**Purpose:**

The purpose of this standard operating procedure is to walk you, the user, through the joint measurement analysis (JMA) toolbox. This toolbox will allow you to import bone models (.stl files) and calculate joint space distance and congruence index at correspondence particles. These correspondence particles can easily be created from ShapeWorks.

**Scope:**

**Notes:**

**Programs Used:**

Statistical shape model from <http://sciinstitute.github.io/ShapeWorks/latest/>

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

MATLAB from <https://www.mathworks.com/>

Parallel Computing Toolbox

Statistics and Machine Learning Toolbox

**Pre-requisites:**

Correspondence particles from a statistical shape model (.particles file)

Bone models or reconstructions (.stl files)

Kinematic data (if desired) from biplane fluoroscopy or other motion capture (.txt files)

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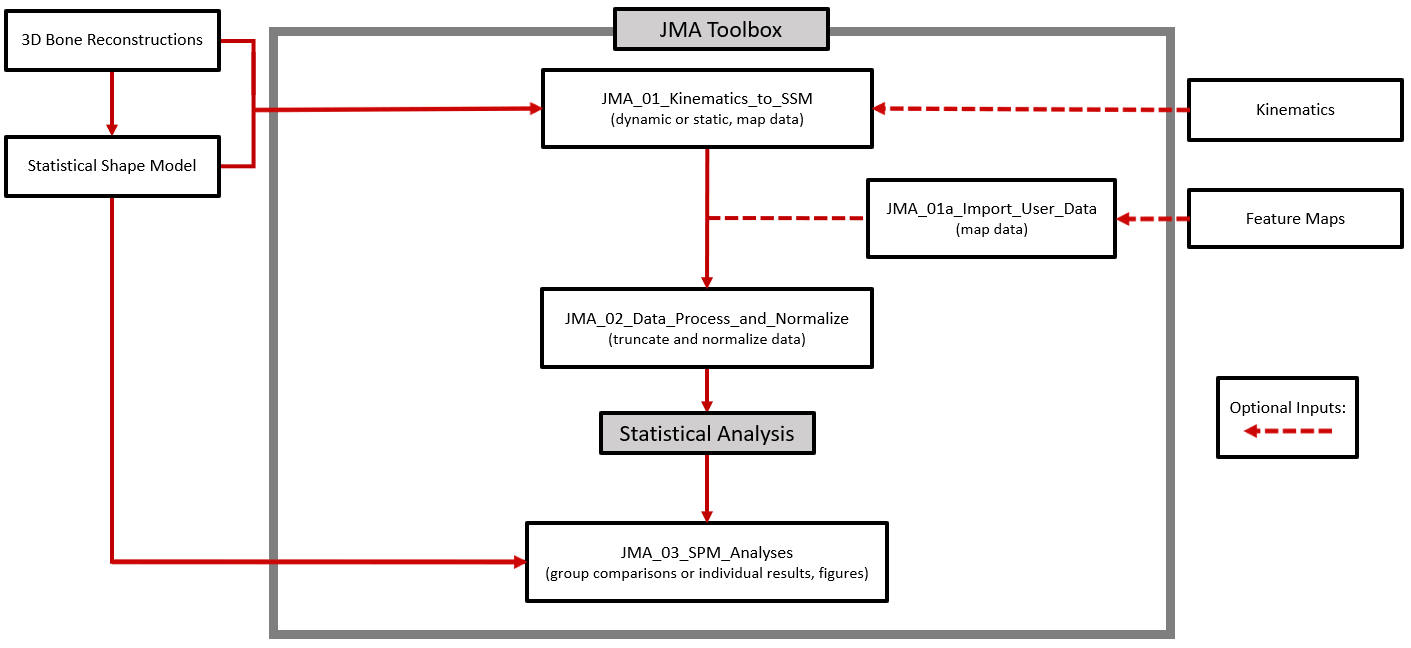
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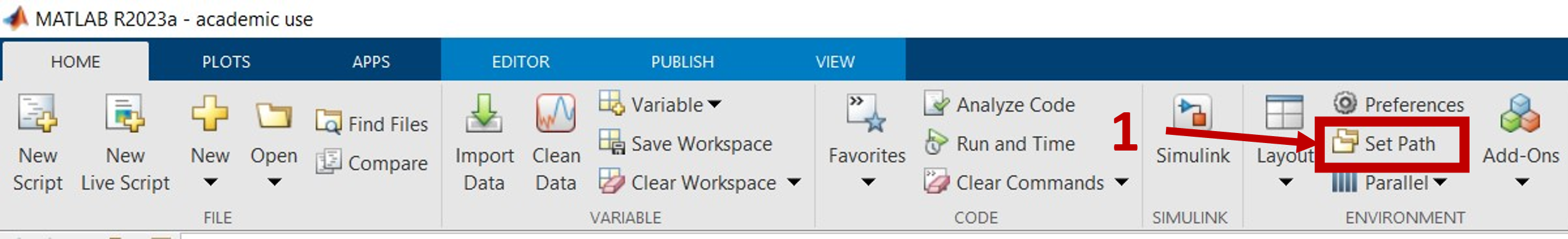
**Procedures:**

# **Workflow**

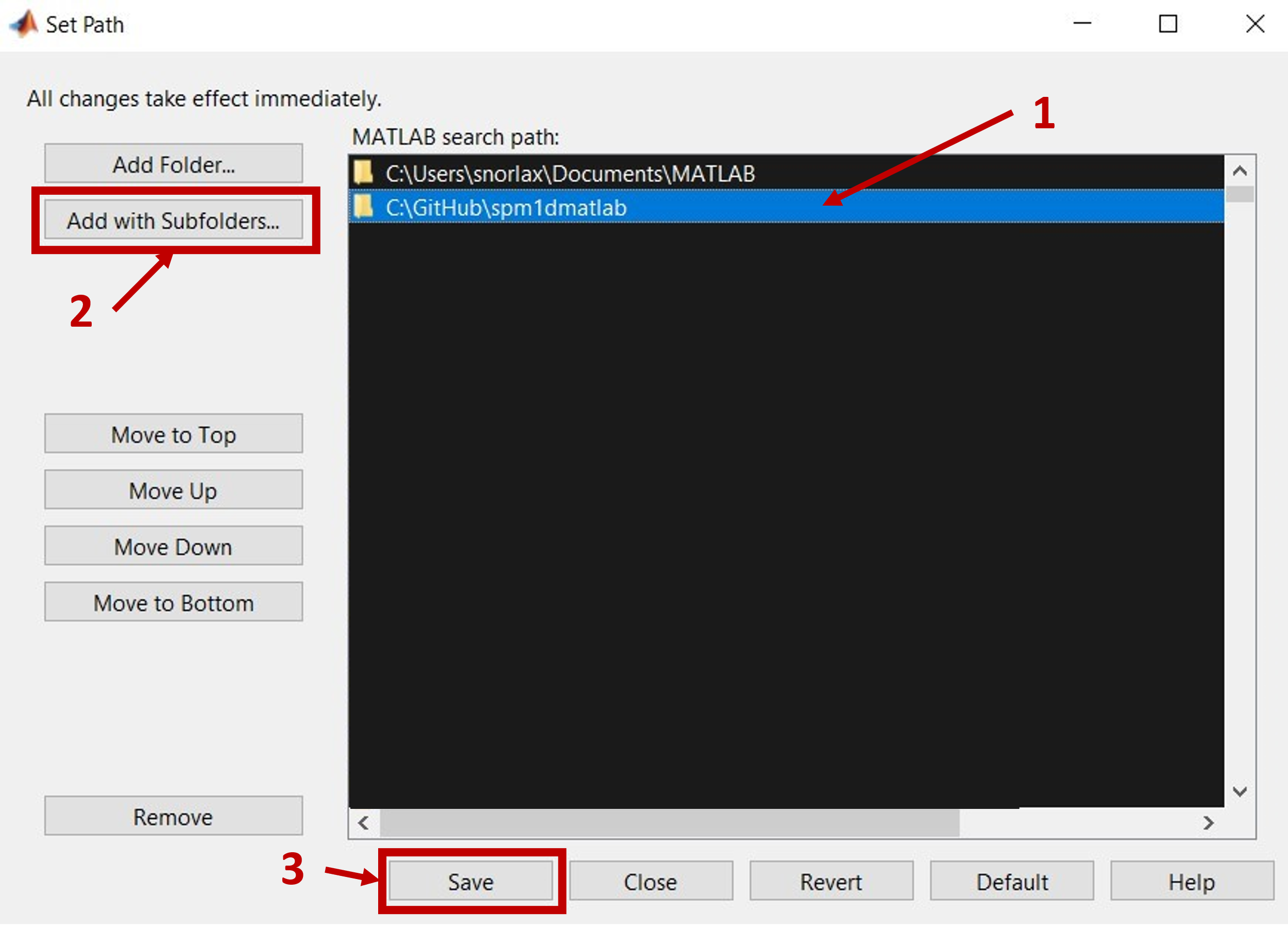


# **Statistical Parametric Mapping (SPM) Toolbox**

* 1. Download the spm1D package (<https://spm1d.org/>), extract wherever you need, and then add the package to the MATLAB path. This will allow the spm1D package to be called upon from any function or script without needing to be in the same file path.

****

*MATLAB > Home > Set Path (1)*

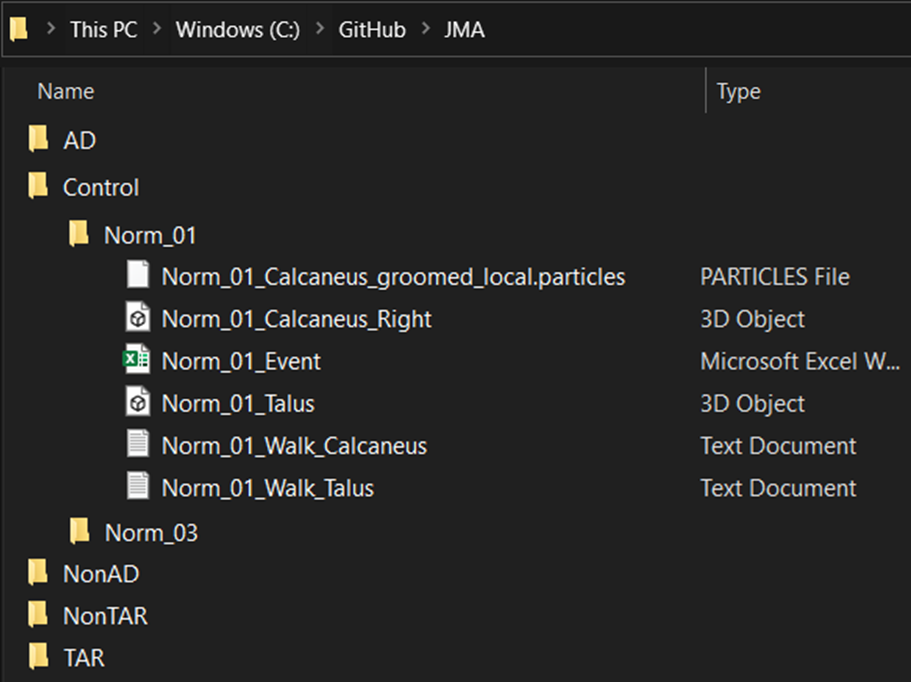
****

*Select the folder location (1) > Add with Subfolders… (2) > Save (3)*

# **Participant Files**

* 1. **Creation of participant-specific files:**

In order to run the JMA you will need to have several specific files for each participant placed in a nested folder. The idea is that these folders are created so it should be easy point and click to run. You will only need the Event spreadsheet and kinematic text files if you are conducting a dynamic analysis using the toolbox.

****

* 1. **Kinematic files** (.txt)
     1. **Purpose:** The kinematic files contain bone-specific 4x4 transformation matrices for each frame (or time point) of a tracked activity. The purpose of this is to transform the bone models to their tracked location for each frame. ***This file is not necessary for single time point static JMA.*** If the .txt file is not within the participant-specific folder the script will assume a static single time point and will automatically proceed using an identity matrix.
     2. **Naming Convention:** In order for this script to load the data properly it just needs to have the name of the bone within its filename. The spelling needs to be consistent and specific as one of the user inputs of the JMA\_01 script is the names of the bones.
     3. **Format:** Within the file each row is a single frame or time point and there are 16 columns. Every four values are a row of the 4x4 matrix. For example, when constructing an identity matrix in this format it will look like this: [**1,0,0,0,0,1,0,0,0,0,1,0,0,0,0,1]** with each color denoting a different row.
  2. **Event files** (.xlsx or .csv)
     1. **Purpose:** The event file is for truncation and normalization of the data to percentage of the activity. From the test dataset it is from heel-strike to toe-off. ***This file is not necessary for single time point static JMA or if you do not have specific events that you would like to normalize to.*** If you would like to normalize to the tracked activity and have provided a kinematic file that is longer than one time point, then by not including this file it will normalize to the length of the kinematic file (i.e., the length of the activity).
     2. **Naming Convention:** In order for this script to load the data properly it just needs to have the name of the bone within its filename. The spelling needs to be consistent and specific as one of the user inputs of the JMA\_01 script is the names of the bones.
     3. **Format:** Within the file it will have a single row and 4 columns. It will be truncated to common percentages of the normalized activity from the first tracked frame to the last tracked frame. The frame selected for heel-strike frame will be 0% and the frame selected for toe-off frame will be 100% of the normalized activity. From the test dataset the excel sheet will have [**first tracked frame, heel-strike frame, toe-off frame, last tracked frame**].
  3. **Bone files** (.stl)
     1. **Purpose:** The bone models are the surfaces that the distances and curvatures will be calculated from. These bone models should be smoothed, decimated, and the mesh resolution constructed to your needs. It is recommended that you mesh with edge lengths that result in a high-resolution mesh, as a sparse mesh will lead to erroneous measurement calculations. For example, the test dataset each bone was meshed with a maximum edge length of 0.5 mm and then smoothed to eliminate rough triangle edges. The coordinate space of these bone models should be those that match the kinematic transformation matrices.
     2. **Naming Convention:** Each of the bone .stl files will need to have the name of the bone in the filename. The spelling needs to be consistent and specific as one of the user inputs of the JMA\_01 script is the names of the bones. So, if there are any variations or inconsistencies from what you input into JMA\_01 you will have issues and the files will not properly load. For any specific joint analysis at least one of the .stl bone files of that joint will need to have the laterality of those bones included in the name. This can be done by including “\_right\_”, “\_left\_”, “\_R\_”, or “\_L\_” (upper or lower case it doesn’t matter) somewhere within the file name. For example, if you were running JMA on the subtalar joint, as in the test dataset, you will need to include the laterality in either the talus or the calcaneus .stl filenames, *ParticipantID*\_Talus\_left.stl. If no laterality is included in either of the .stl filenames it will be assumed that they are a right sided limb. Laterality is needed as the kinematic files are likely not reflected to match the reflection of the bones needed for a good correspondence model within ShapeWorks (right is the assumed convention here).
  4. **Correspondence Particle files** (local.particles)
     1. **Purpose:** The correspondence particle files for each participant are outputs from ShapeWorks and can be found within its project file. The world.particles particle locations are on the surface of the models from the groom steps. The local.particles particle locations are on the surface of the models when they are imported into ShapeWorks. This toolbox uses the **local.particles** and aligns the bone model to their respective correspondence particles using an iterative closest point algorithm in order to pair bone model surface nodes to the correspondence particles. If you ran Procrustes on your shape model and insert world.particles into the participant-specific folders, you will run into issues. Namely it will not map correctly because of difference in scale and JMA\_01 will crash. Verify that you are using the correct particle files and bone model .stl files.
     2. **Naming Convention:** In order for this script to load the data properly it just needs to have the name of the bone within its filename. The spelling needs to be consistent and specific as one of the user inputs of the JMA\_01 script is the names of the bones.

# **Study Group Files**

**Creation of group files (Mean\_Models folder):**

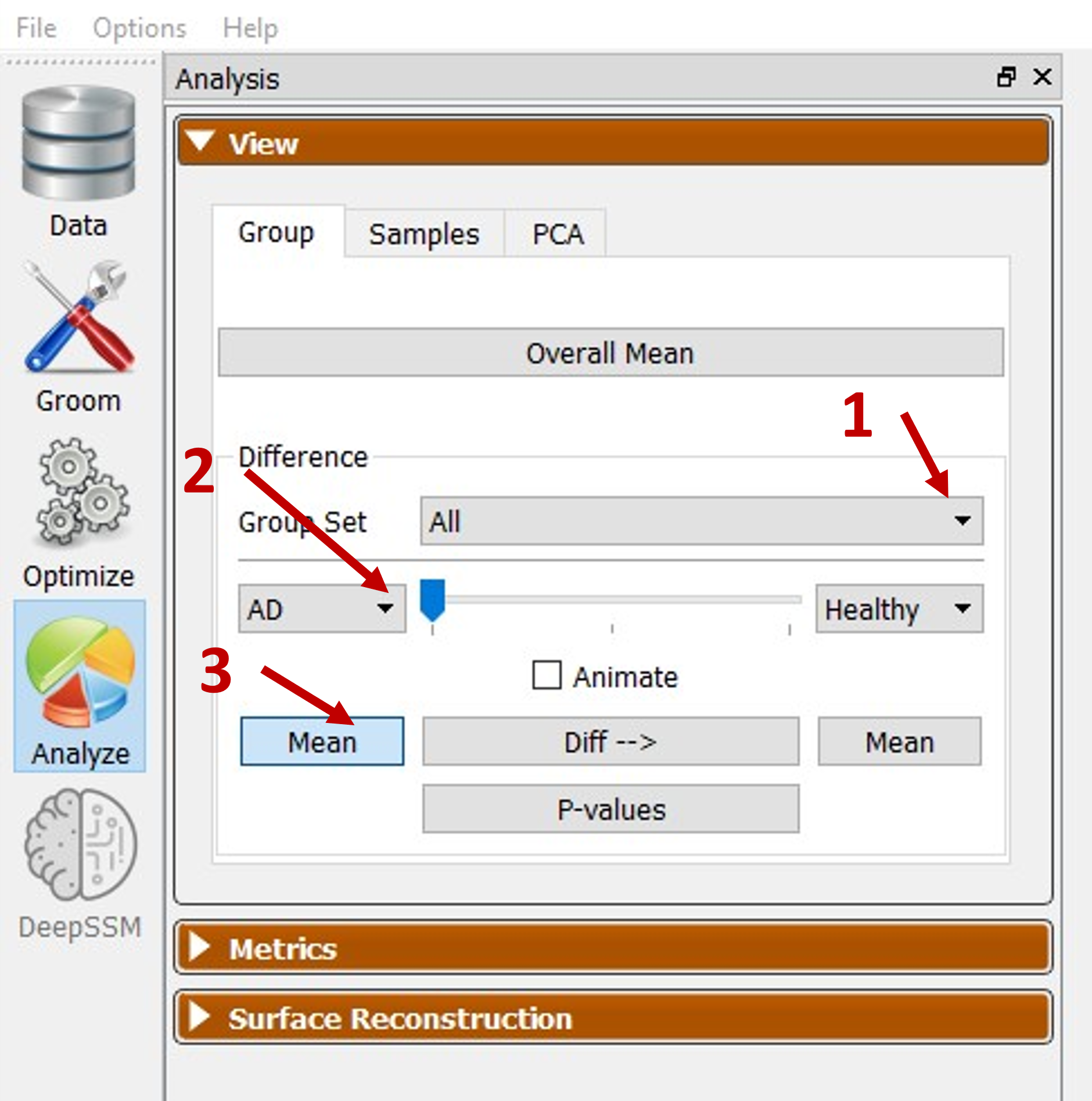
* 1. **Bone files** (.stl)
     1. **Purpose:** The mean shape of a study group is used for creating figures showing the joint space results. See the figure below for example of how to locate where to export the mean shape for a specific group. From this same place you can also export the correspondence particles for that study group mean shape. (See below figure for example)

*ShapeWorks > Analyze > Group Set (1) > Group (2) > Mean (3) > File > Export > Current Mesh*

* + 1. **Naming Convention:** In order for this script to load data properly it just needs to have the name of the bone and the study group within its filename separated by underscores (e.g., *Mean\_StudyGroup\_BoneName.*stl).
  1. **Correspondence Particles** (.particles)
     1. **Purpose:** The mean shape of a study group is used for creating figures showing the joint space results. See the figure below for example of how to locate where to export the mean shape for a specific group. From this same place you can also export the correspondence particles for that study group mean shape.

*ShapeWorks > Analyze > Group Set (1) > Group (2) > Mean (3) > File > Export > Current Particles*

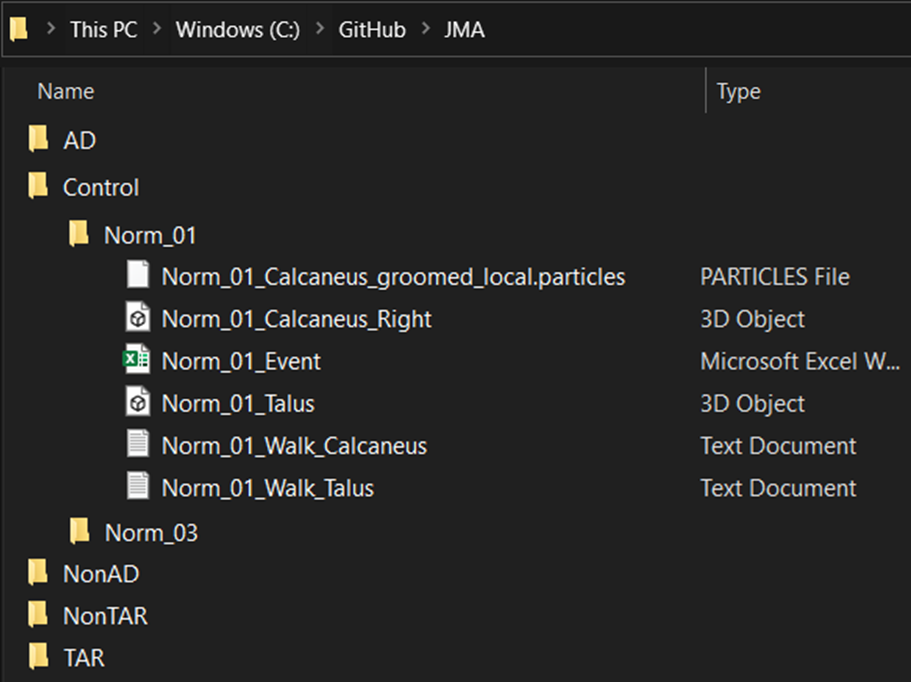
* + 1. **Naming Convention:** In order for this script to load data properly it just needs to have the name of the bone and the study group within its filename separated by underscores (e.g., *Mean\_StudyGroup\_BoneName.*particles).



# **Data Consolidation**

**Consolidate data for each participant:**

* 1. The JMA Toolbox operates out of a project directory and therefore you will need to copy/move files into folders within that location to be able to proceed. It is suggested to place outside of the JMA directory so that your data is not deleted by GitHub when pulling any future releases. A test case dataset has been included within the toolbox GitHub repository as an example. Please see below section **Test Case Data** for more information on the included dataset.
  2. The JMA Toolbox utilizes study group folders with nested participant-specific folders to load and save data (see below figure). Each study group will have its own folder (e.g., Controls, Pathologic, etc.) and nested within each of those folders will be that study group’s participant-specific folders containing the necessary files. The name of the study group folder (AD, Control, NonAD, etc.) and the name of the participant-specific folders dictates the names of the data structures used in the MATLAB script. A few things to note, the names should not start with numbers as this will cause the scripts to crash (cannot be structure names starting with numbers), cannot include hyphens or dashes (‘-‘), and the participant-specific folders do not need to match the study group folder name. The scripts will check each folder directory for specific file types and query the filename for identifying naming conventions (listed above in section 2) which includes the bone name and laterality.

****

* 1. **Importing your own data:**

If you want to import your own data to be compared at the correspondence particle locations, you just need to add an .xlsx or .csv file of the participant-specific data into their respective folders. Please refer to section 7 for more information.

# **Test Case Dataset**

**Test Case Dataset:** 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 respectivegroups.

# **Processing Data – JMA\_01 Mapping Data**

**Processing Data:**

* 1. **JMA\_01\_Kinematics\_to\_SSM.m**
     1. **Disclaimer:** This script will take the longest to run and is the most computationally expensive portion of the JMA 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 30 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. The number of faces on each of the surface files is what greatly affects this.
     2. **Running the Script:** After arranging the files into the appropriate folder structures you are ready to start processing some data.
* Open and run the MATLAB script JMA\_01\_Kinematics\_to\_SSM.m. You will be prompted with a popup asking you to enter user inputs.
* Enter the name of bone that data will be mapped to and therefore visualized on.
* Enter the name of opposite bone – this is the name of the opposing bone that distances from the previous bone will be calculated to.
* Enter number of study groups – this is how many groups you want to process; you can process them separately or consecutively.
* Would you like to overwrite previous data? – If selected it will save over previous .mat files for that specific joint. If selected it will start from the first frame and ignore previous .mat files. If it is not selected it will load any previous .mat files for that joint and continue where it was last saved.
* How often would you like to save the .mat file in case of interruptions? – Every x number of frames will save the structures to a .mat file. Only applies to dynamic and is especially helpful if running for long periods of time and in case of power outage, unexpected software updates, etc.
* Do you want to calculate the surface area on both bone surfaces? – Will calculate the surfaces not only on the mapped bone surface but also on the opposing surface as well. However, it will take double the time as it will need to calculate intersecting surface normal from the opposing surface as well.

Would you like to save coverage area .stl files for each time step? – Setting to 1 will save the coverage surface bone .stl files. Specifically, it will only save the mapped surface unless the surface area on both surfaces are being calculated (from previous input), in which case it will save both surfaces.

A screenshot of a computer

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* + - 1. **Location of data:** Nex you will be prompted to select the directory/folder where the data is located. Each script will ask you this so that it can path to the correct location.

# **Processing Data – JMA\_01a Import User Data**

**Processing Data:**

* 1. **JMA\_01a\_Import\_User\_Data.m**

The JMA\_01a\_Import\_User\_Data.m script will load data from spreadsheets and pair to their correspondence particles. The spreadsheets will need to be within each participant specific folder. The structure of this spreadsheet is as follows: the first column is the node indices and the following columns starting at cell B, are the data at that node for each time point. For example, see the figure below. The output structure and file names will be in lower case and will be named the spreadsheet name without the participant-specific identifier. **So, it is important to have the names other than the identifiers be consistent!** For example, if you are running it with FEA results a control participant could be called Control\_01 and the FEA data spreadsheet named FEA\_Control\_01.csv and the outputs for the FEA results will have ‘fea’ in their name rather than ‘Distance’ or ‘Congruence’.

Graphical user interface, table, Excel

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# **Processing Data – JMA\_02 Normalize Data**

**Processing Data:**

* 1. **JMA\_02\_Data\_Process\_and\_Normalize.m**
     1. The JMA\_02\_Data\_Process\_and\_Normalize.m script will normalize and truncate the data to consistent percentages of stance for the data measured from the JMA\_01 script. When you run it, you will be asked to enter the names of the bones and enter the number of study groups then prompted to select the folders just as you did with JMA\_01. It is important to note that it will only normalize across those that are selected. I suggest selecting all of your groups so they are consistent, and it will be easier to make comparisons in the stats JMA\_03 script.
     2. The results from this script will be stored in a structure and saved as a .mat file with a name starting in ‘Normalized\_Data’ within the …\Outputs\JMA\_02\_Outputs\ folder. The beginning of the file name will be concatenated with the names of the groups processed (e.g., ‘Normalized\_Data\_Calcaneus\_Talus\_AD\_Control\_NonAD\_NonTAR\_TAR.mat’).

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# **Processing Data – JMA\_03 Stats**

**JMA\_03\_Statistical\_Analyses.m**

* 1. The JMA\_03\_Satistical\_Analyses.m script has several options for comparing or visualizing results. Each statistical analysis is performed at each correspondence particle and currently is not spatially connected. Options for analysis include: Mann Whitney *t-*test and/or Wilcoxon rank-sum test, one-way ANOVA and/or Kruskal-Wallis test, temporal 1D statistical parametric mapping (SPM) analysis, group visualization, or individual participant visualization. ANOVA SPM has not been included to date, but will be in the future.

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* 1. **Running the script: User Inputs**
* Enter the name of the comparison. The script will automatically name any output based on what was selected and performed. However, adding a string here will place this name at the beginning of those names to make them easily identifiable. This is helpful when making figures with different colormaps, viewing perspectives, or simply wanting to keep them separate from other outputs.
* Alpha Value – the threshold for statistical significance
* Frame Rate – only applicable for dynamic analyses but sets the framerate for the saved video

A screenshot of a computer

Description automatically generated

* If any option other than SPM or individual results was selected, you will be prompted to enter the minimum percentage of participants that must be included for each group. What this is asking is if you want to include in the analysis any correspondence particles that do not have data for each participant within a group. In short, reducing this percentage will likely increase the number of particles visualized, but may not have results for each participant. This is likely due to morphology or kinematic differences. When making comparisons with SPM, to be included, a particle must have data for each participant or SPM will not work properly. The other comparisons on the other hand are not connected or corrected across time and are handled on a frame-by-frame basis. Therefore, you can set the threshold for the minimum amount of data needed at a particle to be included. It is important to note that there is a minimum of 5 participants within each group needed in order to perform a Shapiro-Wilk normality test.

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* Would you like to include multiple results (more than one bone, or one bone with multiple results mapped)? This option allows you to visualize multiple results on the same figure. The limit thresholds will be applied across all results. See examples below.

A screenshot of a computer

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A screenshot of a computer

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* + Example multiple results on one bone (Calcaneus: Subtalar and Calcaneocuboid joints):

A colorful dot pattern on a white surface

Description automatically generated

* + Example results on multiple bones (Tibia: Tibiofibular joint, Talus: Talofibular joint):

A close-up of a white object

Description automatically generated

* 1. **Running the script: Selecting and loading .mat file**

A screenshot of a computer error

Description automatically generated

Select the project directory.

A screenshot of a computer error

Description automatically generated

Then select the .mat file(s) with the normalized data to be processed. It will have the title Normalized\_Data\_*BoneName1\_BoneName2\_StudyGroup1\_...StudyGroupN*.mat. The field *BoneName1* is the bone with the correspondence particles and *BoneName2* is the opposing bone. It will then list off the groups included in the .mat file. This is so that multiple variations can be run and saved from the same directory depending on your needs.

A screenshot of a computer error message

Description automatically generated

If not SPM, then you will be asked to select groups. Select all of those that you wish to include (if only two are selected it will perform t-test or rank-sum, if more than two are selected it will perform ANOVA or Kruskal-Wallis test). Otherwise, if SPM you will be asked to pick the two groups to perform the comparison on.

* 1. **Running the script: Selecting first group to compare**

Graphical user interface, text, application

Description automatically generated

The first group to compare is which study group bone model will be used and that group’s mean results will be displayed on the bone model. Select the first group and select “OK”.

* 1. **Running the script: Selecting the second group to compare**

Graphical user interface, text, application

Description automatically generated

The second group to compare is which study group the first group will be compared against. If measurements at a correspondence particle are statistically significant (p<0.05) they will be circled in pink. Select the second group and select “OK”.

* 1. **Running the script: Select which data to analyze**

Select which data you would like to analyze, if more than one is selected (using shift or control click) you will process each of those selected. **NOTE: The colormap and figure settings will be the same for each. It may be beneficial to run separately.**

Graphical user interface, text, application

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The default is if any results at any particle are nonparametric it will default to only show nonparametric results. However, by choosing to combine the analyses onto the same plot it will show both parametric and nonparametric results. Meaning, that it will not omit parametric results. Since the normality test is performed at each particle some may be found to be normal while others are not. Obviously, if the results at a particle were found to be nonparametric only the nonparametric test results will be visualized for that particle, and vice versa.

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A screenshot of a computer error

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# **JMA\_03 – Figure Settings**

**Changing/Loading Figure Settings:**

* 1. **Loading figure settings:** You will not be given the option to load figure settings until you have saved them. Once populated in …\Outputs\JMA\_03\_Outputs you will be able to load previous settings.
  2. **Randomized data for visualization:** When configuring the figure settings, the correspondence particles are all those that have any data mapped to them, and the data at the particles are randomly created using a Gaussian distribution and some are randomly selected as statistically significant so you will be able to see what it will look like. Your data is not used as it has not had the stats performed on them yet. **Do not panic, these are for visualization only.**

A screenshot of a computer error message

Description automatically generated

A close-up of a structure

Description automatically generated

* + 1. Once the figure is generated you will be given the option to modify the figure settings, proceed with the current settings, or proceed and save the current settings.

A screenshot of a computer menu

Description automatically generated

* + 1. If you choose to modify the figure settings a menu will pop up with several options. Every time you select OK it will reload the figure with the new settings and give you the option to proceed or not. You can iterate and change the settings as much as you would like until you are ready to proceed.

A screenshot of a computer

Description automatically generated

* + - 1. **Glyph Size:** Scale the correspondence particle and ring glyphs
      2. **Ring Color:** Click to bring up several options. The two on the top right let you toggle between standard colors and custom colors (can enter RGB values here).
      3. **Viewing Perspective:** The two values are the figure perspective when it was populated. If the “capture current viewing perspective” is unchecked, you can manually enter values here to change to that perspective. MATLAB’s rotation within a 3D figure is not great and can clip. If this happens you may need to manually manipulate the .stl and .particle files for visualization externally and then reload them.
      4. **Bone Transparency:** Each of these values (currently showing one because only one bone is visualized) is a scalar for the transparency of that bone. The order is based on the order you selected from the .mat files.
      5. **Colormap:** Dropdown that lets you pick some default MATLAB colormaps. Note: if you do not see one that you would like to use, select “type in your own” and enter the name. An option to upload your own colormaps will be added in a future release.

A computer screen with a computer screen and a computer screen

Description automatically generated

* + - 1. **Check to capture current viewing perspective:** If this is checked when you select OK it will save the current viewing perspective of the figure.
      2. **Glyph Transparency:** Adjusts the transparency of the particle and the ring.
      3. **Load Figure Settings:** Dropdown that if any are selected will load them when you select OK. If you do not want to load any keep it as blank.
    1. **Changing Limits:** For each of the data you wish to analyze you will be able to set the colormap limits and flip the colormap. For example, below shows the Distance data limits. Note that it is Distance followed by the mean and the ±2 standard deviation. The editable field for distance is default set to 0 to 6 mm, while congruence index is set at 0 to the mean +2 standard deviations, and all other user loaded feature maps are -2 standard deviations and +2 standard deviations from the mean.
    2. **Set distance limits for removing particles from analysis:** The default is set at 0 to 6 mm. These values give the lower and upper limit. When performing the stats, any data will only be included if it the distance results at that particle for that individual are within these distance limits. This allows you to control what is included in the analysis as any results at a distance of 12 mm for example is likely too far away to realistically be in articulation and therefore should not be included in the analysis. These ranges may change from joint to joint and it is up to you to make the best call of what thresholds you should set.

A screenshot of a computer

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# **Interpreting Results – Location**

**Interpreting Results:**

* 1. **Finding the results:** All of the figures and videos created are saved in the “Results” folder. Within the Results folder there will be multiple folders created as you process and analyze data.
     1. Naming conventions:

*Comparison\_Data\_Bone1\_Bone2\_Extra*

Comparison: Name of the statistical test performed, or if no stats labeled as group or individual

Data: Distance, Congruence, or user imported name (fea, dea, etc)

Bone1: Bone data is visualized on

Bone2: Opposite bone

Extra:

\_diff if “Difference” colormap was selected

\_NonParametric if only nonparametric results were shown

\_Parametric if only parametric results were shown

\_combined\_*BoneName­* if a multi-result figure was created

* + 1. Data name is the name of the data structure (Distance, Congruence, etc.)
    2. Lastly the joint. The joint will be named by the two bone name inputs from the User Input prompt when it was executed. The first bone name is the bone with the data mapped correspondence particles and the second bone name is the opposing bone.
  1. Each stack of .tif images are saved into their respective folder and the .mp4 video will be saved one directory up of the location of the images used to create that video.

Graphical user interface, text

Description automatically generated

* 1. **Data structures:** Each of the output files are located in the “Outputs” folder and will have a specific folder for JMA\_01, JMA\_02, and Coverage\_Models. The .mat files in the JMA\_01 folder will contain compiled raw data from each participant. The .mat files in the JMA\_02 folder will have the truncated and normalized data for each participant and group within it. The .mat files in the JMA\_03 folder are the saved figure settings.
     1. **Coverage Models**

Each of the models for both bones will be saved following similar architecture within the SOP. Within the Outputs directory there will be a Coverage\_Models folder. Nested within the Coverage\_Models folder are the folders of each participant with saved coverage models, and they will be named following the *Bone1* and *Bone2* format and within their respectively named folders. **Note that these surface coverage models are created by intersecting normal calculations between the two full bone models**.

* + 1. **Coverage Area Results**

The coverage area results are saved to a spreadsheet following the bone name conventions used in every other output filename. The location of these spreadsheets are within the JMA\_02\_Outputs directory. Each row is the surface area calculated at that frame. **Note that these surface area calculations are not normalized to percentage of the activity.**

* + 1. **JMA\_02 .mat results**

The architecture of these truncated normalized data when loaded is as follows:

|  |  |  |
| --- | --- | --- |
| Variable Name | Type | Description |
| bone\_names | cell array | The names of the bones of the analyzed joint with the first being the bone with the mapped correspondence particles |
| DataOut | structure | Participant-specific mapped data at each particle across the normalized activity |
| DataOut\_Mean | structure | Group mean results at each particle across the normalized activity |
| DataOut\_SPM | structure | Compiled group results at each particle across the normalized activity |
| DataOutAll | structure | All of the results placed in one array, used for calculating mean and standard deviations of the data across the entire dataset |
| max\_frames | double | The total number of common percentages, used for iteration in future scripts |
| per\_stance | double | Common percentages of the normalized activity |
| SPM\_check\_list | structure | Logical cell array identifying particles at specific time points that are suitable for SPM analysis (1 = has data of each participant at that particle) |
| subj\_group | structure | The study group names and the participant identifiers within each group |

# **Frequently Asked Questions – FAQs**

* Q: Why are particles missing from the figure?

A: Could be for a variety of different reasons:

1. Depending on the percentage of participants that you selected it may not have enough participant’s data there to be included in the analysis (most often the case)
   1. This could be due to one or more participant’s morphology affecting the coverage area identification around that particle
   2. The particle in question is outside of the distance thresholds for one or more participants
2. Poor correspondence and gaps within the distribution of the correspondence particles

A close-up of a colorful structure

Description automatically generated

* Q: How do I run a Statistical Shape Model?

A: Perfectly good question, ShapeWorks is an open-source tool that is simple and easy to use to get started with. <https://www.sci.utah.edu/software/shapeworks.html>

* Q: Can I run multiple scripts at the same time?

A: With the parallel computing, you will not be able to as it will set aside “workers” to be dedicated for use within the script. This will also affect other desktop applications so it is suggested to not do anything major while the scripts are running.

* **If you have your own questions, please reach out!** [rich.lisonbee@utah.edu](mailto:rich.lisonbee@utah.edu)

|  |  |  |
| --- | --- | --- |
| **Revision Date** | **Revision Author** | **Revision Description** |
| 2023-08-23 | R. J. Lisonbee | Drafted |
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