# Dynamic Joint Measurement Analysis – Standard Operating Procedures

Test Case – Data

The test case data provided includes three individuals surgically treated with tibiotalar arthrodesis and their untreated contralateral limb (AD\_02, AD\_04, and AD\_10), two individuals surgically treated with total ankle replacement and their untreated contralateral limb (TAR\_04 and TAR\_06), and two healthy asymptomatic controls (Norm\_01 and Norm\_03). The data for each of these participants is in participant-specific folder within their respective *Subj* groups.

When processing your own data be sure to have it in a similar folder structure.

* Each participant group has its own folder (Group Folder)
  + Within the group folder each participant for that group will have their own folder

**Data for each participant includes:**

(*Subj* = Subject Group Identifier [AD, TAR, and Norm])

*Subj\_##\_*Calcaneus\_groomed.vtk (Not included but needed if not aligned in ShapeWorks. See below.)

*Subj\_##\_*Calcaneus\_groomed\_local.particles

*Subj\_##\_*Calcaneus\_groomed\_world.particles

*Subj\_##\_*Calcaneus\_*Side*.stl

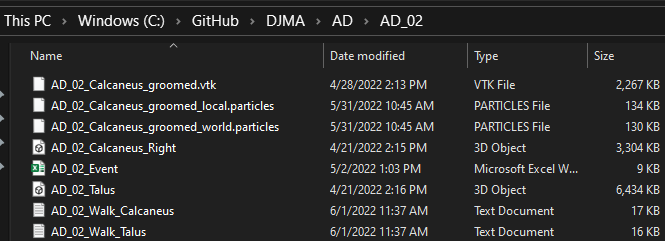
*Subj\_##\_*Talus.stl

*Subj\_##\_*Event.xlsx

*Subj\_##\_*Walk\_Calaneus.txt

*Subj\_##\_*Walk\_Talus.txt

**Participant-specific Folder Example**



**Data generation and descriptions:**

For each of the files below when using your own data set, they do not need have the exact same names. The DJMA\_01\_Kinematics\_to\_SSM.m script reads in the file type not the file name. You can use whatever naming convention you would like, given that the respective bone file names are consistent, e.g., Calcaneus and Talus apart from adding *\_Side* in .stl files aligned outside of ShapeWorks (see below).

*Subj\_##\_*Calcaneus\_groomed.vtk

* This file is necessary if the bones were aligned outside of ShapeWorks before the statistical shape model was created. (The shape model for the test case was aligned in ShapeWorks so the .vtk is not included)
* Exported from ShapeWorks. Can be exported as a .vtk or .ply file and will work.
  + Optimize Tab > File > Export > Current Mesh
* This file is used to align (using iterative closest point algorithm) the bone with correspondence particles to identify correspondence particle and node pairing.

*Subj\_##\_*Calcaneus\_groomed\_local.particles

* Exported from ShapeWorks. Both the local and world particles will be exported.
  + Optimize Tab > File > Export > Current Particles
* This file contains the correspondence particle 3D locations within the local space. This local space is whatever coordinate system the bones were in when imported into ShapeWorks. If bone models were imported into ShapeWorks straight from the segmentations they will live within the imaging space that the segmentations were generated in (CT, WBCT, MRI, etc).

*Subj\_##\_*Calcaneus\_groomed\_world.particles

* Exported from ShapeWorks. Both the local and world particles will be exported.
  + Optimize Tab > File > Export > Current Particles
* This file contains the correspondence particle 3D locations within the world space. The world space is the coordinate system after any pre-processing within the groom tab (such as aligning).

*Subj\_##\_*Calcaneus\_*Side*.stl

* Calcaneus bone model file that was imported into ShapeWorks to create SSM and is in the coordinate space that the transformation matrices are applied to. In the example case all these files are within the CT coordinate space.
  + *\_Side* needs to be ‘Left’ or ‘Right’ unless you are aligned within ShapeWorks.
  + If ­*\_Side* is not included, it will assume that the bone model is a ‘Right’ and will not flip during the alignment section of code (see section starting at Line 240 of DJMA\_01\_Kinematics\_to\_SSM.m)

*Subj\_##\_*Talus.stl

* Talus bone model file and is in the coordinate space that the transformation matrices are applied to. In the example case all these files are within the CT coordinate space.

*Subj\_##\_*Event.xlsx

* This file is used for normalizing the events to percentage of stance.
  + [heelstrike frame, first frame tracked, last frame tracked, toe off frame]

*Subj\_##\_*Walk\_Calcaneus.txt

* This file contains the 4x4 transformation matrices. The below identity matrix example shows how for one frame the matrix is changed for every four delimited values are a row of the transformation matrix.
* Identity Matrix transformed to -> 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1 0, 0, 0, 0, 0, 1
* Each row is a frame.

*Subj\_##\_*Walk\_Talus.txt

* This file contains the 4x4 transformation matrices. The below identity matrix example shows how for one frame the matrix is changed for every four delimited values are a row of the transformation matrix.
* Identity transformed to -> 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1 0, 0, 0, 0, 0, 1
* Each row is a frame or time step from the tracked biplane fluoroscopy overground walking activity.

**Mean\_Models Folder Example**

A screenshot of a computer

Description automatically generated with medium confidence

When running the DJMA\_03\_SPM\_Analysis.m for visualization of the joint measurement and statistical parametric mapping results the bone models and their respective correspondence particle files are required.

**Data generation and descriptions:**

Mean\_*Subj.stl*

* Group specific mean shape from the SSM and exported from ShapeWorks
  + Analyze Tab > Group > Difference – Group Set (1) – *Select the Group* (2) > *Select Mean* (3) > File > Export > Current Mesh (For reference see below figure)

Mean\_*Subj*\_Particles.particles

* Group specific correspondence particle locations from the SSM and exported from ShapeWorks
  + Analyze Tab > Group > Difference – Group Set (1) – *Select the Group* (2) > Select Mean(3) > File > Export > Current Particles (For reference see below figure)

MeanShape.stl

* Overall mean shape from all of the subjects created and exported from ShapeWorks
  + Analyze Tab > Group > Overall Mean > File > Export > Current Mesh

MeanShape\_Particles.particles

* Overall mean shape from all of the subjects created and exported from ShapeWorks
  + Analyze Tab > Group > Overall Mean > File > Export > Current Particles

Graphical user interface

Description automatically generated

**1**

**2**

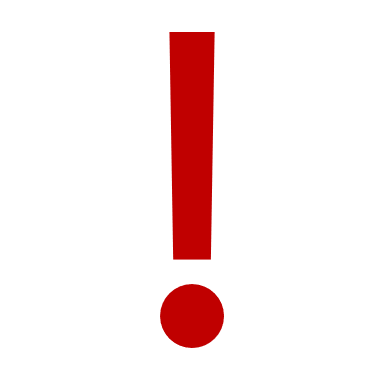
**3**

Test Case – How to process the data

There are three main scripts for processing the data.

1. DJMA\_01\_Kinematics\_to\_SSM
   1. Calculates the joint space distance and congruence index at paired calcaneal indices during the dynamic walking activity using transformation matrices obtained from tracked markerless biplane fluoroscopy. Compiles and saves each individual participant’s results to a data structure and into a .mat file (Data\_*Subj\_##*.mat) for use in DJMA\_02. These .mat files are saved within the participant specific folders.
2. DJMA\_02\_Data\_Process\_and\_Normalize
   1. Loads the data structures created in DJMA\_01 and truncates and normalizes the data to common percentages of stance. It then compiles the data into a single .mat file in the main directory for use in the DJMA\_03 script.
   2. You will be able to select the group folder that you wish to process, and they will only be truncated and normalized between those groups. For consistency we suggest processing all the groups together as you will be able to make group comparisons in DJMA\_03.
3. DJMA\_03\_SPM\_Analysis
   1. Performs the temporal statistical parametric mapping analysis on the normalized data from DJMA\_02. It will also create .tif files of the joint measurement data that are stitched together to make a .avi file to visualize the results.

**DJMA\_01\_Kinematics\_to\_SSM.m**

**Disclaimer:** This script will take the longest to run and is the most computationally expensive portion of the DJMA process. Depending on your computer you will have varying computational times. The machine used for processing the data for the manuscript had an AMD Ryzen 9 5950X 16-Core Processor and 64 GB of DDR4-32000 RAM. With 16 workers it took on average 180 seconds per frame (excluding the first frame) to calculate the joint space measurement data. Future work may implement further developments for optimizations and reduce computational time.

**Toolboxes:**

You will need the Parallel Computing Toolbox for Matlab. To process the data in any feasible amount of time the parpool function is implemented.

**Variables to be updated**:

Line 22: bone\_names – needs to be updated with the names of the bones of interest with the exact spelling and capitalization of the bone file names. In the example data set this is {‘Talus’,’Calcaneus’}.

Line 68: overwrite\_data – will need to be changed if you would like to overwrite existing .mat files from previous iterations or continue from the last saved frame and participant. Setting to 1 will overwrite the current .mat files for a participant and 0 will load the participant .mat files and continue from the last saved. The current code will save every 50 frames. To change how often it will save go to Line 678 and change the 50 in the statement “if rem(frame\_count,**50**) == 0”.

Line 81: pool = parpool([1 100]); The 100 for initiating the parallel pool is so that it will grab as many as it can on your computer. If you are not wanting to commit all your resources and workers to the parallel pool change the 100 to the maximum number that you would like to allocate for computing.

**Running the script:**

After arranging the files into the appropriate folder structures and updating variables, it is time to start crunching some data.

Open and run the Matlab script DJMA\_01\_Kinematics\_to\_SSM.m. You will be prompted with a popup asking how many study groups you would like to process. For the example data set you can run each group individually by entering 1 or batch process all 5 in tandem by entering 5.

Graphical user interface, application

Description automatically generated

After entering the number of study groups you will need to select the folder for each group. This will be done one at a time and will process from first selected to last.

There is a tic toc function to measure the elapsed time for each frame processed. This is to help give an idea how long it will take to process the data for a participant.

**DJMA\_02\_Data\_Process\_and\_Normalize.m**

**Toolboxes:**

**Variables to be updated**:

**Running the script:**

The DJMA\_02\_Data\_Process\_and\_Normalize.m script will normalize and truncate the data to consistent percentages of stance for the data measured from the DJMA\_01\_Kinematics\_to\_SSM.m script. When you run it, you will be asked to enter the number of study groups and then prompted to select the folders just as you did with DJMA\_01. It is important to note that it will only normalize across those that are selected. I suggest selecting all your groups, or all 5 in the example data set, so they are consistent, and it will be easier to make comparisons in the last DJMA\_03 script.

The results from this script will be stored in a structure and saved as a .mat file with a name ending in ‘SPM\_Data.mat’ within the DJMA folder. The beginning of the file name will be concatenated with the names of the groups processed (e.g., ‘AD\_Control\_NonAD\_NonTAR\_TAR\_SPM\_Data.mat’).

**DJMA\_03\_SPM\_Analysis.m**

**Toolboxes:**

You will need the SPM toolbox listed below.

<http://www.spm1d.org/install/InstallationMatlab.html>

**Variables to be updated**:

Depending on which joint you are evaluating or your constraints, you will want to adjust the distance at which the joint space distance at a particle is removed from the analysis.

Line 19: Distance\_Upper – sets the upper limit and any group mean joint space distance measurements above this will be removed from the analysis. This will also remove it from the congruence index comparison as well.

Line 22: Distance\_Lower – sets the lower limit. There should not be anything lower than 0 unless you are having overlap of the bones in which case something went wrong and you should investigate your transformation matrices or the .stl files for the bones to ensure that they are in the right coordinate space.

Line 24: view\_perspective – sets the angles for the view perspective of the .tif files. This may need to be adjusted based on where your data is on the bone surface to get good visualization.

Line 294: video.FrameRate – change the frame rate of the .avi video files created.

**Files needed:**

You will need to export from ShapeWorks the group specific MeanShape.stl and MeanShape.particles for each of the groups and place them in the folder Mean\_Models. If they follow the similar naming structure of Mean\_*GroupName*.stl and Mean\_*GroupName*\_Particles.particles, and the *GroupName* matches the name of their group folder, then you will not need to make any changes to load these files into the script.

**Running the script:**

You will be prompted to select the .mat file to load and then have you select the two groups you want to process and compare. **The first group you select will be the group results displayed in the figures.** So, to get both sides of the comparison you will need to run both groups twice, flipping which one is selected first upon running it the second time. The results are individual .tif files. These files will be populated within a ‘Results’ folder created by the script. The Particles\_*GroupName* folder will contain each of the individual .tif files in sequential order.

The naming convention may be confusing but is as follows. The first group identifier in the file name is which group’s results are displayed followed by ‘vs’ and the group it is compared against.

For example: Congruence\_Index\_AD\_vs\_TAR.tif – this image will have the tibiotalar arthrodesis congruence index results displayed on the arthrodesis group’s mean calcaneus shape from SSM and at any correspondence particle where the results were determined to be statistically significant when compared to the TAR group will have a pink circle placed on the particle.

After each of the .tif files are created it will create a .avi file in the Particles\_*JointMeasurement* folder. The frame rate is set to 7 fps. You can change this setting on Line 294.

Now you should have some results!