joint and muscle files.

The wrap object definition is saved in the joint file. Here is an example of a wrap object definition:

```
/* WRAP OBJECT: example */
beginwrapobject example_wrap_object
wraptype ellipsoid
segment lab1femur
xyz_body_rotation 0.00 0.00 0.00
translation 0.00 0.00 0.00
radius 0.05 0.02 0.05
endwrapobject
```

This wrap object is an ellipsoid (`wraptype`), attached to the `lab1`femur segment (`segment`) with its origin (`translation`) and axes (`xyz_body_rotation`) oriented with the `lab3femur` segment's reference frame. The radii (`radius`) of the ellipsoid are: 0.05, 0.03, and 0.05. See the SIMM manual (Chapter 3) for more details.

The name of the object over which the muscle wraps is saved in the muscle file:

```
beginmuscle example_muscle_that_wraps
beginpoints
-0.09029 -0.11766 -0.08387 segment pelvis
-0.02503 -0.03921 0.02126 segment tibia
endpoints
wrapobject example_wrap_object
endmuscle
```

VII-D.3. Create and Evaluate Muscle Path #3.

In this section, you will study the sensitivity of the semitendinosus moment arms to knee kinematics. Specifically, you will add a new muscle, `semiten_hinge`, to your muscle file, `lab3.msl`, whose path exactly aligns with the path of your final `my_semiten` muscle in the scanned position, but whose insertion is attached to the `lab3tibia1` segment. You will then compare the knee flexion moment arms of `semiten_hinge` computed about Knee Joint #1 (hinge joint about an axis through the epicondyles) with the knee flexion moment arms of `my_semiten` computed about Knee Joint #2 (joint with relative translations and 3D rotations between the femur and tibia).

VII-D.3.1. Attach Muscle Path #3 to the lab3tibia1 segment.

FIRST: Add a new muscle called `semiten_hinge` to your muscle file, `lab3.msl`:

- Open `lab3.msl` in a text editor
- Copy `my_semiten` to a new muscle called `semiten_hinge`.
- Edit `semiten_hinge` so that its insertion and other distal via points are connected to `lab3tibia1` (instead of `lab3tibia2`).
- In the definition for `semiten_hinge`, change the name of the `wrapobject` over which the muscle wraps to `st_hinge_wrap_object`.
- Save the muscle file.

SECOND: Add a new wrap object associated with `semiten_hinge` to your model files.

- Open `lab3.jnt` in a text editor
- Copy the wrap object you have defined for `my_semiten` to a new wrap object called `st_hinge_wrap_object`
- Edit `st_hinge_wrap_object`, if necessary, so that it is connected to `Lab3tibia1` (instead of `lab3tibia2`):
- Save the joint file.

THIRD: Load your model.

- Load `lab3.jnt` and `lab3.msl`.
- Put the model in the "scanned" position.

VII-D.3.2. Analyze the sensitivity of the semitendinosus moment arms to knee kinematics.

Plot the knee flexion moment arms for the `my_semiten` and `semiten_hinge` muscles compared to the experimental data. Include these plots in your report.

Summarize your knee kinematics-moment arms sensitivity study by answering the following questions:

- How and why are the moment arms of the two muscles different?
- Do you think the differences in the knee kinematics affect the muscle moment arms enough to matter?
- For what applications might a hinge joint knee be sufficient? When would a hinge knee not be sufficient?

VII-E. Discussion

In your written report, comment on the factors that influence the accuracy of muscle moment arms computed with a kinematic musculoskeletal model.

What techniques might you use (computational or experimental) to increase the accuracy of a model if necessary?

VIII. References

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