Tutorial 3 – Muscle-tendon Personalization

The Muscle–tendon Model Personalization tool finds an optimal set of subject-specific muscle–tendon properties and muscle activations from EMG, joint kinematic, and joint moment data by balancing optimization cost function terms related to muscle properties, similarity of properties among grouped muscles, and matching of EMG-driven and experimental inverse dynamics joint moments. Muscle activation and force predictions are sensitive to optimal muscle fiber length and tendon slack length. Therefore, reliable personalization of these parameters is essential for generating reliable predictions of muscle activations and forces during predictive simulations of movement.

The inputs to the MTP tool are a post-JMP OpenSim model as well as IK motion, ID load, muscle–tendon length and velocity, and muscle moment arm data from one or more motion trials of interest.

1. **Before running MTP:**
2. Open the OpenSim model “UF\_Subject\_3\_reduced\_muscles.osim” in the OpenSim GUI.
3. Under the “Forces” tab on the model, explore the muscles available.
4. Take note of the extra groups added.
   1. These are added for organization so that MTP/NCP knows which model muscles to group together in the optimization.
   2. The four important groups are:
      1. Activation Muscle Groups – Muscles that we would expect to have similar activation profiles (ie lateral hamstrings; BFSH and BFLH will have similar activations to each other)
      2. Normalized Fiber Length Muscle Groups – Muscles that we would expect to have similar normalized fiber lengths.
      3. Collected EMG Muscle Groups – Muscle groups that we **do** **have** experimental EMG data for. These must have the same name as the respective EMG channel name your EMG data file (preprocessed\EMGData\gait\_1.sto)
      4. Missing EMG Muscle Groups – Muscle groups that we **do not** **have** experimental EMG data for.
   3. These groups need to be created manually in a text editor such as Notepad++, but we have example groups for lower limb models in the “NMSM Article” download on SimTK: <https://simtk.org/frs/?group_id=2397>
5. **Setting up an MTP settings file:**
6. Activate the NMSM GUI in OpenSim by navigating to “Tools>User Plugins”, and click “rcnlPlugin.dll”
7. With “UF\_Subject\_3\_reduced\_muscles.osim” selected in the OpenSim GUI, navigate to “Tools>Model Personalization>Muscle-tendon Personalization”
   1. The following window should be opened:

A screenshot of a computer

AI-generated content may be incorrect.

1. Leave the Osimx File field empty. This tool outputs an Osimx file, but we do not have one to work with yet. If this field is filled out, the MTP tool will concatenate new elements to the existing Osimx file.
2. For the data directory, select the “preprocessed” folder in the tutorial directory.
3. Set the results Directory to be “MTPResultsV1”
4. For the coordinate list, select: [hip\_flexion\_r, knee\_angle\_r, ankle\_angle\_r].
5. For activation muscle groups, select [HipFlexorsActivationGroupR, GlutmaxActivationGroupR, HamslatActivationGroupR, VasActivationGroupR, GasActivationGroupR]
   1. Tip: The filter box at the top is very helpful to filter only activation groups
6. For normalized fiber length groups, select [GlutmaxNormalizedFiberLengthGroupR, HamsNormalizedFiberLengthGroupR, VasNormalizedFiberLengthGroupR, GasNormalizedFiberLengthGroupR]
7. For missing EMG muscle groups, select [HipFlexorsMissingEMGChannelGroup]
8. For collected EMG muscle groups, select [GlutMaxLat, RecFem, BicFemLong, BicFemShort, VastMed, GasMed, Sol, TibAnt]
9. Enable Muscle Tendon Length Initialization (MTLI) and set the passive data input directory to “passive\_moment\_data”
10. Enable Muscle tendon Synergy Extrapolation (SynX) with 3 synergies.
11. Save this settings file as “MTPSettingsV1.xml”
12. Open up MTPSettingsV1.xml in a text editor of your choice and explore the settings file.
    1. What elements could you directly edit in the GUI?
    2. Were there any elements that show up in the file that you didn’t specify in the GUI?
    3. Why do some cost terms have error centers while others don’t?
    4. Where do you think the default values for max allowable error and error center for each term came from?
    5. Explore the optimization settings near the top of the settings file. These can be edited to change how fast the optimization will terminate.
13. **Running MTP:**
14. Open MATLAB and create a new script called runMTP.m in your MTP tutorial directory.
15. In the script, type: MuscleTendonPersonalizationTool("MTPSettingsV1.xml")
16. To plot results, type: plotMtpResultsFromSettingsFile("MTPSettingsV1.xml")
17. Press Run
    1. Make sure the NMSM project file is open!
18. **Post MTP Analysis:**
19. Look through the plots created by the script. If everything was done correctly, there should be 6 plots.
    1. Plot 1 – Joint Moment Matching: Joint moments generated by muscle forces (with and without SynX) compared to Inverse Dynamics joint moments.
    2. Plot 2 – Muscle Activations: Muscle excitations and activations (with and without SynX) for all muscles included in the MTP run.
    3. Plot 3 – Normalized Fiber Lengths: Normalized fiber lengths for all muscles included in the MTP run. Red dashed lines at 1.0 and 0.6 indicate the optimal working range for muscles.
    4. Plot 4 – Passive Muscle Force: The passive force generated by each muscle in the MTP run. This plot is only generated if MTLI is enabled.
    5. Plot 5 – Passive Joint Moment Matching: The passive moment matching achieved by the MTLI optimization.
    6. Plot 6 – Hill-type Muscle Model Parameters: The muscle model parameters for all optimized muscles in this MTP run. These parameters are the primary output of the MTP tool.
20. Explore the Osimx file created in the MTP results directory. This file is used as an input for the Neural Control Personalization (NCP) tool, and for Treatment Optimization tools if using synergy controls.
21. **Experiment with different numbers of synergies:**
22. Open MTPSettingsV1.xml in a text editor of your choice.
23. Change the results directory to mtpResultsV2
24. Change the number of synergies in SynX to 4.
25. Save this settings file as MTPSettingsV2.xml
26. Run this new settings file in MATLAB.
27. To compare different MTP runs, type: plotMtpResultsFromSettingsFile("MTPSettingsV1.xml", "MTPSettingsV2.xml")
    1. This will create a lot of results plots.
28. Questions:
    1. Which number of synergies had the lowest joint moment matching error? Is this expected?
    2. What might be the benefits or drawbacks of using more synergies for SynX?
    3. Did the muscle model parameters change significantly between runs? Which muscles changed the most? Of the muscles that changed the most, do they cross the same joint as the Iliacus, or a different joint?
29. **Run MTP without SynX:**
30. Open MTPSettingsV1.xml in a text editor of your choice.
31. Change the results directory to mtpResultsV3
32. Disable SynX.
33. Save this settings file as MTPSettingsV3.xml
34. Run this new settings file in MATLAB.
35. To compare different MTP runs, type: plotMtpResultsFromSettingsFile("MTPSettingsV1.xml", "MTPSettingsV3.xml")
36. Questions:
    1. Compare the joint moments and muscle excitations/activations in this MTP run to the dashed red lines in your first MTP run. Why do you think the solutions are different?
       1. Hint: The dashed red lines are constructed simply by removing the muscles without SynX from joint moment calculations.
    2. Which solution do you think is better? Why?