

## Tutorial 1 - Joint Model Personalization

The Joint Model Personalization (JMP) tool optimizes joint parameters, body scaling, and marker placement to minimize IK marker distance errors. Reducing inverse kinematics marker distance errors reduces downstream errors in calculated inverse dynamic joint moments, muscle–tendon lengths and velocities, muscle moment arms, and ultimately muscle activations and forces. These quantities are used by subsequent Model Personalization tools.

The inputs to JMP are a scaled generic OpenSim model, kinematic marker data from one or more motion trials, and a JMP settings file. This tutorial will explore the creation of JMP settings file using both the NMSM Pipeline GUI in OpenSim, and by directly editing the settings file in a text editor.

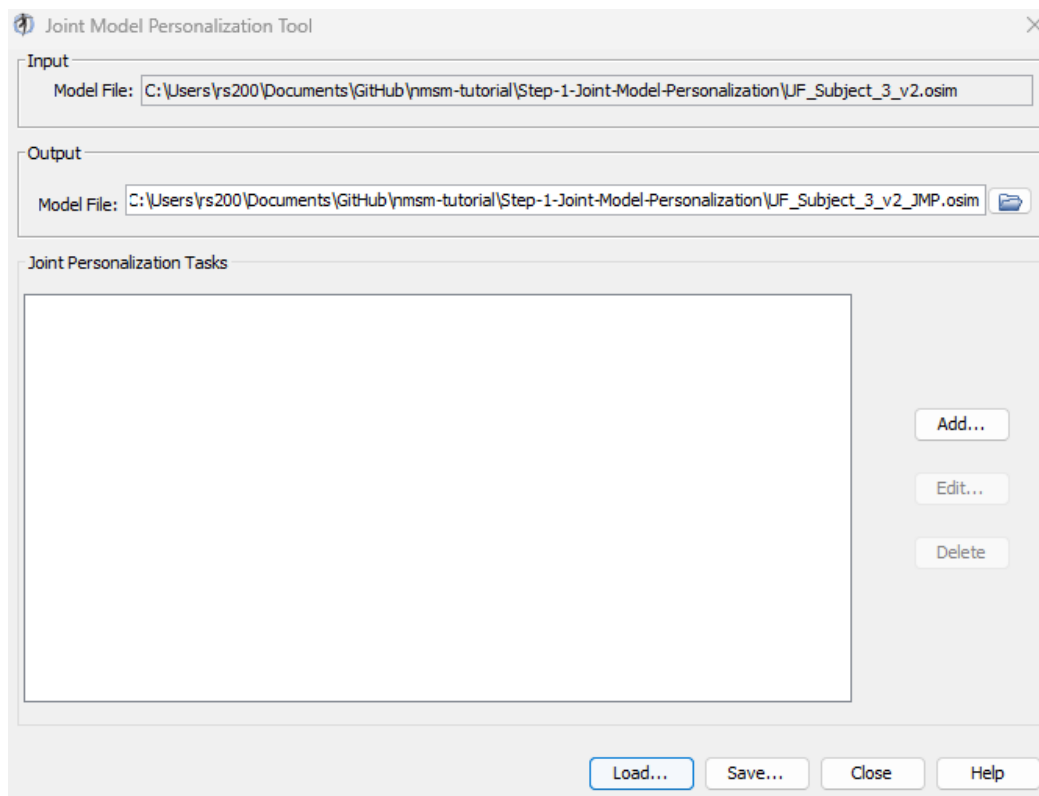
### Before running JMP:

The primary input to a JMP run is a scaled generic OpenSim model. JMP is designed for small adjustments to model parameters, so large scaling adjustments should still be done with OpenSim's *Scale Model* Tool.

1. Open **RCNL2023.osim** in the OpenSim GUI.
2. Open the *Scale Model* Tool.
3. Load the settings file **ScaleSettings.xml**.
4. Run the scale tool
5. With the new model **UF\_Subject\_3\_v2** selected in the *Navigator* window, click on the *Coordinates* window.
6. Lock **knee\_adduction\_r** and **knee\_adduction\_l**
  - a. The knee adduction angle models varus/valgus deformity and doesn't change much during gait. The scale tool modifies this angle using static pose data, and then we don't change it afterwards.
7. Save the scaled model as **UF\_Subject\_3\_scaled.osim**.

## Setting up a JMP settings file:

1. Activate the NMSM GUI in OpenSim by navigating to *Tools>User Plugins*, and click **rcnlPlugin.dll**
2. Open **UF\_Subject\_3\_scaled.osim** in the OpenSim GUI
3. With **UF\_Subject\_3\_scaled.osim** selected in the OpenSim GUI, navigate to *Tools>Model Personalization>Joint Model Personalization*
  - a. The following window should be opened:



4. Rename the output model file to **UF\_Subject\_3\_scaled\_JMP.osim**
5. Create a new JMP Task:
  - a. Name this task **Hips and Knees**
  - b. Select the *Markers File* to be **MarkerFiles\GaitTrial\_markers.trc**
  - c. Include the *markers* (**R\_Asis L\_Asis Sacral R\_Thigh\_Superior R\_Thigh\_Inferior R\_Thigh\_Lateral R\_Shank\_Superior R\_Shank\_Inferior R\_Shank\_Lateral R\_Heel R\_Midfoot\_Superior R\_Midfoot\_Lateral L\_Thigh\_Superior L\_Thigh\_Inferior L\_Thigh\_Lateral L\_Shank\_Superior**)

**L\_Shank\_Inferior L\_Shank\_Lateral L\_Heel L\_Midfoot\_Superior  
L\_Midfoot\_Lateral)**

- d. Add a new joint to this task.
  - i. Joint name: **knee\_r**
  - ii. Parent frame translation: **None**
  - iii. Parent frame rotation: **X-, Y- axes**
  - iv. Child frame translation: **None**
  - v. Child frame rotation: **X-, Y- axes**
- e. Add a new joint to this task.
  - i. Joint name: **knee\_l**
  - ii. Parent frame translation: **None**
  - iii. Parent frame rotation: **X-, Y- axes**
  - iv. Child frame translation: **None**
  - v. Child frame rotation: **X-, Y- axes**
- f. Add a new body to this task:
  - i. Body name: **pelvis**
  - ii. Scale body: **true**
  - iii. Move markers: **Y-axis**
- g. Add a new body to this task:
  - i. Body name: **femur\_r**
  - ii. Scale body: **No**
  - iii. Move markers: **X-, Y-axes**
- h. Add a new body to this task:
  - i. Body name: **femur\_l**
  - ii. Scale body: **No**
  - iii. Move markers: **X-, Y-axes**
- i. Add a new body to this task:
  - i. Body name: **tibia\_r**
  - ii. Scale body: **No**
  - iii. Move markers: **Y-axis**
- j. Add a new body to this task:

- i. Body name: **tibia\_l**
  - ii. Scale body: **No**
  - iii. Move markers: **Y-axis**
- 6. Create a new JMP Task:
  - a. Name this task **Move markers**
  - b. Select the *Markers File* to be **MarkerFiles\GaitTrial\_markers.trc**
  - c. Select the *markers* (**R\_Thigh\_Lateral R\_Thigh\_Superior R\_Thigh\_Inferior R\_Shank\_Superior R\_Shank\_Inferior R\_Shank\_Lateral**)
  - d. Add a new body to this task:
    - i. Body name: **femur\_r**
    - ii. Scale body: **No**
    - iii. Move markers: **Y-, Z-axes**
  - e. Add a new body to this task:
    - i. Body name: **tibia\_r**
    - ii. Scale body: **No**
    - iii. Move markers: **Y-, Z-axes**
- 7. Save the settings file as **JMPSettings.xml**
- 8. Open **JMPSettings.xml** in a text editor of your choice, and explore the document

## Running JMP:

1. Open MATLAB and open **runJMP.m** in your tutorial directory.
2. Open the project file (**Project.prj** inside your installation of nmsm-core.)
3. Ensure MATLAB is set up to use multi-processing, not multi-threading:
  - a. In the bottom left of MATLAB, click the parallel processing icon, and click *parallel preferences*.
  - b. In the drop down menu for *Default Profile*, select **Processes**.
4. Run the MATLAB file **runJMP.m**

## Post JMP Analysis:

1. In the OpenSim GUI, open **UF\_Subject\_3\_scaled\_JMP.osim**.
2. Visually inspect this new model compared to **UF\_Subject\_3\_scaled.osim**. What changed?
3. Analyze the plots created by **runJMP.m**
  - a. How do the post-JMP marker errors compare to the `<max_allowable_error>` specified in the settings file?
  - b. Note that the biggest reductions in error are around peaks. If the error was already low, JMP doesn't make a big difference.

## Alternate JMP Formulations:

The JMP run we did in this tutorial was a “sequential” run. We personalized the knee first, then the hip, and then moved markers. This approach potentially has errors because the personalization of one joint can affect the IK results of another joint. An alternative approach is to personalize every joint at once. This approach generally takes longer to run but has the potential to reduce error even further because all joint errors are being minimized simultaneously.

You can explore simultaneous JMP runs versus sequential JMP runs by creating new settings files with the knee, hip, and ankle for both sides. For the sequential run, every joint and body

should have its own task, and for the simultaneous run, everything should be in a single task. With the simultaneous run, you should change your `<max_function_evaluations>` field to a large number such as 2000. Plot the marker errors for the two runs against each other and compare results.