

# KinematicsToolbox

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## Overview

The goal of KinematicsToolbox is to provide a complete data processing pathway for integrating radiographic motion capture data with anatomical models. This pathway includes initial radiographic motion capture protocol development (Design Module), calculating anatomical morphology (Morphology Module), calculating and visualizing joint kinematics, proximity patterns, and instantaneous helical axes (Analysis Module), and aggregating and compiling data within and between subjects (Compiler Module).

## Legal

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## Responsibilities of the User

This program was written and extensively tested by Becky Lawrence. However, there is no guarantee that the program is error-free both in terms of usability and accuracy. Consequently, it is the sole responsibility of the user to verify the accuracy of all results.

## Release Notes

### Major modifications

1. None.

### Minor modifications

1. AnalysisModule: Added the ability to visualize anatomical landmarks in the Motion Viewer.
2. AnalysisModule: Fixed bugs throughout the code that occurred when the ACS name is not the same as the segment name.
3. AnalysisModule: Added the ability to visualize the x-ray source in the lab setup in the Motion Viewer tab.
4. All modules: Made numerous changes to allow for software citation including removed software expiration date and added citation and license information to help menu.
5. AnalysisModule: Added the ability to visualize segment output ACS in the Proximities Viewer.
6. All modules: Ensured that the program cleared all variables upon exiting a module.

## Potential and Known Issues

1. The acetabular coordinate system has not yet been rigorously tested.

## Design Module

Goal: Simulate different biplane x-ray system configurations and subject positioning to assist in the protocol planning phase of a study. Currently, only shoulder scapular plane abduction can be simulated, but more joints and motions may be implemented in future versions.

### Menu Bar

#### File

Allows the user to load existing simulations, save the current simulation, and clear or quit the program.

- Open: Loads an existing simulation (keyboard shortcut: ctrl+O).
- Save: Saves the current simulation to a location specified by the user (keyboard shortcut: ctrl+S).
- Reset: Clears the current simulation from the program.
- Quit: Quits the program.

#### Load

Allows the user to load joints, motions, and biplane configuration presets.<sup>1</sup>

- Joints: Allows the user to load anatomical and kinematic data for different joint systems.
- Shoulder: Includes the humerus, scapula, and clavicle.
- Presets: Allows the user to load sample biplane configurations.
- Clinical c-arms: Loads a biplane configuration with two 12-inch image intensifiers (e.g., clinical c-arms).
- Custom system: Loads a biplane configuration with two 16-inch image intensifiers from a custom, high-speed system.

#### View

Allows the user to interact with the 3D plots in various ways.

- Rotate: Rotate the 3D plot in space (keyboard shortcut: ctrl+R).
- Pan: Pan (or shift) the view of the 3D plot in the plane of the viewer (keyboard shortcut: ctrl+P).
- Zoom: Zooms in and out of the 3D plot (keyboard shortcut: ctrl+Z).
- Data tips: Allows the user to click on a plot and get the coordinates of the point clicked (keyboard shortcut: ctrl+D).

#### Help

Provides information about the program, including help documentation and license and citation information.

- Help Documentation: Opens the help documentation.
- About: Provides information about the program (including version).
- License Information: Provides information about the license under which KinematicsToolbox is provided.

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<sup>1</sup> The program is currently only capable of simulating shoulder scapular plane abduction, but more joints and motions are planned for future versions.

- Citing KinematicsToolbox: Provides information about how to appropriately cite KinematicsToolbox.

## Running a Simulation

The program can be run by either creating a new simulation or by loading an existing simulation.

### Create a New Simulation

1. Select the joint system to be simulated by navigating to Load --> Joint.
2. Use the slider bars in the "System Distances" panel to define the source-to-image distance (SID) and image intensifier (II) distance for each system.
3. Use the slider bars in the "Biplane Geometry" to define the biplane configuration. This moves System #2 (red) relative to System #1 (green). The simulation will begin with the two biplane systems in the same position and orientation, which effectively results in a single plane simulation assuming the system distances are the same between System #1 and System #2.
4. Use the slider bars in the "Subject Positioning" panel to set the position of the research subject. Note that the kinematic descriptors (e.g., roll, pitch, yaw) describe the movement of the subject relative to System #1 (green).
5. Use the "Frame" slider bar in the "Subject Positioning" panel to simulate shoulder motion using the current system configuration.
6. Once a configuration is defined, the object-to-image distance (OID), source-to-object distance (SOD), image magnification, and effective image intensifier diameter are calculated for each system and reported in the "System Distances" panel. The "System #1" and "System #2" plots display simulated views for each system given the biplane configuration and subject positioning, and any image magnification that will occur. Any anatomy that falls outside the bounds of the simulated image intensifier will not be captured in a radiographic image. The "Laboratory View" plot displays simulated biplane configuration and subject positioning.

### Load Existing Simulation

1. Navigate to File --> Open and select the file to be loaded.

### Save Current Simulation

1. Navigate to File --> Save.
2. Specify the location and filename for the simulation to be saved.

## Morphology Module

Goal: Calculate anatomical morphology variables including a glenoid-based coordinate system, which may be used in the Analysis Module to describe glenohumeral kinematics. Bone-specific morphology calculations are currently limited to the scapula and humerus.

### Setting up the Parameter File

The parameter file provides all the necessary input for the program to run. A single parameter file may be used across multiple bones if the bones are on the same side of the body. If calculating morphology for two sides, a second parameter file is required.

#### Info Sheet

The purpose of this sheet is to provide basic information on the subject (i.e., subject variables) and technical specs. An unlimited number of subject variables can be specified by adding rows to the Excel sheet.

#### Subject parameters

- Subject ID: The study ID of the participant.
- Side: The laterality of the data. Valid input is Right (or R) or Left (or L). Required if calculating scapular and humeral morphology.

#### Project parameters

- Scale: The unit of distance (e.g., mm). Required. It is assumed that all STL files are on the same scale.
- Pixel size in X: The X pixel dimensions of the image stack that made the bone volumes. Required if anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking).
- Pixel size in Y: The X pixel dimensions of the image stack that made the bone volumes. Required if anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking).
- Pixel size in Z: The X pixel dimensions of the image stack that made the bone volumes. Required if anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking).
- Flip image axis: Specifies which axis (if any) to flip to express voxel coordinates relative to the original image stack. Required if anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking). Valid values are: FALSE, X, Y, or Z.

Note: If anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking), then the pixel size in X, Y, and Z and flip image axis are required.

#### Output Sheet

The purpose of this sheet is to specify the output directory for the results output files written by the program. Directories can be specified using absolute paths (e.g., "C:\user\data\output\") or relative paths (e.g., ".\output\"). It is highly recommended to use relative paths when specifying the location of the kinematic tracking files, STLs, etc. For more information on relative paths, see Appendix A – Relative Path Specification.

### Parameters

- **Destination:** The absolute or relative path to where the results should be written.

### Segments and ROIs Sheet

The purpose of this sheet is to specify information for the segments and ROIs that will be analyzed. ROIs can be full segments or portions of a segment (e.g., glenoid). An unlimited number of segments and ROIs can be specified. To add segments and/or ROIs, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names. The required file format for bone geometries is a binary STL. File paths can be specified using absolute paths (e.g., "C:\user\data\boneKinematics.csv") or relative paths (e.g., ".\boneKinematics.csv"). For more information on relative paths, see Appendix A – Relative Path Specification.

### Parameters for each segment/ROI

1. **Name:** Specifies the name of the segment/ROI.
  - Value1: Segment or ROI name. Names must be unique and cannot contain spaces. Required.
  - Value2: ignored.
  - Value3: ignored.
2. **Type:** Specifies whether the anatomical volume is a segment or an ROI.
  - Value1: Valid inputs are segment or ROI. Required.
  - Value2: ignored.
  - Value3: ignored.
3. **STL path:** Specifies the path for the segment/ROI STL. Required.
  - Value1: The absolute or relative path for binary STL for the segment/ROI.
  - Value2: ignored.
  - Value3: ignored.
4. **Image stack dimensions:** The dimensions of the image stack used to create the 3D bone mode. These parameters are required if anatomical landmarks are to be digitized and need to be reported in voxel coordinates (e.g., for use in HFHS MarkerlessTracking).
  - Value1: stack dimension in X
  - Value1: stack dimension in Y
  - Value1: stack dimension in Z

### Anatomical Landmarks

The purpose of this sheet is to specify information regarding the anatomical coordinates to be digitized in preparation for kinematic tracking and/or to be used for morphology calculations. An unlimited number of landmarks can be specified. To add landmarks, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names.

### Parameters for each anatomical landmark

- **Name:** Specifies the name of the anatomical landmark. Required
  - Value1: Landmark name. Names must be unique and cannot contain spaces.
  - Value2: ignored.
  - Value3: ignored.
- **Associated segment:** Specifies the name of the segment to which the landmark belongs. Required.



- Value1: Segment name. Names must be specified exactly (case insensitive) as they are listed in the Segments and ROIs sheet of the parameter file.
- Value2: ignored.
- Value3: ignored.
- **Type:** Specifies the type of landmark based on how it will be defined. Required.
  - Value1: Landmark type. Valid inputs are:
    - Digitize, when landmark coordinates will be manually digitized within the program
    - Specify, when landmark coordinates will be specified in the parameter file
    - Midpoint, when landmark coordinates will be calculated as the mean of two landmarks
    - Calculate, when landmark coordinates will be calculated by the program, e.g., during scapular morphology calculation)
  - Value2: ignored.
  - Value3: ignored.
  - If midpoint is specified, then the two anatomical landmarks that will be used to calculate the midpoint are specified by the value2 and value3 parameters. Otherwise, these parameters are ignored.
  - Only landmarks that are of type “specify” and “digitize” can be included in a midpoint calculation.
- **Coordinates:** The coordinates of an anatomical landmark. Required if the landmark is of type specify. Otherwise, these parameters are ignored.
  - Value1: X coordinate
  - Value2: Y coordinate
  - Value3: Z coordinate

### ACSs Sheet (optional)

The purpose of this sheet is to specify the anatomical coordinate systems (ACSs) for each segment. An unlimited number of ACSs can be specified. To add ACSs, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names.

#### Parameters for each ACS

- **Name:** Specifies the name of the ACS. Required.
  - Value1: The unique name of the ACS. Names must be unique and cannot contain spaces.
  - Value2: ignored.
  - Value3: ignored.
- **Associated segment:** Specifies the name of the segment to which the ACS belongs. Required.
  - Value1: Segment name. Names must be specified exactly (case insensitive) as they are listed in the Segments and ROIs sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **1st axis:** Information that is required to define the first axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.

- Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- Intermediate axis: Information that is required to define the intermediate axis of the ACS. Required.
  - Value1: axis name (int).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- 2nd axis: Information that is required to define the second axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z).
  - Value2: first axis in cross-product calculation.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- 3rd axis: Information that is required to define the third axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z). The first, second, or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. The first, second, or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- Origin: Specifies the landmark that serves as the origin of the ACS. Required.
  - Value1: Landmark name. Name must be specified exactly (case insensitive) as is listed in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.

### Scapula Sheet (optional)

The following morphology variables will be calculated: glenoid-based coordinate system, glenoid anatomical points (i.e., anterior, posterior, superior, inferior, center), glenoid inclination, glenoid version, and critical shoulder angle. Details of these calculations are provided in *Appendix B – Description of Morphology Calculations*. The following segments and ROIs are required (and specified in the Segments and ROIs sheet of the parameter file) to calculate scapular morphology variables:

1. Scapula (segment)
2. Glenoid (ROI)
3. Acromion (ROI)

The following parameters are specified in the parameter file. Note that the glenoid coordinate system and glenoid inclination and version vectors are related to a reference coordinate system that is specified by the parameters.

### Parameters

- Calculate morphology: Indicator of whether to calculate scapular morphology variables, including a glenoid-based coordinate system. Required.
  - Value1: TRUE/FALSE. If FALSE, is specified, then all other inputs in this sheet are ignored.
  - Value2: ignored.
  - Value3: ignored.

- Segments and ROIs: Specifies the name of the segment and ROIs required for scapular morphology calculations. Required if scapular morphology is to be calculated.
  - Value1: name of the scapular segment. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value2: name of the glenoid ROI. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value3: name of the acromion ROI. Name must match those specified in the Segments and ROIs sheet of the parameter file.
- Glenoid S/I Landmarks: The landmark names to be assigned to the superior and inferior glenoid landmarks calculated during Scapular Morphology calculations. Required if scapular morphology is to be calculated.
  - Value1: name assigned to the superior glenoid point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: name assigned to the inferior glenoid point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value3: ignored.
- Glenoid A/P Landmarks: The landmark names to be assigned to the anterior and posterior glenoid landmarks calculated during Scapular Morphology calculations. Required if scapular morphology is to be calculated.
  - Value1: name assigned to the anterior glenoid point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: name assigned to the posterior glenoid point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value3: ignored.
- Center glenoid landmark: The landmark name to be assigned to the center glenoid landmark calculated during Scapular Morphology calculations. Required if scapular morphology is to be calculated.
  - Value1: name assigned to the center glenoid point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- Lateral acromial landmark: The landmark names to be assigned to the lateral acromial landmark calculated during Scapular Morphology calculations. Required if scapular morphology is to be calculated.
  - Value1: name assigned to the lateral acromial landmark. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- Glenoid axes: The names to be assigned to the glenoid coordinate system axes during Scapular Morphology Calculations. Required if scapular morphology is to be calculated.
  - Value1: name assigned to the anterior/posterior glenoid axes.
  - Value2: name assigned to the superior/inferior glenoid axes.
  - Value2: name assigned to the medial/lateral glenoid axes.
- 1st axis: Information that is required to define the first axis of the scapular reference coordinate system. Required if scapular morphology is to be calculated.
  - Value1: axis name (X, Y, or Z)

- Value2: landmark at tip of vector. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- Intermediate axis: Information that is required to define the intermediate axis of the scapular reference coordinate system. Required if scapular morphology is to be calculated.
  - Value1: axis name (int)
  - value2: landmark at tip of vector. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- 2nd axis: Information that is required to define the second axis of the scapular reference coordinate system. Required if scapular morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- 3rd axis: Information that is required to define the third axis of the scapular reference coordinate system. Required if scapular morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). The first, second, or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. The first, second, or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- Origin: The landmark that serves as the origin of the scapular reference coordinate system. Required if scapular morphology is to be calculated.
  - The landmark must be specified exactly (case insensitive) as is listed in the Anatomical Landmarks sheet of the parameter file. Landmarks of type “calculate” cannot be specified.
  - Input in the value2 and value3 fields will be ignored.
- Anatomical directions: The axis directions that correspond to the anterior, superior, and lateral anatomical directions. Required if scapular morphology is to be calculated.
  - Value1: anterior anatomical direction.
  - Value2: superior anatomical direction.
  - Value3: lateral anatomical direction.
  - Valid inputs for all values are +X, +Y, +Z, -X, -Y, or -Z.

### Humerus Sheet (optional)

The following morphology variables will be calculated: center and radius of a sphere fit to the humeral articular surface, humeral retroversion, and humeral length. Details of these calculations are provided in *Appendix B – Description of Morphology Calculations*. The following segments and ROIs are required (and specified in the *Segments and ROIs* sheet of the parameter file) to calculate humeral morphology variables:

1. Humerus (segment)
2. Articular surface (ROI)

The following parameters are specified in the parameter file. Note that the humeral retroversion is related to a reference coordinate system that is specified by the parameters.

### Parameters

- **Calculate morphology:** Indicator of whether to calculate scapular morphology variables. Required.
  - Value1: TRUE/FALSE. If FALSE, is specified, then all other inputs in this sheet are ignored.
  - Value2: ignored.
  - Value3: ignored.
- **Calculate retroversion:** Indicator of whether to calculate humeral retroversion.
  - Value1: TRUE/FALSE.
  - Value2: ignored.
  - Value3: ignored.
- **Segments and ROIs:** Specifies the name of the segment and ROIs for the humerus (value1) and articular surface (value2). Required if humeral morphology is to be calculated.
  - Value1: Name of humerus segment. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value2: Name of articular surface ROI. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value3: ignored.
- **Articular surface sphere fit landmark:** The landmark name to be assigned to the center of a sphere fit to the humeral articular surface. Required if humeral morphology is to be calculated.
  - Value1: name assigned to the humeral head center landmark. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **1st axis:** Information that is required to define the first axis of the humeral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- **Intermediate axis:** Information that is required to define the intermediate axis of the humeral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (int).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.

- Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- **2nd axis:** Information that is required to define the second axis of the humeral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation.
- **3rd axis:** Information that is required to define the third axis of the humeral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first, second, or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first, second, or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- **Origin:** The landmark that serves as the origin of the humeral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: landmark name. Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Anatomical directions:** The axis directions that correspond to the anterior, superior, and lateral anatomical directions. Required if humeral morphology is to be calculated.
  - Value1: anterior anatomical direction.
  - Value2: superior anatomical direction.
  - Value3: lateral anatomical direction.
  - Valid inputs for all values are +X, +Y, +Z, -X, -Y, or -Z.

### Pelvis Sheet (optional)

The following morphology variables will be calculated: acetabular-based coordinate system, acetabular anatomical points (i.e., anterior, posterior, superior, inferior, center), and acetabular dimensions (height and width). Details of these calculations are provided in *Appendix B – Description of Morphology Calculations*. The following segments and ROIs are required (and specified in the Segments and ROIs sheet of the parameter file) to calculate pelvis morphology variables:

1. Pelvis (segment)
2. Acetabulum (ROI)

The following parameters are specified in the parameter file. Note that the acetabular coordinate system is related to a reference coordinate system that is specified by the parameters.

### Parameters

- **Calculate morphology:** Indicator of whether to calculate pelvis morphology variables, including an acetabular-based coordinate system. Required.
  - Value1: TRUE/FALSE. If FALSE, is specified, then all other inputs in this sheet are ignored.

- Value2: ignored.
  - Value3: ignored.
- **Segments and ROIs:** Specifies the name of the segment and ROIs required for pelvis morphology calculations. Required if pelvis morphology is to be calculated.
  - Value1: name of the pelvis segment. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value2: name of the acetabular ROI. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value3: ignored.
- **Acetabular S/I Landmarks:** The landmark names to be assigned to the superior and inferior acetabular landmarks calculated during Pelvis Morphology calculations. Required if pelvis morphology is to be calculated.
  - Value1: name assigned to the superior pelvis point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: name assigned to the inferior pelvis point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value3: ignored.
- **Acetabular A/P Landmarks:** The landmark names to be assigned to the anterior and posterior acetabular landmarks calculated during Pelvis Morphology calculations. Required if pelvis morphology is to be calculated.
  - Value1: name assigned to the anterior pelvis point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: name assigned to the posterior pelvis point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value3: ignored.
- **Acetabular center landmark:** The landmark name to be assigned to the center acetabular landmark calculated during Pelvis Morphology calculations. Required if pelvis morphology is to be calculated.
  - Value1: name assigned to the center pelvis point. Name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Acetabular axes:** The names to be assigned to the acetabular coordinate system axes during Pelvis Morphology Calculations. Required if pelvis morphology is to be calculated.
  - Value1: name assigned to the anterior/posterior acetabular axes.
  - Value2: name assigned to the superior/inferior acetabular axes.
  - Value2: name assigned to the medial/lateral acetabular axes.
- **1st axis:** Information that is required to define the first axis of the pelvis reference coordinate system. Required if pelvis morphology is to be calculated.
  - Value1: axis name (X, Y, or Z)
  - Value2: landmark at tip of vector. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- **Intermediate axis:** Information that is required to define the intermediate axis of the scapular reference coordinate system. Required if pelvis morphology is to be calculated.

- Value1: axis name (int)
- value2: landmark at tip of vector. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file and cannot be of type “calculate”.
- 2nd axis: Information that is required to define the second axis of the scapular reference coordinate system. Required if pelvis morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- 3rd axis: Information that is required to define the third axis of the scapular reference coordinate system. Required if pelvis morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). The first, second, or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. The first, second, or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2).
- Origin: The landmark that serves as the origin of the pelvis reference coordinate system. Required if pelvis morphology is to be calculated.
  - The landmark must be specified exactly (case insensitive) as is listed in the Anatomical Landmarks sheet of the parameter file. Landmarks of type “calculate” cannot be specified.
  - Input in the value2 and value3 fields will be ignored.
- Anatomical directions: The axis directions that correspond to the anterior, superior, and lateral anatomical directions. Required if pelvis morphology is to be calculated.
  - Value1: anterior anatomical direction.
  - Value2: superior anatomical direction.
  - Value3: lateral anatomical direction.
  - Valid inputs for all values are +X, +Y, +Z, -X, -Y, or -Z.

### Femur Sheet (optional)

The following morphology variables will be calculated: center and radius of a sphere fit to the femoral articular surface. Details of these calculations are provided in *Appendix B – Description of Morphology Calculations*. The following segments and ROIs are required (and specified in the *Segments and ROIs* sheet of the parameter file) to calculate femoral morphology variables:

1. Femur (segment)
2. Articular surface (ROI)

The following parameters are specified in the parameter file. Note that the humeral retroversion is related to a reference coordinate system that is specified by the parameters.

### Parameters

- Calculate morphology: Indicator of whether to calculate femoral morphology variables. Required.



- Value1: TRUE/FALSE. If FALSE, is specified, then all other inputs in this sheet are ignored.
  - Value2: ignored.
  - Value3: ignored.
- Segments and ROIs: Specifies the name of the segment and ROIs for the femur (value1) and articular surface (value2). Required if femoral morphology is to be calculated.
  - Value1: Name of femur segment. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value2: Name of articular surface ROI. Name must match those specified in the Segments and ROIs sheet of the parameter file.
  - Value3: ignored.
- Articular surface sphere fit landmark: The landmark name to be assigned to the center of a sphere fit to the femoral articular surface. Required if femoral morphology is to be calculated.
  - Value1: name assigned to the femoral head center landmark. Landmark name must match those specified in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- 1st axis: Information that is required to define the first axis of the femoral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- Intermediate axis: Information that is required to define the intermediate axis of the femoral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (int).
  - Value2: landmark at tip of vector. Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Landmark name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- 2nd axis: Information that is required to define the second axis of the femoral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation.
- 3rd axis: Information that is required to define the third axis of the femoral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: axis name (X, Y, or Z). Only the first, second, or intermediate axes may be specified.

- Value2: first axis in cross-product calculation. Only the first, second, or intermediate axes may be specified.
- Value3: second axis in cross-product calculation (value1 cross value2).
- **Origin:** The landmark that serves as the origin of the femoral reference coordinate system. Required if humeral morphology is to be calculated.
  - Value1: landmark name. Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Anatomical directions:** The axis directions that correspond to the anterior, superior, and lateral anatomical directions. Required if humeral morphology is to be calculated.
  - Value1: anterior anatomical direction.
  - Value2: superior anatomical direction.
  - Value3: lateral anatomical direction.
  - Valid inputs for all values are +X, +Y, +Z, -X, -Y, or -Z.

## Menu Bar

### File

Controls the information being calculated and/or displayed by the program.

- **Load:** Loads one parameter file.
- **Reset:** Resets the program by clearing all non-GUI variables.
- **Quit:** Quits the program (keyboard shortcut: ctrl+Q).

### Edit

Allows the user to modify the appearance of the 3D plots.

### Models

Allows the user to change how the segment models appear.

- **Model color:** Changes the color of the segment model(s).
- **Triangulation:** Toggles on/off the visualization of the mesh faces and vertices on the segment model(s).
- **Transparency:** Changes the transparency of the segment model(s).

### Plot objects

Allows the user to change aspects of how lines and markers are displayed.

- **Line color:** Changes the color of line objects (e.g., glenoid inclination vector).
- **Line thickness:** Changes the thickness of line objects (e.g., coordinate systems, glenoid inclination vector).
- **Marker color:** Changes the color of the markers (e.g., anatomical landmarks).
- **Marker size:** Changes the size of the markers (e.g., anatomical landmarks).

### Restore defaults

Restores the default visualization settings for the model appearance and plot objects.

### View

Allows the user to enable various interactions and visualizations with the 3D plots in the *Landmark Setup and Viewer* and *Morphology Viewer* tabs.

- Rotate: Rotate the 3D plot in space (keyboard shortcut: ctrl+R).
- Pan: Pan (or shift) the view of the 3D plot in the plane of the viewer (keyboard shortcut: ctrl+P).
- Zoom: Zooms in and out of the 3D plot (keyboard shortcut: ctrl+Z).
- Data tips: Allows the user to click on a plot and get the coordinates of the point clicked (keyboard shortcut: ctrl+D). This option is disabled in the *Landmark Setup and Viewer* tab.

## Export

Allows the user to export still images and movies of the 3D plot.

- Image: Exports a still image (.jpg and .fig) the current view and all plot options. JPG images are exported at 150 dpi.
- Error report: Exports a .txt file containing the errors found during the input verification process.

## Help

Provides information and help about KinematicsToolbox.

- About: Provides information about KinematicsToolbox (including version).
- Permissions: Provides the date and number of days until current permissions to use KinematicsToolbox expires.
- Documentation: Opens the help documentation.

## Running the Module

### Load Parameter File

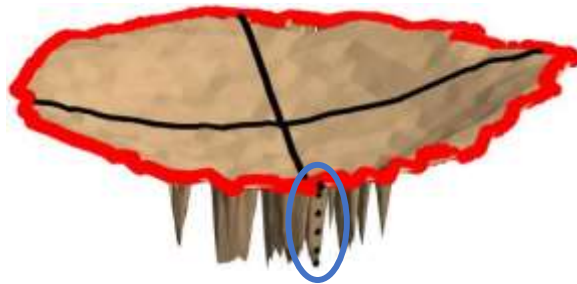
1. Load a parameter file for a subject (1 side only) by clicking on "Load Parameter File" or by navigating to File --> Load. A file selection dialog box will appear allowing the user to navigate to the parameter file to analyze. Once the file is selected, the program will first search for any existing results.
2. If no existing results are detected, the program will proceed to verify the parameter file, which helps prevent code errors downstream. This process may not catch 100% of potential issues; however, it should catch most.
  - a. If errors are detected, a list is populated in the "Input Verification Report" to help identify what to fix in the parameter file. These errors can be exported to a .txt file for easier troubleshooting by navigating to Export --> Error report.
  - b. If no errors are detected, then the "Digitize Landmarks" and "Calculate Morphology" buttons will be enabled.
3. If existing results are detected, the user will be asked whether to load existing results, edit the existing results, or overwrite them.
  - a. If the user selects "Load", the program will run a check to make sure the results loaded were created from the same version of the parameter file by checking the date and time. If the versions do not match, then the user will be asked whether they want to load the results anyway (in which case the changes to the parameter file will not be reflected in the results), edit the results, or overwrite the files (see descriptions below).
  - b. If the user selects "Edit", the program will perform the input verification process then load in any previously digitized anatomical landmarks that share the same name as those specified in the current parameter file. Morphology variables will need to be recalculated given the potential for changes.

- c. If the user selects "Overwrite", the program will delete any existing results files and recalculate morphology variables as specified in the parameter file.

### Running the Program

Landmarks can be viewed and digitized by selecting the "Digitize Landmark" button. Only landmarks that are of type "digitize" can be changed. ACS and morphology variables are calculated by selecting the "Calculate Morphology" button.

If scapular morphology is calculated, a dialog box will appear allowing the user to review and approve or reject the glenoid face points that are detected. This is an important step to ensure that the glenoid radius of curvature is calculated correctly. In particular, make sure that the points detected on the glenoid face along the S/I and A/P axes do not lie medial to the glenoid face. If so, revise the STL by removing the faces corresponding to the points that lie outside the glenoid face. Note that faces outside the glenoid that do not lay along the S/I and A/P axes (black lines) do not need to be removed as they are not included in the radius of curvature calculation (see figure below).



Once morphology calculations are complete, results can be saved by pressing the "Save Results" button. *Note: Changes to landmark coordinates will not be reflected in ACSs until "Calculate Morphology" is re-run.*

### Landmark Setup and Viewer

The purpose of this tab is to digitize anatomical landmarks (if necessary) and to verify the accuracy of the anatomical landmarks that were specified within the parameter file. This step is not necessary but helps to ensure the correctness of the output.

#### View Options

In addition to the options in the View menu, the user can specify whether to visualize additional parameters.

**Segments:** Indicates which segment(s) to view in the plot area. Only one segment can be viewed at a time. Selecting a segment automatically updates the anatomical landmarks listed in the "Landmark(s)" list box.

- **Landmarks:** Indicates which anatomical landmark(s) to view in the plot area. Only one landmark can be selected at a time from the list box.
- **ACSs:** Indicates which ACS(s) to view in the plot area. Multiple ACSs can be selected at a time from the list box.
- **Viewer's Orientation:** Indicates which direction is the viewer's vertical. The axes are defined by the option selected in the Viewer's Perspective drop-down menu. The viewer's orientation can also be changed by pressing F1-F6 keys as follows:
  - F1: +X
  - F2: +Y
  - F3: +Z

- F4: -X
- F5: -Y
- F6: -Z

*Note that these keyboard shortcuts cannot be used when rotate, pan, zoom, or data tip mode is turned on.*

- Global coordinate system: Toggles on/off visualization of the global coordinate system axes.
- Show all landmarks for segment: Toggles on/off visualization of all anatomical landmarks for the currently selected segment.
- Digitize a landmark: Turns on the ability to digitize the surface of the segment. Only one point can be digitized at a given time.
- Save landmark coordinates: Saves the coordinates to the currently selected anatomical landmark.
- Clear landmark coordinates: Clears the coordinates to the currently selected anatomical landmark.
- Coordinates table: Displays the X, Y, and Z coordinates of all landmarks specified in the Anatomical Landmarks sheet of the parameter file.

### Model Appearance

Model color can be changed by navigating to Edit --> Model appearance --> Color. The mesh triangulation of the segments can be viewed on the segments by navigating to Edit --> Model appearance --> Triangulation. Segment transparency can be changed by navigating to Edit --> Model appearance --> Transparency.

### Morphology Viewer

The purpose of this tab is to view the morphology results.

#### View Options

- Data type: Indicates which data to view in the plot area. When a morphology analysis is selected (e.g., scapular morphology), additional segment-specific objects appear, which are described below.
- Viewer's Perspective: Indicates which coordinate system from which to view the data.
- Viewer's Orientation: Indicates which direction is the viewer's vertical. The viewer's orientation can also be changed by pressing F1-F6 keys as follows:
  - F1: +X
  - F2: +Y
  - F3: +Z
  - F4: -X
  - F5: -Y
  - F6: -Z

*Note that these keyboard shortcuts cannot be used when rotate, pan, zoom, or data tip mode is turned on.*

- Model color can be changed by navigating to Edit --> Model appearance --> Color. Segment transparency can be changed by navigating to Edit --> Model appearance --> Transparency.
- Scapular Morphology Objects: When "Scapular Morphology" is selected from the Data Type drop-down menu, the following objects appear:
  1. Scapular reference coordinate system: Enables visualization of the scapular coordinate system specified in the Scapula sheet of the parameter file.

2. Glenoid coordinate system: Enables visualization of the glenoid coordinate system.
  3. Glenoid rim contour: Enables visualization of the glenoid rim points that were detected while calculating the glenoid coordinate system.
  4. Glenoid points: Enables visualization of the superior, inferior, anterior, and posterior glenoid points.
  5. Glenoid inclination: Enables visualization of the glenoid inclination vector.
  6. Glenoid version: Enables visualization of the glenoid version vector.
  7. Glenoid S/I ROC: Enables visualization of a circle fit to the glenoid to calculate the superior/inferior radius of curvature.
  8. Glenoid A/P ROC: Enables visualization of a circle fit to the glenoid to calculate the anterior/posterior radius of curvature.
  9. Critical shoulder angle: Enables visualization of the two vectors used to calculate the critical shoulder angle.
- Humeral Morphology Objects: When "Humeral Morphology" is selected from the Data Type drop-down menu, the following objects appear:
    1. Humeral reference coordinate system: Enables visualization of the humeral coordinate system specified in the Humerus sheet of the parameter file.
    2. Retroversion: Enables visualization of humeral retroversion vectors.
    3. Sphere fit to articular surface: Enables visualization of a sphere fit to the humeral articular surface ROI.

## Output Files

- MorphologyResults.xlsx: Provides results for all anatomical landmark coordinates (in distance and voxel units) and bone-specific morphology variables.

## Error Reports

In the event of a program error, a dialog box will appear displaying the error code. The user has the option to save an error report which contains the error code, the software version, and the computer's operating system. This information will be useful for troubleshooting the error.

## Analysis Module

Goal: Calculate and visualize joint kinematics, proximity patterns, and instantaneous helical axes by integrating kinematic and anatomical data across data collection trials. Kinematic data is calculated from markerless tracking program output files. Currently supported programs include JointTrack, C-Motion, Autoscooper, and HFHS in-house software.

### Setting up the Parameter File

The parameter file provides all the necessary input for the program to run. A separate parameter file is required for each trial of data.

#### Info Sheet

The purpose of this sheet is to provide basic information on the subject (i.e., subject variables) and technical specs from the data collection (i.e., project variables). Subject variables are written to all output files as column variables. An unlimited number of subject variables can be specified by adding rows to the Excel sheet. Project variables are not transferred to output files but are used internally by the program to ensure correct calculations and visualizations. Input from the following tracking software is currently supported: JointTrack, C-Motion, and HFHS. An unlimited number of project variables can be specified by adding rows to the Excel sheet. However, non-required project variables will not be used by the program or appear in output files.

#### Subject parameters

- Subject ID: The study ID of the participant.
- Side: The laterality of the data. Valid input is Right (or R) or Left (or L). Required if calculating scapular and humeral morphology.
- Trial: The unique trial identifier for the motion data to be analyzed.

#### Project parameters

- Software: The software used for radiographic kinematic tracking. Valid inputs are JointTrack, C-Motion, or HFHS.
- Modality: The modality from which the bone models were generated. Valid inputs are MR or CT.
- Scale: The unit of distance (e.g., mm). Required. It is assumed that all STL files are on the same scale.<sup>2</sup>
- Frame rate (Hz): The frame rate (in Hz) at which the radiographic images were acquired.
- Image dimensions in X: The X dimensions of the radiographic image in number of pixels. Required if lab setup is to be visualized.
- Image dimensions in Y: The Y dimensions of the radiographic image in number of pixels. Required if lab setup is to be visualized.
- II size: The diameter of the image intensifier in the units specified by the variable scale. Required if lab setup is to be visualized.

#### Considerations for later processing in the CompilerModule

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<sup>2</sup> It is assumed that all distance measures (e.g., kinematic position inputs, calibration object dimensions, and STL files) are on the same scale, which is defined by the variable "scale". Therefore, pre-processing may be required to ensure all inputs are on the same scale.

If the CompilerModule will be used later to reduce and compile data both within and between subjects, then it is necessary to think carefully about how to set up the subject variables in the AnalysisModule. This is because these variables are written to each results file, including the .mat file that is queried by CompilerModule.

For example, let's say your study has two visits (pre, post) and during each visit you collect two trials each of SAB and ER (4 trials per visit). You will need to come up with a unique trial name for each of the trials collected for the subject in the study and create 2 additional subject variables (motion, time) to classify these trials as follows:

Trial	Motion	Time
SAB1pre	SAB	Pre
SAB2pre	SAB	Pre
SAB1post	SAB	Pre
SAB2post	SAB	Pre
ER1pre	ER	Pre
ER2pre	ER	Pre
ER1post	ER	Pre
ER2post	ER	Pre

The subject variables “motion” and “time” are necessary so that data across different trial types aren't averaged together during the CompilerModule. These variables will be specified as grouping variables in the CompilerModule parameter file.

### Output Sheet

The purpose of this sheet is to specify the output directories for any results output files written by the program. There are two primary types of output: Kinematics and Proximities. Directories can be specified using absolute paths (e.g., “C:\user\data\output\”) or relative paths (e.g., “.output\”). It is highly recommended to use relative paths when specifying the location of the kinematic tracking files, STLs, etc. For more information on relative paths, see Appendix A – Relative Path Specification.

#### Parameters for each output type

- Destination: The absolute or relative path to where the results should be written.

An output path for “Kinematics” is required because it is necessary to calculate kinematics to create any visualization, which are the most basic function of the program. “Proximities” is not required, and proximity patterns will not be calculated if it not listed in the “output type” column.

### Segments Sheet

The purpose of this sheet is to specify information for the segments that have been tracked by the radiographic motion capture system. Generally, segments are bones but they can also be prostheses, assuming they were tracked in the same manner as other tracked segments. An unlimited number of segments can be specified. To add segments, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names. If proximity patterns are to be calculated, all segments associated with an ROI need to be closed surfaces (i.e., watertight). The required file format for bone geometries is a binary STL. The required file format for kinematics depends upon the software used for kinematic tracking (i.e., JointTrack, C-Motion, HFHS) but assumes data



represents the segment's anatomical coordinate system relative to the lab coordinate system (i.e., calibration cube). File paths can be specified using absolute paths (e.g., "C:\user\data\boneKinematics.csv") or relative paths (e.g., ".\boneKinematics.csv"). For more information on relative paths, see Appendix A – Relative Path Specification.

#### *Parameters for each segment*

- **Name:** Specifies the name of the segment. Required.
  - Value1: Segment name. Names must be unique and cannot contain spaces.
  - Value2: ignored.
  - Value3: ignored.
- 5. **STL path:** Specifies the path for the segment's binary STL. Required.
  - Value1: The absolute or relative path.
  - Value2: ignored.
  - Value3: ignored.
- 6. **Kinematics path:** Specifies the path for the segment's kinematic tracking file. Required.
  - Value1: The absolute or relative path.
  - Value2: ignored.
  - Value3: ignored.
- **Butterworth filter:** The parameters to be used to filter the segment's kinematic data using a Butterworth filter. Filtering can only be applied for internally tracked segments and for trials with >12 frames of data. Required.
  - Value1: TRUE/FALSE indicator of whether to apply filtering.
  - Value2: filter order (valid values are positive integers). Required if Value1 is TRUE.
  - Value3: low-pass cutoff frequency (Hz; valid values are positive numbers). Required if Value1 is TRUE.

#### *ROIs Sheet*

If proximity patterns are desired, the information provided in this sheet specifies the names of each region of interest (ROI) for the proximity patterns, their type, their associated segments, and the locations of the geometries (binary STL format). An unlimited number of ROIs can be specified. To add ROIs, duplicate the entire block including header and modify value(s) accordingly. ROIs can be surfaces of a tracked segment or soft tissue assumed to be rigidly fixed to the ROI's associated segment. ROIs will be linked to their associated kinematics by correctly specifying the name of the segment to which they belong. Therefore, it is critical to use the exact spelling (case insensitive) of the segment here and in the Segments sheet of the parameter file. File paths can be specified using absolute paths (e.g., "C:\user\data\ROI.stl") or relative paths (e.g., ".\ROI.stl"). For more information on relative paths, see Appendix A – Relative Path Specification.

#### *Parameters for each ROI*

- **Name:** The name of the ROI. Names must be unique, cannot contain spaces, and must not exceed 21 characters in length. Required.
- **Type:** An indicator specifying the type of ROI. Valid inputs are bone, tendon, muscle, and ligament. Required.
- **Associated segment:** The name of the segment to which the landmark belongs. Segment names must be specified exactly (case insensitive) as they are listed in the Segments sheet of the parameter file. Required.
- **STL path:** The absolute or relative path for binary STL for the segment. Required.

### *Considerations on how to prepare ROIs*

- The degree to which the ROI mesh is highly refined will significantly impact computation time and program performance. Consequently, it is recommended that ROI mesh are prepared with no more resolution than necessary to fulfill the aims of the study.
- If an ROI is a region on the surface of the segment and it is made such that it follows that segment surface exactly, the colormapping may be impacted because the two surfaces (which are essentially the same surface) are being plotted on top of each other. This appears to be the case when surfaces are cut using planes in Mimics. To prevent this issue, create the ROI mesh in a way that remeshes the surface once it is defined from the segment. This can be done in Meshlab or 3-Matic and gives the ROI a slightly different definition of the surface topography and allows the colormap to be seen. Any differences between surface definitions are likely less than the distance between neighboring mesh vertices (i.e., generally much less than 1 mm but depends on the resolution of the mesh).
- A maximum of 16,000 faces is allowed on an ROI. This is both for computational and practical reasons (i.e., maximum columns allowed in Excel for "FaceDistances.xlsx" output file).

### *Calibration Sheet*

The purpose of this sheet is to specify the calibration coefficients for each radiographic imaging plane (listed in columns). Calibration coefficients are not required input. However, if specified, then the variables image dimensions in X (px), image dimensions in Y (px), and II size are required in the Info sheet. Together, this data allows for visualizing the lab setup in the Motion Viewer tab. An unlimited number of imaging planes can be specified.

### *Coefficients for HFHS software (9 required)*

- SID (source-to-image distance)
- X position of the source relative to the calibration object
- Y position of the source relative to the calibration object
- Z position of the source relative to the calibration object
- Roll (X) orientation of the source relative to the calibration object
- Pitch (Y') orientation of the source relative to the calibration object
- Yaw (Z'') orientation of the source relative to the calibration object
- X coordinates of the principal point relative to the image corner
- Y coordinates of the principal point relative to the image corner

### *Coefficients for C-Motion software (10 required)*

- SID (source-to-image distance)
- X position of the source relative to the calibration object ("Source Position in Lab Coordinates")
- Y position of the source relative to the calibration object ("Source Position in Lab Coordinates")
- Z position of the source relative to the calibration object ("Source Position in Lab Coordinates")
- X position of the image relative to the calibration object ("Image Position in Lab Coordinates")

- Y position of the image relative to the calibration object ("Image Position in Lab Coordinates")
- Z position of the image relative to the calibration object ("Image Position in Lab Coordinates")
- Roll (X) orientation of the image relative to the calibration object ("Image Orientation in Lab Coordinates")
- Pitch (Y) orientation of the image relative to the calibration object ("Image Orientation in Lab Coordinates")
- Yaw (Z) orientation of the image relative to the calibration object ("Image Orientation in Lab Coordinates")

#### *Coefficients for JointTrack and Autoscooper software (11 required)*

- DLT coefficients in the order specified in the MergedDIts\_Frame0.csv file, which is export from XMALab.

#### *Anatomical Coordinates Sheet*

The purpose of this sheet is to specify the coordinates of the anatomical landmarks used to define each segment's anatomical coordinate system (ACS). Note that "landmarks" may include both anatomical points and vectors. For example, if the 3 unit vectors describing a glenoid-based coordinate system are known, they may be input as separate landmarks of type vector. Along with an origin anatomical landmark, these vectors can be reconstructed into a full glenoid-based coordinate system in the ACSs sheet of the parameter file. An unlimited number of anatomical landmarks can be specified. To add landmarks, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names. It is critical that the coordinates be described in the same reference frame as the segment and (if specified) ROI STLs, which is typically the scanner coordinate system. If the coordinates and STLs are not in the same coordinate system, motion visualization will not be correct.

#### *Parameters for each anatomical landmark*

- **Name:** Specifies the name of the anatomical landmark. Required
  - Value1: Landmark name. Names must be unique and cannot contain spaces.
  - Value2: ignored.
  - Value3: ignored.
- **Type:** Specifies the type of anatomical landmark. Valid inputs are "point" and vector.
  - Value1: Landmark type. Valid inputs are:
    - Point, when the landmark is an anatomical landmark.
    - Vector, when the landmark is an anatomical vector (i.e., axis).
  - Value2: ignored.
  - Value3: ignored.
- **Associated segment:** Specifies the name of the segment to which the landmark belongs. Required.
  - Value1: Segment name. Names must be specified exactly (case insensitive) as they are listed in the Segments sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Coordinates:** The coordinates of an anatomical landmark. Required.
  - Value1: X coordinate for landmarks,  $i$  component for unit vectors
  - Value2: Y coordinate,  $j$  component for unit vectors
  - Value3: Z coordinate,  $k$  component for unit vectors

- Note: If the landmark is of type “vector”, then the vector must have a magnitude of 1.

#### *Additional considerations and requirements*

- At least three landmarks are required per segment.

#### *ACSs Sheet*

The purpose of this sheet is to specify the anatomical coordinate systems (ACSs) for each segment. An unlimited number of ACSs can be specified. To add ACSs, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names.

Coordinate systems can be specified as either point-based or vector-based. For point-based anatomical coordinate systems, at least three non-collinear landmarks (i.e., anatomical points) are required resulting in the definition of a first axis and an intermediate axis. The second and third axes are defined using cross-products. For vector-based anatomical coordinate systems, 3 unit vectors (i.e., anatomical vectors) are specified. For example, if the 3 unit vectors describing a glenoid-based coordinate system are known, they may be input as separate "landmarks" with type "vector" in the Anatomical Coordinates sheet of the parameter file. Along with an origin anatomical landmark, these vectors can be reconstructed into a full glenoid-based coordinate system.

#### *Parameters for each ACS*

- **Name:** Specifies the name of the ACS. Required.
  - Value1: ACS name. Names must be unique, cannot contain spaces, and must not exceed 31 characters in length. Input for value2 and value3 will be ignored.
  - Value2: ignored.
  - Value3: ignored.
- **Type:** Specifies the type of ACS to be defined. Required.
  - Value1: Type of ACS. Valid inputs are:
    - Input: The ACS that was used to track a segment, and all input kinematic data (path to data specified in the Segments sheet of the parameter file) must be defined in the input coordinate systems. Input ACSs are required for data tracked with HFHS, JT, or C-motion software. However, Autoscooper tracks segments in the image coordinate system; therefore, the input ACS is already known (i.e., an identity matrix). Only one input coordinate system is allowed per segment.
    - Output: An ACS that will be used to describe the kinematics in all output files. If the input coordinate system is the same as the output coordinate system, then simply duplicate the entry and update the type parameter. At least one output coordinate system is required for each segment.
    - External: Used when a segment was tracked externally (i.e., not by the x-ray system). For example, the trunk can be tracked using Vicon and then related to the scapula to result in the description of scapulothoracic kinematics. The axes of this coordinate system do not need to be defined.
  - Value2: ignored.

- Value3: ignored.
- **Associated segment:** Specifies the name of the segment to which the ACS belongs. Required.
  - Value1: Segment name. Names must be specified exactly (case insensitive) as they are listed in the Segments sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **1st axis:** Information that is required to define the first axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z)
  - Value2: landmark at tip of vector. Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- **Intermediate axis:** Information that is required to define the intermediate axis of the ACS. Required.
  - Value1: axis name (int)
  - Value2: landmark at tip of vector. Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
  - Value3: landmark at tail of vector (vector points from value2 to value1). Name must be specified exactly (case insensitive) as they are listed in the Anatomical Landmarks sheet of the parameter file.
- **2nd axis:** Information that is required to define the second axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z)
  - Value2: first axis in cross-product calculation
  - Value3: second axis in cross-product calculation (value1 cross value1). Only the first or intermediate axes may be used to define the second axis.
- **3rd axis:** Information that is required to define the third axis of the ACS. Required.
  - Value1: axis name (X, Y, or Z). Only the first, second, or intermediate axes may be specified.
  - Value2: first axis in cross-product calculation. Only the first, second, or intermediate axes may be specified.
  - Value3: second axis in cross-product calculation (value1 cross value2). The first, second, or intermediate axes may be used to define the third axis.
- **Origin:** The landmark that serves as the origin of the ACS. Required.
  - Value1: Landmark name. Name must be specified exactly (case insensitive) as is listed in the Anatomical Landmarks sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Correction factor: rotation:** The magnitude of correction about each axis of the ACS. Required.
  - Value1: X rotation. Specify 0 if no correction factor should be applied.
  - Value2: Y' rotation. Specify 0 if no correction factor should be applied.
  - Value3: Z" rotation. Specify 0 if no correction factor should be applied.
  - Correction factors can only be specified for ACS of type "input". Specify 0 if no correction factor should be applied and for all other ACS types (i.e., output and external).

- Correction factor: position: The magnitude of correction along each axis of the ACS. Required.
  - Value1: X position. Specify 0 if no correction factor should be applied.
  - Value2: Y position. Specify 0 if no correction factor should be applied.
  - Value3: Z position. Specify 0 if no correction factor should be applied.
  - Correction factors can only be specified for ACS of type "input". Specify 0 if no correction factor should be applied and for all other ACS types (i.e., output and external).

#### *Additional considerations and requirements*

- The output coordinate system "type" allows for a segment's kinematics to be described in multiple systems. For example, if the scapula was tracked using the ISB standard but the user would like to also describe scapular kinematics in a glenoid-based coordinate system (GCS), then specify ScapulaISB as the input ACS and both ScapulaISB and ScapulaGCS as output ACSs. Then, in the Kinematics sheet of the parameter file, list two separate joints: GH\_ISB and GH\_GCS. This will result in a full description of glenohumeral kinematics in both ISB and GCS.
- Any external data specified must be in the same input format as the segments tracked by the software. For example, if the thorax is tracked using Vicon and the bones are tracked using JointTrack, then the thorax kinematics must be pre-processed such that they are in the same format as JointTrack output.
- For output or internal coordinate systems, landmarks and axes are required to define the coordinate system. None are required for externally tracked segments since it is assumed that the data is already defined in an anatomically meaningful way and does not need to be reconstructed.
- A correction factor must be specified for all coordinate systems (if none, then enter 0 for each of the 6 values). However, only those specified for an input coordinate system will be considered. The correction factor describes the orientation and position of the "corrected" segment ACS relative to the segment's input coordinate system as 3 rotations (using arbitrary X-Y'-Z" sequence) and X, Y, Z positions. Use this specification to employ a clavicle correction or to adjust for an average magnitude of humeral retroversion when the epicondyles are not present. In this case, the correction factor is the rotation that would have to occur (about the local axes) to align the bone with the desired axis. Since the correction factor is applied to the segment's input kinematic data, the correction factor will be applied to any joint segment in which the segment is specified, regardless of whether it is the proximal or distal segment. Note that only one angular correction factor should be applied to not have the outcome affected by the arbitrary (but necessary) choice of rotation sequence. Example #1: clavicle correction – If the clavicle needs to be rotated posteriorly 3° about its medial/lateral axis to be aligned with the trunk vertical axis. If the +Z axis points laterally, then the correction factor would be: 0, 0, 3, 0, 0, 0. Since the correction factor is applied to any joint involving the segment, both the sternoclavicular and acromioclavicular joint kinematics are adjusted. Example #2: humeral retroversion – If the humerus was tracked using a biceps groove-based coordinate system, an adjustment can be made so that the resulting humeral kinematics can approximate what would be expected if the epicondyles were present. In this case, the humeral ACS would need to be rotated about its superior/inferior axis approximately 57.2° (the average retroversion magnitude). If the +Y axis points superiorly, then the correction factor would be: 0, 57.2, 0, 0, 0, 0.

Since the correction factor is applied to any joint involving the segment, both the glenohumeral and humerothoracic kinematics are adjusted.

- Data filtering is applied to anatomical landmarks. This is done by determining where each segment anatomical landmark is in the lab coordinate system given the known transformations between 1) the segment input ACS and the lab coordinate system, 2) the segment input ACS and the CT/MRI scanner, and 3) the position of the anatomical landmarks wrt the CT/MRI scanner. Filtering can only be specified for ACS of type "input" but is done prior to applying any correction factors and calculating kinematics; therefore, it will be automatically applied to all output kinematics. Filtering cannot be specified for segments tracked externally as the anatomical landmark coordinates are not known. Therefore, all kinematics from externally tracked segments need to be filtered prior to running KinematicsToolbox.

### Kinematics Sheet

The purpose of this sheet is to specify the joint kinematics that will be described from the tracked segment kinematics. An unlimited number of joints can be specified. To add joints, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names.

#### Parameters for each joint

- **Name:** Specifies the name of the joint. Required.
  - Value1: Joint name. Names must be unique and cannot contain spaces.
  - Value2: ignored.
  - Value3: ignored.
- **Reference segment ACS:** Specifies the output ACS that will be used to define the joint motion of the reference (typically proximal) segment. Required.
  - Value1: Name of output ACS. It is critical to use the exact spelling (case insensitive) of the ACS here and in the ACSs sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Moving segment ACS:** Specifies the output ACS that will be used to define the joint motion of the moving (typically distal) segment. Required.
  - Value1: Name of output ACS. It is critical to use the exact spelling (case insensitive) of the ACS here and in the ACSs sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- **Rotation sequence:** The Cardan or Euler rotation sequence from which to describe the joint kinematics. Required.
  - Value1: rotation sequence. Valid inputs: X-Y'-Z'', X-Z'-Y'', Y-X'-Z'', Y-Z'-X'', Z-X'-Y'', Z-Y'-X'', X-Y'-X'', X-Z'-X'', Y-X'-Y'', Y-Z'-Y'', Z-X'-Z'', and Z-Y'-Z''.
  - Value2: expected sign of the second rotation (i.e., beta). Valid values are either 1 (i.e., positive beta) or -1 (i.e., negative beta). Required if a repeating Euler sequence is selected, otherwise enter 1.
  - Value3: ignored.
- **DOF names: rotation:** Names for the three rotational degrees of freedom. Names must be unique across all joints, cannot contain spaces, and must not exceed 9 characters in length. Required.
  - Value1: name for alpha rotation.
  - Value2: name for beta rotation.
  - Value3: name for gamma rotation.



- DOF names: position: Names for the three translational degrees of freedom. Names must be unique across all joints, cannot contain spaces, and must not exceed 9 characters in length. Required.
  - Value1: name for X translation.
  - Value2: name for Y translation.
  - Value3: name for Z translation.
- Transformations: rotations: The transformation to be applied to the three rotational degrees of freedom. Required.
  - Value1: X transformation.
  - Value2: Y transformation.
  - Value3: Z transformation.
  - Valid values are either 1 or -1. A value of 1 indicates no transformation will be applied, while a value of -1 indicates the kinematic value will be multiplied by -1.
- Transformations: positions: The transformation to be applied to the three translational degrees of freedom. Required.
  - Value1: X transformation.
  - Value2: Y transformation.
  - Value3: Z transformation.
  - Valid values are either 1 or -1. A value of 1 indicates no transformation will be applied, while a value of -1 indicates the kinematic value will be multiplied by -1.

#### *Additional considerations and requirements*

- The reference segment ACS is typically the proximal segment ACS (e.g., scapula for glenohumeral), and the moving segment ACS is typically the distal segment ACS (e.g., humerus for glenohumeral).
- Unique names are required for each degree of freedom. For example, the name “upward rotation” cannot be shared across multiple joints. If this descriptor is to be used for describing scapulothoracic and acromioclavicular motion, then distinguish them using a unique name (e.g., ACur, STur).
- In the specification of DOF names for rotation, alpha refers to the first rotation, beta to the second, and gamma to the third. Therefore, alpha, beta, and gamma will depend on the rotation sequence specified. For example, if an X-Y-Z” rotation sequence was specified, then alpha corresponds to the rotation about the X axis, beta corresponds to the rotation about the Y’ axis, and gamma to the rotation about the Z” axis.
- Specify transformations if a left-to-right conversion is necessary.

#### **Proximities Sheet**

The purpose of this sheet is to specify the proximity patterns that will be described and visualized. The scale of proximity values is defined by the dimensionality of the STL files (typically mm). An unlimited number of proximity patterns can be specified. To add proximity patterns, duplicate the entire block including header and modify value(s) accordingly. Do not change header or parameter names. Proximities are only calculated if an output destination is specified for “Proximity patterns” in the Output sheet of the parameter file. Consequently, proximity patterns will not be calculated if an output destination is not specified even if the Proximities Sheet is completed.

#### *Parameters for each proximity pattern*

- Name: Specifies the name of the proximity pattern. Required.



- Value1: Pattern name. Names must be unique and cannot contains spaces.
  - Value2: ignored.
  - Value3: ignored.
- ROI #1: Specifies the name of the first ROI in the proximity pattern. Required.
  - Value1: ROI name. Name must match those in the ROIs sheet (case insensitive) of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- ROI #2: Specifies the name of the second ROI in the proximity pattern. Required.
  - Value1: ROI name. Name must match those in the ROIs sheet (case insensitive) of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- Output reference frame: ROI #1: The output reference frame from which to describe contact center locations on ROI #1. Required.
  - Value1: Output ACS name. Name must match an ACS in the ACSs sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- Output reference frame: ROI #2: The output reference frame from which to describe contact center locations on ROI #. Required.
  - Value1: Output ACS name. Name must match an ACS in the ACSs sheet of the parameter file.
  - Value2: ignored.
  - Value3: ignored.
- Transformation: contact center: The transformation to be applied to the contact center coordinates. Since contact center coordinates are defined in a local ACS, it may be necessary to transform the coordinates to ensure they are described consistently physiologically. Required.
  - Value1: X transformation (1 or -1).
  - Value2: Y transformation (1 or -1).
  - Value3: Z transformation (1 or -1).
  - A value of 1 indicates no transformation will be applied, while a value of -1 indicates the kinematic value will be multiplied by -1.
- Test vector penetration: Indicator of whether to test for penetration of a face's minimum distance vector with either segment. Details about the centroid constraint can be found in Appendix C – Description of Proximity Calculations. Required.
  - Value1: TRUE or FALSE.
  - Value2: ignored.
  - Value3: ignored.
- Test normal opposition: Indicator of whether to test the opposition between pairwise face normals. Details about the centroid constraint can be found in Appendix C – Description of Proximity Calculations. Required.
  - Value1: TRUE or FALSE.
  - Value2: threshold angle (in degrees). Valid values are >0 degrees and <= 180 degrees. A value of 180° indicates minimum distance vectors are unconstrained (same as FALSE).
  - Value3: ignored.
- Test angular deviation: Indicator of whether to test the angular deviation between the mapped face normal and the minimum distance vector. Details about the centroid

constraint can be found in Appendix C – Description of Proximity Calculations. Required.

- Value1: TRUE or FALSE, value2: threshold angle (in degrees).
- Valid values are >0 degrees and <= 180 degrees. A value of 180° indicates minimum distance vectors are unconstrained (same as FALSE).
- Value3: ignored.
- **Minimum distance bins:** The minimum distance bin limits for calculating surface areas. Required.
  - Value1: Bin limits. Each value must be separated by a comma. For example, if the values “0,2,4,6,8,10” are specified, then surface areas will be calculated within the bins of 0-2, 2-4, 4-6, 6-8, 8-10, >10 (scale specified by the STLs). At least two bin limit values are required, and they need to be specified in ascending order.
  - Value2: ignored.
  - Value3: ignored.
- **Centroid type:** Specifies the type of centroid to be calculated. Required.
  - Value1: Centroid type. Valid inputs are:
    - Absolute: interprets the centroid bin limits as distances (e.g., mm)
    - Relative: interprets the centroid bin limits as multiples of the minimum distance.
  - Value2: ignored.
  - Value3: ignored.
  - Details about the centroid calculation can be found in Appendix C – Description of Proximity Calculations.
- **Centroid bin limits:** Specifies the bin limits for calculating the proximity centroid. Required.
  - Value1: Bin limits. Each value must be separated by a comma. At least two bin limits values need to be specified, and they need to be specified in ascending order (e.g., 1,2,3).
  - Value2: ignored.
  - Value3: ignored.
  - Details about the centroid calculation can be found in Appendix C – Description of Proximity Calculations.
- **Centroid weights:** Specifies the weight to be applied to the bins in the calculation of the centroid Required.
  - Value1: Bin limits. Each value must be separated by a comma (e.g., 8,2,0). A value of 0 indicates coordinates in the bin will not be included in the centroid calculation. The number of weights must be equal to the number of centroid bins, and all weights must be integers.
  - Value2: ignored.
  - Value3: ignored.
- **Normalization:** Indicator of whether to normalize minimum distances and centroid distances. Required.
  - Value1: TRUE or FALSE.
  - Value2: normalization value (ignored if value1 is FALSE)
  - Value3: ignored.

#### *Additional considerations and requirements*

- Only one output reference frame can be specified for each ROI within a proximity pattern. Therefore, if contact center coordinates are needed in multiple output

reference frames (e.g., ScapulaISB, ScapulaGCS), then duplicate the proximity pattern and give the new proximity pattern a unique name.

- Test for vector penetration may not be necessary for all proximity patterns. For example, the minimum distance vector between the glenoid and the rotator cuff footprint often penetrates the humeral segment STL at low angles of elevation. Specifying TRUE will invalidate this minimum distance vector; however, the required computational time will be substantially increased. In contrast, the constraint may not be necessary for calculation of glenohumeral joint contact patterns.

## Menu Bar

### File

Controls the information being calculated and/or displayed by the program.

- Load: Loads one or more parameter files.
- Individual: Loads a single subject and is equivalent to pressing the “Load Parameter File” button on the “Project Info” tab.
- Batch: Allows the user to load multiple parameter files so that the results can be calculated successively. Note that this does not allow for the visualization of results but allows the user to process multiple subjects at once and not be physically present to load each individual subject. Also, input verification will be performed on all subjects prior to calculation results. Therefore, critical errors should be caught before calculations begin.
- Reset: Resets the program by clearing all non-GUI variables.
- Quit: Quits the program (keyboard shortcut: ctrl+Q).

### Edit

Allows the user to modify the appearance of the 3D plots.

### Models

Allows the user to change how the segment models appear (enabled for the Anatomical Verification, Motion Viewer, and Proximities tabs).

- Model color: Changes the color of the segment model(s).
- Triangulation: Toggles on/off the visualization of the mesh faces and vertices on the segment model(s).
- Transparency: Changes the transparency of the segment model(s).

### Colorbar

Allows the user to change the appearance of colormapping on proximity patterns (enabled for the Proximities tab only).

- Distance measure: Toggles the type of distance measure to view (i.e., absolute or normalized values).
- Colormap: Changes the type of colormap based on existing MATLAB colormaps.
- Limits: Changes the scale of the colorbar by specifying minimum and maximum values.

### Plot objects

Allows the user to change aspects of how lines and markers are displayed.

- Line color: Changes the color of line objects (e.g., vector connecting contact centers).
- Line thickness: Changes the thickness line objects including axes in the Anatomical Verification and Motion Viewer tabs, instantaneous helical axes and traces in the Motion Viewer tab, and contact center path and vectors in the Proximities tab.
- Marker color: Changes the color of markers(s) including anatomical landmarks on the Anatomical Verification tab, instantaneous helical axis trace points on the Motion Viewer tab, and contact center points on the Proximities tab.
- Marker size: Changes the size of the marker(s) including anatomical landmarks on the Anatomical Verification tab, instantaneous helical axis trace points on the Motion Viewer tab, and contact center points on the Proximities tab.
- Axis length: Changes the length of the anatomical coordinate system in the Anatomical Verification tab, instantaneous helical axis trace points on the Motion Viewer tab.

### *Restore defaults*

Restores the default visualization settings for the model appearance, colorbar, and plot objects.

### *View*

Allows the user to enable various interactions and visualizations with the 3D plots in the Anatomical Verification, Motion Viewer, and Proximities tabs.

- Rotate: Rotate the 3D plot in space (keyboard shortcut: ctrl+R).
- Pan: Pan (or shift) the view of the 3D plot in the plane of the viewer (keyboard shortcut: ctrl+P).
- Zoom: Zooms in and out of the 3D plot (keyboard shortcut: ctrl+Z).
- Data tips: Allows the user to click on a plot and get the coordinates of the point clicked (keyboard shortcut: ctrl+D).
- Lab setup: Allows the user to visualize motion trial relative to the laboratory setup. This option is only enabled in the Motion Viewer tab when the necessary calibration information is provided in the parameter file.
  - X-ray system(s): Toggles on/off the visualization of the 3D motion capture volume including x-ray source(s), image intensifier(s), and image and lab coordinate systems (keyboard shortcut: ctrl+X). For biplane systems, the inter-beam angle is also calculated and displayed at the bottom of the window.
  - Calibration cube: Toggles on/off the visualization of the calibration cube within the 3D motion capture volume (keyboard shortcut: ctrl+C).
- Helical axes: Allows the user to visualize the motion trial about one or more instantaneous helical axes. This option is only enabled in the Motion Viewer tab.
  - Instantaneous: Toggles on/off the visualization of instantaneous helical axes (keyboard shortcut: ctrl+H).
  - Trace: Toggles on/off the visualization of a trace that connects the instantaneous helical axes between frame #1 and the current frame (keyboard shortcut: ctrl+T). The length of the IHA can also be changed depending on the size of the anatomy.
- Instantaneous velocity vectors: Allows the user to visualize instantaneous surface velocity vectors of selected segment(s). Velocity vectors are calculated within the reference frame selected. This option is only enabled in the Motion Viewer tab.

- Pairwise vectors: Allows the user to visualize pairwise minimum distance vectors between ROIs (keyboard shortcut: ctrl+V). This option is only enabled in the Proximities tab.<sup>3</sup>
- Proximity path type: Allows the user to select which proximity (i.e., contact) path to visualize: Euclidean or geodesic (default).

## Export

Allows the user to export still images and movies of the 3D plot.

- Image: Exports a still image (.jpg and .fig) the current view and all plot options.
- Video: Exports a movie (.mp4) of all frames in the motion trial using the current view and all plot options. A dialog box will appear asking for the following video parameters:
  1. Start frame: The first frame of the motion trial to be written to the video.
  2. End frame: The last frame of the motion trial to be written to the video.
  3. Playback speed: The speed at which the video will be viewed. The default is 100%, which corresponds to the frame rate specified in the Info sheet of the parameter file. However, a slower/faster playback speed can be specified as a percentage of the real-time value. For example, if the data was collected at 60 Hz and the user specifies a playback speed of 50%, the video will be written at 30 fps.
- Error report: Exports a .txt file containing the errors found during the input verification process.

## Help

Provides information and help about KinematicsToolbox.

- About: Provides information about KinematicsToolbox (including version).
- Permissions: Provides the date and number of days until current permissions to use KinematicsToolbox expires.
- Documentation: Opens the help documentation.

## Running the Module

### Load Parameter File(s)

The program can be run in one of two modes: individual or batch. In “individual mode”, a parameter file is loaded for a single subject. If necessary, kinematics and proximity patterns (if specified) are calculated. The results can be visualized once calculations are complete. In “batch mode”, parameter files are loaded for multiple subjects so that the kinematics and proximity patterns (if specified) can be calculated successively without the need for user input. In this mode, results visualization is disabled. However, the program can be reset and results for an individual subject can be loaded.

### Individual Mode

1. Load a parameter file for the trial by clicking on “Load Parameter File” or by navigating to File --> Load --> Individual. A file selection dialog box will appear allowing the user to navigate to the parameter file to analyze.
2. Once the file is selected, the program will check for existing results.

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<sup>3</sup> Plotting pairwise vectors will slow down the visualization, especially when done for both ROIs simultaneously.

- a. If existing results are detected: the user will be asked whether to load existing results or to recalculate them.
  - i. If the user selects “Load”, the program will run a check to make sure the results loaded were created from the same version of the parameter file by checking the date and time. If the versions do not match, then the user will be asked whether they want to load the results anyway or re-calculate.
  - ii. If the user elects to load existing results (regardless of whether the parameter file matches), the program will first check to make sure that the kinematic tracking files (specified in the Segments sheet of the parameter file) and STL files for each ROI (specified in the ROIs sheet of the parameter file, if specified) are the same version by checking the file’s name and time stamp. All files specified in the current parameter file need to exactly match those used to calculate the results to be loaded to ensure the integrity of the visualization. For example, the results may no longer be valid if kinematic tracking for a segment were updated since the last run of the program, or if an ROI was redefined resulting in a new STL file.
  - iii. If no existing results are detected, the program will calculate kinematics (and if specified, proximity patterns) as specified in the parameter file.
3. The program will verify the parameter file to help prevent code errors downstream. This process may not catch 100% of potential issues; however, it should catch most.
  - a. If errors are detected, a list is populated in the “Input Verification Report” to help identify what to fix in the parameter file. These errors can be exported to a .txt file for easier troubleshooting by navigating to Export --> Error report.
  - b. If no errors are detected, then the “Calculate Results” button will be enabled.
4. Once a parameter file has been verified, click on the “Calculate Results” button. The program will first search for any existing results.

### *Batch Mode*

1. Navigate to File --> Load --> Batch
2. Populate the list of parameter files to include in the batch processing by navigating to each file and adding them to the list. Once populated, press “Enter”.
3. Input verification will be performed on all parameter files prior to calculating results. Therefore, critical errors should be caught before calculations begin. If errors are found, a list is populated in the “Input Verification Report” to help identify what to fix in the parameter file. These errors can be exported to a .txt file for easier troubleshooting by navigating to Export --> Error report. If no errors are found, the user can proceed to calculating results.
4. Unlike “individual mode”, “batch mode” does not check for existing results. Therefore, any existing results will be overwritten.
5. Once calculations are complete, all visualization tabs are disabled. However, the program can be reset and results for an individual subject can be loaded.

### *Anatomical Verification*

The purpose of this tab is to verify the accuracy of the anatomical landmarks and coordinate systems that were specified within the parameter file. This step is not necessary but helps to ensure the correctness of the output.

### View Options

In addition to the options in the View menu, the user can specify whether to visualize additional parameters.

- **Segments:** Indicates which segment to view in the plot area. Only one segment can be viewed at a time.
- **Landmark(s):** Indicates which anatomical landmark(s) to view in the plot area. Landmarks can be viewed individually or in groups (by holding down the ctrl key).
- **Input ACS:** Indicates which input ACS(s) to view in the plot area. ACS(s) can be selected (or deselected) individually or in groups (by holding down the ctrl key).
- **Output ACS:** Indicates which output ACS(s) to view in the plot area. ACS(s) can be selected (or deselected) individually or in groups (by holding down the ctrl key).
- **ACS Correction Factor:** Indicates whether to adjust the ACS(s) based on the correction factor specified in the ACSs sheet of the parameter file.
- **Viewer's Orientation:** Indicates which direction is the viewer's vertical. The axes are defined by the option selected in the Viewer's Perspective drop-down menu. The viewer's orientation can also be changed by pressing F1-F6 keys as follows:
  - F1: +X
  - F2: +Y
  - F3: +Z
  - F4: -X
  - F5: -Y
  - F6: -Z

*Note that these keyboard shortcuts cannot be used when rotate, pan, zoom, or data tip mode is turned on.*

### Model Appearance

Model color can be changed by navigating to Edit --> Model appearance --> Color. The mesh triangulation of the segments can be viewed on the segments by navigating to Edit --> Model appearance --> Triangulation. Segment transparency can be changed by navigating to Edit --> Model appearance --> Transparency.

### Kinematics

The purpose of this tab is to view plots of the joint kinematics specified within the Kinematics sheet of the parameter file. A single kinematic variable (or frame number) can be plotted on the x-axis, while one or multiple variables can be plotted on the y-axis. Multiple variables can be selected by holding down ctrl key.

### Motion Viewer

The purpose of this tab is to view the motion trial by animating the segments with the kinematics. Drag the slider bar on the bottom of the plot to advance the visualization through the frames of the data collection trial.

### View Options

- **Segments:** Indicates which segment(s) to view in the plot area. Segments can be viewed individually or in groups (by holding down the ctrl key).
- **Axes:** Indicates which segment ACS(s) to view in the plot area. Segment ACS(s) can be selected (or deselected) individually or in groups (by holding down the ctrl key). The ACS(s) that are displayed are output coordinate systems which have been adjusted using the correction factor specified in the ACSs sheet of the parameter file.



- Landmarks: Indicates which anatomical landmark(s) to view in the plot area. Anatomical landmark(s) can be selected (or deselected) individually or in groups (by holding down the ctrl key).
- Viewer's Perspective: Indicates which coordinate system from which to view the data. This perspective is kept fixed across the motion trial. In other words, the viewer will view the motion trial as though they were fixed to the entity that it is selected. Options include the laboratory frame and the ACS of each segment. Note: Because all calculations are initially performed using input ACSs, the perspective is defined by the selected segment's input ACS.
- Viewer's Orientation: Indicates which direction is the viewer's vertical. The axes are defined by the option selected in the Viewer's Perspective drop-down menu. The viewer's orientation can also be changed by pressing F1-F6 keys as follows:
  - F1: +X
  - F2: +Y
  - F3: +Z
  - F4: -X
  - F5: -Y
  - F6: -Z

*Note that these keyboard shortcuts cannot be used when rotate, pan, zoom, or data tip mode is turned on.*

#### *Model Appearance*

Model color can be changed by navigating to Edit --> Model appearance --> Color. Segment transparency can be changed by navigating to Edit --> Model appearance --> Transparency.

#### *Instantaneous Helical Axes*

Instantaneous helical axes (IHAs) can be visualized by navigating to View --> Helical Axes --> Instantaneous (keyboard shortcut: ctrl+H). A list will appear containing all joints that were specified in the Kinematics sheet of the parameter file. IHAs can be viewed individually or in groups (by holding down the ctrl key). The visualization can be turned off by navigating back to View --> Helical Axes --> Instantaneous, which unchecks the option and turns off the visualization.

In addition to the IHA itself, the following can also be visualized:

1. Trace: A trace of the helical axis tip can be visualized by navigating to View --> Helical Axes --> Trace. The visualization can be turned off by navigating back to View --> Helical Axes --> Trace, which unchecks the option and turns off the visualization.
2. Surface: A surface (created by connecting IHAs from the first frame to the current frame) can be visualized by navigating to View --> Helical Axes --> Surface.
3. All IHAs: All IHAs from the first frame to the current frame can be visualized by navigating to View --> Helical Axes --> All IHAs.

Each visualization can be turned off by navigating back to View --> Helical Axes --> Trace/Surface/All IHAs, which unchecks the option and turns off the visualization.

Additionally, the thickness of the IHA and trace can be modified by navigating to Edit --> Plot objects --> Line thickness. Additionally, the size of the frame markers in the trace path can be modified by navigating to Edit --> Plot objects --> Marker size. The color of IHAs cannot be changed.



### Laboratory Setup

If the necessary calibration information is provided in the Calibration sheet of the parameter file, the motion trial can be viewed relative to the laboratory setup by navigating to View --> Lab setup. Specifically, View --> Lab setup --> X-ray system(s) toggles on/off the visualization of the 3D motion capture volume including x-ray source(s), image intensifier(s), and image and lab coordinate systems. For biplane systems, the inter-beam angle is also calculated and displayed at the bottom of the window. The calibration cube can be viewed by navigating to View --> Lab setup --> Calibration cube.

### Proximities

The purpose of this tab is to view the proximity patterns. Drag the slider bar on the bottom of the plot to advance the visualization through the frames of the data collection trial. Only one proximity pattern can be visualized at a time.

### View Options

- Proximity Pattern: Indicates which proximity pattern to visualize in the plot area.
- Segments, Axes, and ROIs: Indicates the segment(s) and their respective output ACSs and ROIs to visualize in the plot area. Colormaps are applied to the ROI. Therefore, ROI must be checked to view proximity patterns.
- Contact Centers: Indicates which method for calculating the contact center is visualized: the minimum distance or the weighted centroid. The contact center can be visualized a point, a path between the first and current frame, and/or the vector between coordinates. The points and paths will only be visualized if the respective ROI is visible. Depending on the physical proximities between ROIs and the centroid bin limits specified in the Proximities sheet of the parameter file, it is possible that the weighted centroid does not exist. In these instances, the contact center will not be displayed, and the program status will alert the user. The thickness of the lines showing the contact path and vector between contact centers can be modified by navigating to Edit --> Plot objects --> Line thickness. The size of the contact center markers can be modified by navigating to Edit --> Plot objects --> Marker size. The color of the contact center lines and markers can be modified by navigating to Edit --> Plot objects --> Line color. The average colormap map calculated between the first and current frame can also be visualized by checking "Avg. map". Since the contact path and average colormap are calculated between the first and the current frame, the pattern over the entire motion trial can be visualized by dragging the slider bar to the last frame of the motion trial.
- Viewer's Perspective: Indicates which coordinate system from which to view the data. This perspective is kept fixed across the motion trial. In other words, the viewer will view the motion trial as though they were fixed to the entity that it is selected. Options include the laboratory frame and the ACS of each segment. Note: Because all calculations are initially performed using input ACSs, the perspective is defined by the selected segment's input ACS.
- Viewer's Orientation: Indicates which direction is the viewer's vertical. The axes are defined by the option selected in the Viewer's Perspective drop-down menu. The viewer's orientation can also be changed by pressing F1-F6 keys as follows:
  - F1: +X
  - F2: +Y
  - F3: +Z
  - F4: -X
  - F5: -Y

- F6: -Z

*Note that these keyboard shortcuts cannot be used when rotate, pan, zoom, or data tip mode is turned on.*

- **Data to Plot:** Indicates which data to display on the data plot. Whether the data is based on a minimum distance or centroid contact center depends on what is selected in the "Contact Centers" drop-down menu. Options are:
  1. Distance (i.e., the magnitude of the distance between the contact centers on each ROI)
  2. Normalized distance (if normalization parameter is TRUE for proximity pattern)
  3. Coordinates for ROI #1 (i.e., the X, Y, and Z coordinates of the contact center on ROI #1)
  4. Coordinates for ROI #2 (i.e., the X, Y, and Z coordinates of the contact center on ROI #2)
  5. Surface areas for ROI #1
  6. Surface areas for ROI #2

### Model Appearance

Model color can be changed by navigating to Edit --> Model appearance --> Color. The mesh triangulation of the segments can be viewed on the segments by navigating to Edit --> Model appearance --> Triangulation. Segment transparency can be changed by navigating to Edit --> Model appearance --> Transparency.

### Colorbar Appearance

The colormap can be changed by navigating to Edit --> Colorbar --> Colormap. Additionally, the colorbar limits (i.e., min and max values) can be changed by navigating to Edit --> Colorbar --> Limits.

### Status Log

The purpose of this tab is to record major milestones in the data processing and to alert the user to any errors or warnings.

## Output Files

### Kinematics

- **Kinematics.xlsx:** Provides relative kinematics for each joint specified in the Kinematics sheet of the parameter file.
- **Kinematics\_ACSwrtLab.xlsx:** Provides the 16-element transformation matrix of each output ACS relative to the lab coordinate system for each frame of motion (elements specified as row, column).
- **Kinematics\_IHA.xlsx:** Helical axis variables include the orientation of the helical axis ( $n$ ), the velocity ( $v$ ), and the position of the helical axis ( $s$ ). The variables  $n$  and  $s$  are defined in the proximal coordinate system of the joint (e.g., scapula for glenohumeral). Instantaneous helical axis is calculated for each joint based on the frame rate specified in the Info sheet of the parameter file. **Important Note:** The coordinates of the helical axis ( $n$  and  $s$ ) for left-sided data are NOT transformed to right-sided equivalence. This is to facilitate plotting, since the vector coordinates should plot directly onto the anatomy.
- **Plots:** Frame-by-angle plots for each joint specified in the parameter file.

Note: Code is written but currently commented out to save instantaneous surface velocities. This is because velocities are calculated across all faces on a triangulation, which results in a very large file once these values are reported over all frames and segments.

## Proximity Patterns

- Proximities <<PatternName>>.xlsx: Contains the minimum distance between ROIs and the proximity surface areas (in specified bins) for each frame. One file is written for each proximity pattern specified in the Proximities sheet of the parameter file.
- Proximities <<PatternName>> ContactCenterCoordinates.xlsx: Contains the contact center coordinates for the ROIs in the specified proximity pattern for each frame of the data collection trial. Coordinates are defined using both calculation methods (minimum distance, centroid) and in two coordinate systems (the segment output ACS specified in the parameter file and the lab frame). Contact center coordinates expressed in the local frame are transformed based on the transformations specified in the Proximities sheet of the parameter file. Global coordinates remain in the original lab/global reference frame. One file is written for each proximity pattern specified in the Proximities sheet of the parameter file.
- Proximities <<PatternName>> FaceDistances.xlsx: Contains the minimum distance to each face of the ROI for each frame of the data collection trial. Note: Face indices correspond to a triangulated surface in which duplicate vertices are removed. One file is written for each proximity pattern specified in the Proximities sheet of the parameter file.
- Proximities <<PatternName>> VectorData.xlsx: Contains the indices of the vertex on the opposing ROI that defines the minimum distance vector for each face of the mapped ROI for each frame of the data collection trial. Note: Face indices correspond to a triangulated surface in which duplicate vertices are removed. One file is written for each proximity pattern specified in the Proximities sheet of the parameter file.
- Plots: 10 plots: Minimum distance, normalized minimum distance (if appropriate) contact center coordinates for ROI #1 (minimum distance), contact center coordinates for ROI #1 (centroid), contact center coordinates for ROI #2 (minimum distance), contact center coordinates for ROI #2 (centroid), surface area for ROI #1 (minimum distance), surface area for ROI #1 (centroid), surface area for ROI #2 (minimum distance), and surface area for ROI #2 (centroid). Each of the 9 plots are written for each proximity pattern specified in the Proximities sheet of the parameter file. Contact center coordinates are expressed in the local frame for the ROI and transformed based on the transformations specified in the Proximities sheet of the parameter file.

## Software

- A .mat file is created once all data is processed for a subject based on the parameter file. This file is saved in the directory in which the parameter file is saved. This file needs to be kept in the same directory as its associated parameter file so that existing results can be loaded.

## Error Reports

In the event of a program error, a dialog box will appear displaying the error code. The user has the option to save an error report which contains the error code, the software version, and the computer's operating system. This information will be useful for troubleshooting the error.

## Compiler Module

Goal: Reduce and aggregate trial results within subjects, and compile data across subjects.

### Setting up the Parameter File

The parameter file provides all the necessary input for the program to run.

#### Parameters Sheet

The purpose of this sheet is to provide basic information on the parameters by which to reduce and aggregate data.

#### Data to Compile

- AnalysisModule: Specifies whether to process data from KinematicsToolbox Analysis Module.
  - Value1: TRUE/FALSE indicator of whether to process data from KinematicsToolbox Analysis Module. Required.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.
- MorphologyModule: Specifies whether to process data from KinematicsToolbox Morphology Module. Required.
  - Value1: TRUE/FALSE indicator of whether to process data from KinematicsToolbox Morphology Module. Required.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.

#### Output Specification

- Write files: Specifies whether to write results to file.
  - Value1: TRUE/FALSE indicator of whether to write results to file.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.
- Trial data: Specifies where to write the write output containing a trial's reduced (e.g., data reduced to every 5° of humerothoracic elevation) and summarized (e.g., averaged across the full trial) data.
  - Value1: The absolute or relative path to output directory. Required if "write files" is TRUE.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.
- Combined within-subject data: Specifies where to write the results of the data that will be combined across trials within a particular subject. The files written will be named "ID\_CompiledResults\_AllFrames.xlsx", "ID\_CompiledResults\_ReducedByAngle.xlsx", "ID\_CompiledResults\_LimitedRangeSummary.xlsx", and

- “ID\_CompiledResults\_WholeMotionSummary.xlsx”. If a suffix is specified (Value2), then the specified suffix will be added to the filenames.
- Value1: The absolute or relative path to write output. Required if “write files” is TRUE.
  - Value2: The filename suffix to distinguish files containing the combined results. For example, it may sometimes be necessary to run the Compiler multiple times on one dataset. If this were the case and the output directories (Value1) were the same between program runs, then specifying a unique filename suffix for each run will prevent the results file from getting overwritten in the second run. However, this parameter is optional.
  - Value3: Ignored.
  - Value4: Ignored.
- Combined between-subject data: Specifies where to write the results of the data that will be combined across subjects. The file written will be named “AllSubjects\_CompiledResults.xlsx”. If a suffix is specified (Value2), then the specified suffix will be added to the filenames.
    - Value1: The absolute or relative path to write output.
    - Value2: The filename suffix to distinguish files containing the combined results. For example, it may sometimes be necessary to run the Compiler multiple times on one dataset. If this were the case and the output directories (Value1) were the same between program runs, then specifying a unique filename suffix for each run will prevent the results file from getting overwritten in the second run. However, this parameter is optional.
    - Value3: Ignored.
    - Value4: Ignored.

### *Data Reduction*

- Interval: Input specifies how to define intervals by which to reduce the data. Note: If the data is not to be reduced, then remove the line from the parameter file. Otherwise, an unlimited number of intervals can be specified (e.g., every 5° of humerothoracic and glenohumeral elevation).
  - Value1: The reference variable that defines how the data will be reduced (e.g., HTelev). Only kinematic DOF variables reported in Kinematics results files written by KinematicsToolbox Analysis Module can be specified as a reference variable. In other words, valid reference variables are specified as “DOF names: rotation” or “DOF names: position” in the Kinematics sheet of the AnalysisModule parameter file. Required.
  - Value2: The interval step by which to reduce the data. Valid values are positive numbers. Required.
  - Value3: The tolerance by which to reduce the data at each interval step. In other words, values of the reference variable that are within  $\pm$  the tolerance will be “assigned” to that interval step and included in the average when the data is reduced. For example, if the interval step is 5°, the tolerance is  $\pm 2^\circ$ , and a subject’s reference values are [..., 23.5°, 22.6°, 21.7°, 20.9°, 19.4°, 18.1°, 17.8°, ...], then the values pertaining to the 20° step will be [21.7°, 20.9°, 19.4°, 18.1°] since they are all within the tolerance ( $\pm 2^\circ$ ) of the 20° interval, which is a multiple of the interval step (5°). Consequently, the reduced data for the 20° interval will be the average of the data for the frames in which the reference values are [21.7°, 20.9°, 19.4°, 18.1°]. Valid values are positive numbers. Required.

- Value4: Indicator of whether to include or exclude repeated interval steps. For example, as a person raises their arm, they may begin to lower it at the end, so humerothoracic elevation values may be 150°, 155°, 160°, 155°. Selecting “inclusive” would maintain all data (including the second instance of 155°, when the arm starts to lower again), while “exclusive” would remove the extreme duplicate data from the reduced data (i.e., the second instance of 155°). Similarly, if a person raises their arm, they may start then lower then raise again, so humerothoracic elevation values may be 25°, 30°, 25°, 30°, 35°, etc. Selecting “inclusive” would maintain all data (including the first instance of 25° and 30°, when the arm started to raise for the first time), while “exclusive” would remove the extreme duplicate data from the reduced data (e.g., the first instance of 25° and 30°). Required.

*Note: An unlimited number of intervals can be specified (e.g., reduce the data by every 5 degrees of humerothoracic elevation and 2 degrees of glenohumeral elevation). To do so, duplicate the line parameter file line beginning with “Interval” and update with new parameter values.*

### Range Summary

- Range: Input specifies how to define ranges by which to summarize data. Note: If the data is not to be summarized within a limited range, then remove the line from the parameter file. Otherwise, an unlimited number of ranges can be specified (e.g., summarize the data between 20-80° glenohumeral elevation and 30-150° humerothoracic elevation).
  - Value1: The name of the reference variable that defines the range. Only kinematic DOF variables reported in Kinematics results files written by KinematicsToolbox AnalysisModule can be specified as a reference variable. In other words, valid reference variables are specified as “DOF names: rotation” or “DOF names: position” in the Kinematics sheet of the AnalysisModule parameter file. Required.
  - Value2: The lower limit of the range. Required.
  - Value3: The upper limit of the range. Required.
  - Value4: The tolerance about the values specified as the lower or upper limits. For example, if the parameter file specifies a tolerance of 2°, lower limit of 20°, and upper limit of 80°, then data any data between 18-82° will be included (i.e., averaged) in the range summary. Required.

*Note: An unlimited number of ranges by which to summarize the data can be specified (e.g., summarize between 20-80° glenohumeral elevation and between 30-150° humerothoracic elevation). To do so, duplicate the line parameter file line beginning with “Range” and update with new parameter values.*

### Within-Subject Aggregation

- Subject variable: Specifies the variable name that identifies the subject’s study identifier in the results files (e.g., ID).
  - Value1: Variable name for subject ID. Required.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.

- Grouping variable(s): Specifies the variable(s) by which to combine the data across trials. A maximum of 4 variables can be specified. If none are specified, then data will be aggregated across all trials based on the subject variable only.

### Misc. Parameters

- Proximities: Specifies whether proximity data exist within the results files and should be included in the compilation.
  - Value1: TRUE/FALSE indicator of whether proximity data exists.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.
- Overlap type: Indicator of how to determine whether proximity overlap (i.e., contact) occurred in an interval step during data reduction.
  - Value1: Indicator. Valid values are “any” or “majority”. If “any” is selected, then “overlap” will be deemed TRUE for the reduced data if contact was detected to have occurred at least once in the reduced data (even if it only occurred for 1 frame out of the 10 in the reduced data). If “majority” is selected, then “overlap” will be deemed TRUE only when contact occurred for >50% of the frames within the reduced data. Required if proximities is TRUE.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.
- Path length distance method: Indicator of how to calculate path length during the whole motion and limited range summaries.
  - Value1: Indicator. Valid values are “Euclidean” or “geodesic”. If “Euclidean” is selected, the path length will be calculated as the sum of the shortest 3D distance between contact center points across the motion trial. If “geodesic” is selected, the path length will be calculated as the sum of the shortest 3D distance along the surface curvature between contact center points across the motion trial. Required if proximities is TRUE.
  - Value2: Ignored.
  - Value3: Ignored.
  - Value4: Ignored.

### Paths Sheet

The purpose of this sheet is to specify the KinematicsToolbox results files to be used in the run of the Compiler module.

- Type: The parameter file type. Valid values are “Analysis” or “Morphology”. Required.
- Path: The absolute or relative path to the KinematicsToolbox results file. These are the .mat files that are written out by the Morphology and Analysis Modules, and by default are written to the directory of the parameter file. Required.

## Menu Bar

### File

Controls the information being calculated and/or displayed by the program.

- Load: Loads one parameter file.
- Reset: Resets the program by clearing all non-GUI variables.
- Quit: Quits the program (keyboard shortcut: ctrl+Q).



## Export

- Range verification report: Exports an .xlsx file containing data on whether trials have the upper and lower bounds of each range specified in the parameter file. This helps determine the bounds of the range that will ensure a similar range across trials and subjects.
- Error report: Exports a .txt file containing the report of errors found during the input verification process.

## Help

Provides information and help about KinematicsToolbox.

- About: Provides information about KinematicsToolbox (including version).
- Permissions: Provides the date and number of days until current permissions to use KinematicsToolbox expires.
- Documentation: Opens the help documentation.

## Running the Module

### Load Parameter File

4. Load a parameter file by clicking on “Load Parameter File” or by navigating to File --> Load. A file selection dialog box will appear allowing the user to navigate to the parameter file to analyze.
5. Once the file is selected, the program will proceed to verify that all of the parameters specified in the compiler module parameter file are valid, that all of the analysis and/or morphology module parameter files listed exist and contain all of the necessary information, and that all of the output files contain the same variables so that data can be compiled. The goal of this step is to help prevent code errors downstream. This process may not catch 100% of potential issues; however, it should catch most.
  - a. If errors are detected, a list is populated in the “Input Verification Report” to help identify what to fix in the parameter file. These errors can be exported to a .txt file for easier troubleshooting by navigating to Export --> Error report. If no errors are detected, then the “Digitize Landmarks” and “Calculate Morphology” buttons will be enabled.
  - b. If errors are not detected, then the “Aggregate Data” button will become enabled.

### Compile Within Subject(s)

Compiling data within subject(s) means that individual trial data will be reduced, summarized, and combined as follows:

- **Reduced**: Trial data, consisting of data across all frames of the data collection trial, will be reduced as specified in the “Data Reduction” section of the Compiler Module parameter file. For example, shoulder data can be reduced to every 5° of humerothoracic elevation.
- **Summarized**: Trial data, consisting of data across all frames of the data collection trial, will be summarized across the entire motion and for a specified range of motion as specified in the “Range Summary” section of the Compiler Module parameter file. For example, shoulder data can be summarized (i.e., reported as mean, min, max)



between 30-150° humerothoracic elevation. Contact center path lengths and helical dispersion variables are also calculated across these ranges.

- **Aggregated:** Data is aggregated (i.e., combined) across individual trials based on the grouping variables specified in the “Within-Subject Aggregation” section of the Compiler Module parameter file. In other words, data is averaged across specified trials (e.g., side, condition).

### Compile Across Subject(s)

Compiling data across subject(s) means that reduced, summarized, and aggregated data will be combined into a single file across subjects. These files are written to the destination specified in the “Within-Subject Aggregation” line of the Compiler Module parameter file.

### Data Visualization

This tab allows the user to view within-subject data across trials. Note that only kinematic data can be visualized (i.e., not morphology data).

#### View Options

- **Study ID:** Specifies which subject’s data to view.
- **Data Type:** Specifies which type of data to view.
  - **By frame:** Displays data for all frames of the motion trial. Line plot with individual lines corresponding to the “Trial(s)” listbox selection.
  - **Reduced:** Displays reduced data for the selected reduction interval (specified in the “Data Reduction” section of the Compiler Module parameter file). Line plot with individual lines corresponding to the “Trial(s)” listbox selection.
  - **Whole motion summary:** Displays summary data for the whole motion. Grouped bar plot with the summary statistics grouped according to the “Trial(s)” listbox selection.
  - **Range summary:** Displays summary data for the selected range (specified in the “Within-Subject Aggregation” section of the Compiler Module parameter file). Grouped bar plot with the summary statistics grouped according to the “Trial(s)” listbox selection.
- **Variable:** Specifies which variable to plot. Only one variable can be plotted at a time.
- **Trial(s):** Specifies which trial(s) to plot.

### Output Files

The following files provide compiled data for individual trials and are written to the destination specified in the “Reduced data” line of the Compiler Module parameter file.

- “\_CompiledResults\_ReducedByAngle.xlsx”
  - Separate sheet(s) are written for each data reduction interval specified in the Compiler module parameter file, each with the following 2 suffixes:
    - “All”: Contains the reduced data for all trial(s) used to calculate the summary data for the specified reduction interval
    - “Avg”: Contains the averaged summary data (e.g., mean, helical dispersion, contact path lengths) for the reduction interval across all trials as specified in the Compiler Module parameter file.
  - Note that kinematics and proximity variables have all summary statistics (i.e., mean, median, standard deviation, minimum, maximum, range). However, helical dispersion and contact path lengths do not have summary statistics because they are a single attribute. For example, a path length is not a mean,

it is the sum of individual segment lengths. Likewise, the angular helical dispersion does not have a mean, it has a single value. Therefore, these variables are provided in the “magnitude” column.

- “\_CompiledResults\_WholeMotionSummary.xlsx”
  - Contains two sheets that summarize data (e.g., mean, SD, helical dispersion, contact path lengths) for the whole motion trial.
    - “All|” : Contains the data for all trial(s) used to calculate the summary data across the whole motion trial.
    - “Avg|” : Contains the averaged summary data (e.g., mean, helical dispersion, contact path lengths) for all trials as specified in the Compiler Module parameter file.
  - Note that kinematics and proximity variables have all summary statistics (i.e., mean, median, standard deviation, minimum, maximum, range). However, helical dispersion and contact path lengths do not have summary statistics because they are a single attribute. For example, a path length is not a mean, it is the sum of individual segment lengths. Likewise, the angular helical dispersion does not have a mean, it has a single value. Therefore, these variables are provided in the “magnitude” column.
- “\_CompiledResults\_RangeSummary.xlsx”
  - Separate sheet(s) are written for each range summary specified in the Compiler module parameter file, each with the following 2 suffixes:
    - “All|” : Contains the data for all trial(s) used to calculate the summary data for the specified range.
    - “Avg|” : Contains the summary data (e.g., mean, SD, helical dispersion, contact path lengths) for the specified range.

The following files provide compiled data across trials and are written to the destination specified in the “Combined data” line of the Compiler Module parameter file.

- “\_CompiledResults\_ReducedByAngle.xlsx”
  - Contains aggregated data reduced as specified in the Compiler Module parameter file.
  - Separate sheet(s) are written for each data reduction interval specified in the Compiler module parameter file.
- “\_CompiledResults\_WholeMotionSummary.xlsx”
  - Contains aggregated summary data (e.g., mean, SD, helical dispersion, contact path lengths) for the whole motion trial.
- “\_CompiledResults\_RangeSummary.xlsx”
  - Contains aggregated summary data (e.g., mean, SD, helical dispersion, contact path lengths) for each range summary as specified in the Compiler Module parameter file.
  - Separate sheet(s) are written for each range summary specified in the Compiler module parameter file.
- “AllSubjects\_CompiledResults.xlsx”
  - Contains all of the aggregated data across all subjects.
  - Separate sheets are written for each type of data (e.g., reduced, range summary, whole motion, morphology).

## Error Reports

In the event of a program error, a dialog box will appear displaying the error code. The user has the option to save an error report which contains the error code, the software version, and the computer's operating system. This information will be useful for troubleshooting the error.

## Appendices

### Appendix A – Relative Path Specification

Relative paths make it easy to define default directories and/or file locations if a study utilizes a highly structured directory/file name system. It also allows for the specification of files that may be located on different drives if accessed by different computers (e.g., the server may be V: drive on one computer and Y: drive on another). Since all files are referenced from the location of the parameter file, as long as the project folder structure does not change between computers, the same parameter file can be used regardless of whether the drive and/or path above the level of the project folder changes. It is highly recommended to use relative paths.

For example, assume all subjects have the following folder/file structure:

```
C:\User\Projects\Motion\subjectID\side\trial\subjectID side bone tracking.csv.
```

For example, an absolute path using this generic structure could look like this:

```
C:\User\Projects\Motion\BL08\R\Rep1\BL08 R humerus.csv
```

And also assume the parameter file is located here (i.e., at the trial level within the subject's folder, as recommended):

```
C:\User\Projects\Motion\BL08\R\Rep1\ folder.
```

Then we can specify the relative path for the file "BL08 R humerus.csv" as:

```
.\BL08 R humerus.csv
```

This is because the single '.' indicates the file is located within the current directory, which is defined by where the parameter file is located.

However, say all of the parameter files were located here:

```
C:\User\Projects\Motion\BL08\ParameterFiles\
```

And the humeral kinematics file is located here:

```
C:\User\Projects\Motion\BL08\R\Rep1\BL08 R humerus.csv
```

In this case, the file is located up two levels of the directory. Moving up one level within the directory can be specified using '..'. Therefore, we can specify the humeral kinematics as a relative path as follows:

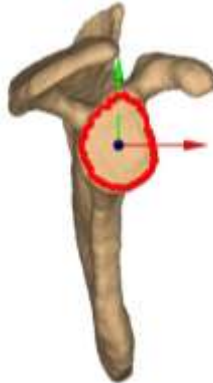
```
..\..\R\Rep1\BL08 R humerus.csv
```

## Appendix B – Description of Morphology Calculations

### Scapular Morphology

#### *Glenoid coordinate system*

1. The glenoid STL is first transformed into the scapular coordinate system specified in the Scapula sheet of the parameter file. This allows us to make sense of anatomical directions.
2. Then we calculate the principal axes of the glenoid ROI to better orient the data to the glenoid shape. We then transform the glenoid STL into this preliminary GCS.
3. Then we find the points belonging to the glenoid rim. To do this we first project a point laterally off the surface of the glenoid by a specified distance (hover). Then we do an iterative search for the points along the rim by casting a ray that starts at the horizontal (0 deg) and then angles downwards towards the glenoid. If this ray intersects the glenoid, then what is intersected is assumed to be the rim. This calculation is done iteratively all the way around the glenoid clockface (360 degrees). Due to the nature of this search, it is best that the glenoid STL does not contain part of the coracoid or scapular body.
4. Then, the principal axes are calculated for the points detected along the glenoid rim. The result of this calculation is the final GCS.

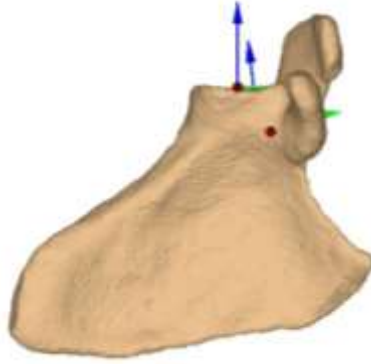


#### *Glenoid anatomical points*

The glenoid anatomical points are calculated as the points along the glenoid rim that have the closest angular distance to each of the glenoid coordinate system axes.

#### *Glenoid inclination*

1. A superior/inferior vector is constructed from the superior glenoid and inferior glenoid landmarks (described above).
2. This axis is projected onto the coronal plane of the scapular coordinate system specified in the Scapula sheet of the parameter file.
3. Glenoid inclination is calculated as the angle between the superior/inferior vector and the glenoid superior axis and expressed in units of degrees. A positive value indicates glenoid inclination and a negative value indicates glenoid declination.



### *Glenoid version*

1. An anterior/posterior axis is constructed from the anterior glenoid and posterior glenoid landmarks (described above).
2. This axis is projected onto the transverse plane of the scapular coordinate system specified in the Scapula sheet of the parameter file.
3. Glenoid version is calculated as the angle between the anterior/posterior vector and the glenoid anterior axis and expressed in units of degrees. A positive value indicates glenoid anteversion and a negative value indicates glenoid retroversion.



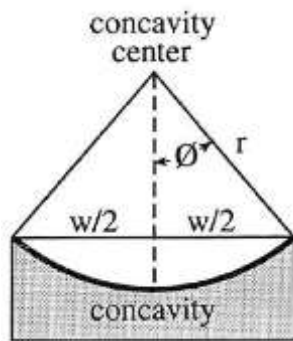
### *Glenoid superior/inferior radius of curvature*

1. All points on the glenoid ROI are projected onto the sagittal plane of the glenoid coordinate system.
2. Points that are on the glenoid face are identified by determining whether the point lies within the glenoid rim contour (defined during the glenoid coordinate system calculation).
3. Points defining the glenoid face are converted to a surface interpolation to increase resolution.
4. A plane is positioned along the superior/inferior axis of the glenoid coordinate system (for superior/inferior ROC) or along the anterior/posterior axis of the glenoid coordinate system (for anterior/posterior ROC), and the points that lie along the plane on the glenoid face are identified.
5. A circle is fit to the points identified. The radius of this circle is glenoid's radius of curvature (ROC) and is expressed in units of mm. A positive ROC indicates the glenoid is concave and a negative ROC indicates the glenoid is convex (which can happen with a very flat glenoid).



### Superior/inferior and anterior/posterior stability angle

Represents the maximum angle (in degrees) that the glenohumeral resultant force vector may deviate from the glenoid concavity center line and be balanced within the glenoid (per Lippitt and Matsen. *Clin Orthop and Related Res*, 1993).

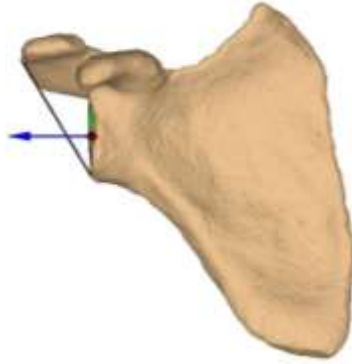


$$\text{Stability angle} = \sin^{-1} \left( \frac{w}{2} \right) / r$$

Where  $w$  is the glenoid height or width (as appropriate), and  $r$  is the glenoid height or width (as appropriate).

### Critical shoulder angle

1. The lateral-most point on the acromial ROI is calculated by transforming the ROI into the GCS. The point with the maximal coordinate value in the lateral dimension is determined to be the lateral acromion.
2. Vector1 is defined as pointing from the superior glenoid from the inferior glenoid.
3. Vector2 is defined as pointing from the lateral acromion from the inferior glenoid.
4. CSA is the 3D angle between vector1 and vector2 via the dot product and expressed in units of degrees.



## Humeral Morphology

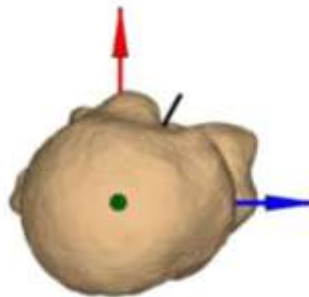
### *Humeral head center*

1. A sphere is fit to the articular surface ROI using a least-squares algorithm.
2. The radius and center coordinates of this sphere are calculated and expressed in units of mm.



### *Retroversion*

1. A vector is constructed between the humeral head center (tail) to the biceps groove (tip) landmarks.
2. This vector is projected onto the transverse plane of the humeral coordinate system specified in the Humerus sheet of the parameter file.
3. Retroversion is calculated angle between the humeral head/biceps groove vector and the lateral axis of the humeral reference coordinate system and expressed in units of degrees. A positive value indicates glenoid retroversion.





### Humeral length

1. The humeral model is transformed so that it is consistent with the humeral reference coordinate system.
2. The superior- and inferior-most points are detected on the humeral model.
3. Humeral length is calculated as the 3D distance between the superior- and inferior-most points and expressed in units of mm.

### Glenohumeral Morphology

#### *Glenohumeral superior/inferior and anterior/posterior conformity index*

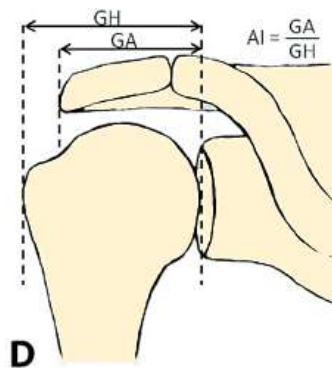
Calculated as the ratio of superior/inferior or anterior/posterior glenoid radius of curvature (ROC) (as appropriate) to the humeral head radius of curvature. A conformity index  $>1$  indicates the glenoid ROC is larger than the humeral ROC, while a conformity index of  $<1$  indicates the humeral ROC is larger than the glenoid ROC.

#### *Glenohumeral superior/inferior and anterior/posterior ratio*

Calculated as the ratio of glenoid height or width (as appropriate) to the humeral head diameter. A ratio  $>1$  indicates the glenoid dimension is larger than the humeral dimension, while a ratio of  $<1$  indicates the humeral dimension is larger than the glenoid dimension.

#### *Acromial index*

Describes the lateral extension of the acromion over the humeral head (per Nyffeler et al. *J Bone Joint Surg Am*, 2006). First, the humerus and scapula are aligned with glenoid ACS. The humerus is translated laterally the distance of the humeral head radius. Second, the lateral-most points on the acromion and humeral head are identified. The lateral distance between the glenoid plane and the lateral acromion (GA) and humeral head (GH) are calculated. Finally, the acromial index is calculated as the ratio of these distances ( $AI = GA/GH$ ). A larger lateral acromial index represents a more lateral acromial extension.

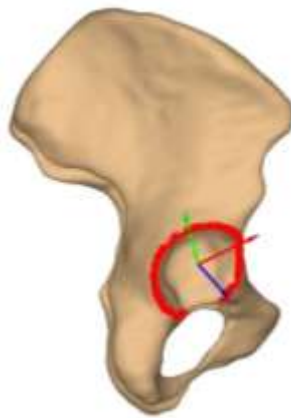


### Pelvis Morphology

#### *Acetabular coordinate system*

1. The acetabulum STL is first transformed into the pelvis coordinate system specified in the Pelvis sheet of the parameter file. This allows us to make sense of anatomical directions.

2. Then we calculate the principal axes of the acetabular ROI to better orient the data to the acetabular shape. We then transform the acetabular STL into this preliminary acetabular coordinate system.
3. Then we find the points belonging to the acetabular rim. To do this we first project a point laterally off the surface of the acetabulum by a specified distance (hover). Then we do an iterative search for the points along the rim by casting a ray that starts at the horizontal (0 deg) and then angles downwards towards the acetabulum. If this ray intersects the acetabulum, then what is intersected is assumed to be the rim. This calculation is done iteratively all the way around the acetabular clockface (360 degrees). Due to the nature of this search, it is best that the acetabular STL does not contain part of the pelvis.
4. Then, the principal axes are calculated for the points detected along the glenoid rim. The result of this calculation is the final acetabular coordinate system.



## Femoral Morphology

### *Femoral head center*

1. A sphere is fit to the articular surface ROI using a least-squares algorithm.
2. The radius and center coordinates of this sphere are calculated and expressed in units of mm.



## Appendix C – Description of Proximity Calculations

### Instantaneous Surface Velocities

This calculation is made by first down-sampling the vertices across the triangulation by 75% to help computational efficiency and prevent the visualization from being overly crowded. Then, the partial derivative of the displacement of each point is calculated across time. Velocity vectors are scaled to 200% of the instantaneous velocity.

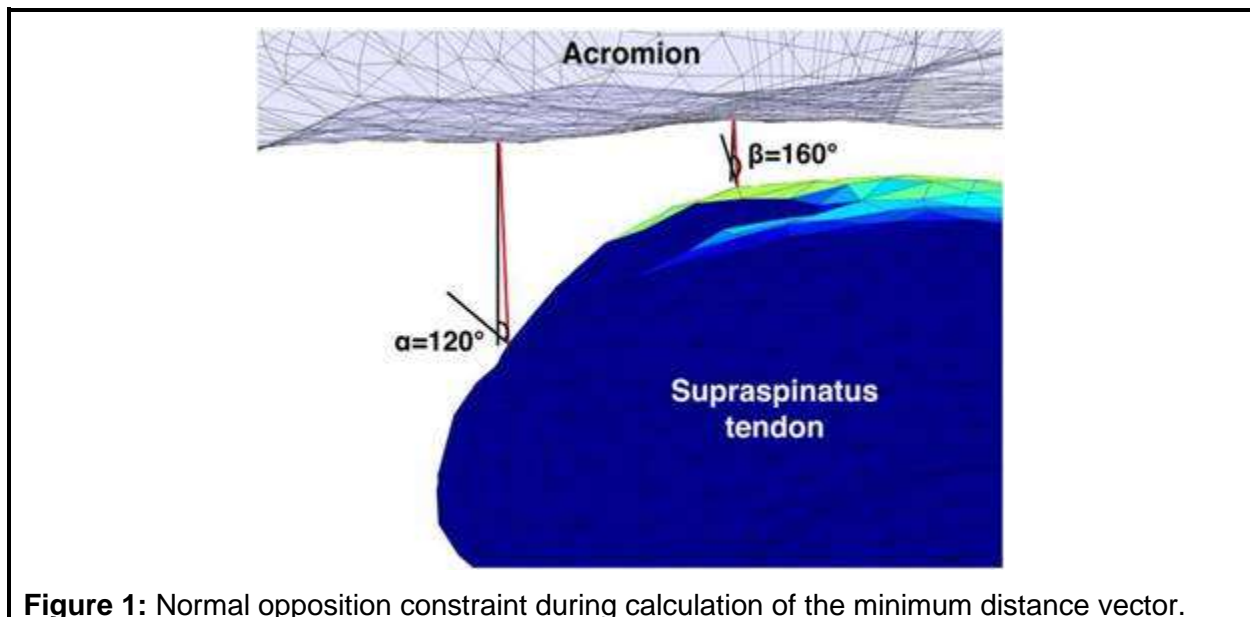
### User-Specified Constraints for Proximity Calculations

#### *Test Vector Penetration*

This constraint tests whether the minimum distance vector penetrates (i.e., intersects) the mapped segment. For example, at lower angles of arm elevation, the shortest distance between the rotator cuff footprint and the glenoid is through the humeral head surface, which is physiologically illogical. When "test vector penetration" is specified as TRUE in the parameter file, the minimum distance vector between each face on the mapped surface is tested to see if it intersects with the whole mapped segment. The entire mapped segment is used in this calculation (not just the ROI) as the minimum distance vector may intersect the segment outside the ROI as in the case of internal impingement (described above). This constraint is computationally intensive and is therefore performed on the minimum distance matrix after it is collapsed.

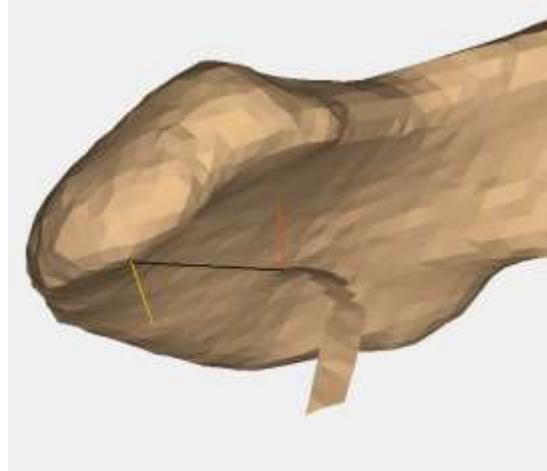
#### *Test Normal Opposition*

This constraint tests whether the opposition angle between pairwise face normals exceeds a specified threshold ([Lawrence et al., J Biomech 2018](#)), and helps ensure that the faces detected as being the closest are reasonably aligned to each other to reflect potential for tissue compression (Figure 1). However, this constraint may result in a minimum distance vector that is illogical because the location on the mapped surface is not under the opposing surface (Figure 2). This calculation is performed on the entire minimum distance matrix (i.e., prior to collapse).



**Figure 1:** Normal opposition constraint during calculation of the minimum distance vector.

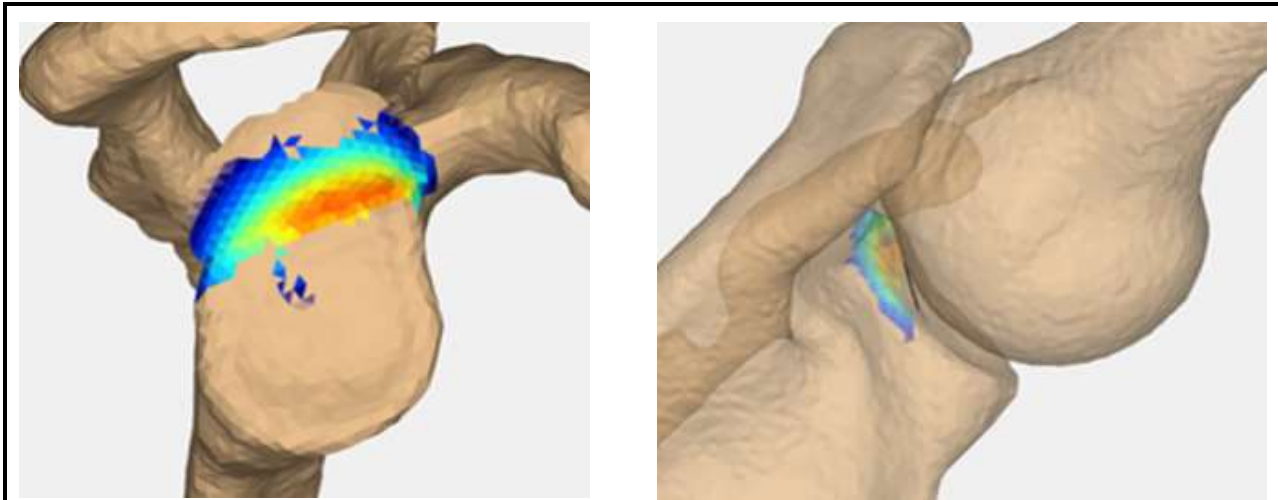
The two red lines represent the unconstrained minimum distance vectors between two pairwise sets of vertices. The threshAng for this example is 30 degrees. The four solid lines represent the vertex normal vectors. When the opposition angle between pairwise vertex normals was  $<150^\circ$  (e.g.,  $\alpha$ ), the minimum distance vector is considered invalid because the surface of the supraspinatus tendon is not oriented towards the coracoacromial arch surface and therefore would not be compressed by it. When the opposition angle between pairwise vertex normals was  $\geq 150^\circ$  (e.g.,  $\beta$ ), the minimum distance vector was retained. Figure from [Lawrence et al., J Biomech 2018](#).



**Figure 2:** An example in which the oppAngle test results in a minimum distance that meets the oppAngle criteria but is shifted and thus illogical (ROI1 = acromion, ROI2 = articular margin). The black vector is the minimum distance vector between the acromion and articular margin of the footprint; the orange vector is the face normal for the minimum distance location on the articular margin; the yellow vector is the face normal for the minimum distance location on the acromion. The oppAngle between the two vectors is 161 degrees and the threshAng = 30. Therefore, it is within the tolerance for this constraint and made valid. However, its distance between these two vertices is still less than a vector between the articular margin and a point directly above it on the acromion. Thus, an issue with the angular constraint is that it can still result in illogical minimum distance vectors. The test for angular constraint may be appropriate in this case.

### *Test Angular Deviation*

This constraint tests whether the angle between the mapped vertex normal and the minimum distance vector exceeds a given threshold. This calculation is useful to ensure the mapped surface is reasonably underneath the opposing surface. An example of when this calculation may be useful is shown in Figure 3. This calculation is performed on the entire minimum distance matrix (i.e., prior to collapse).



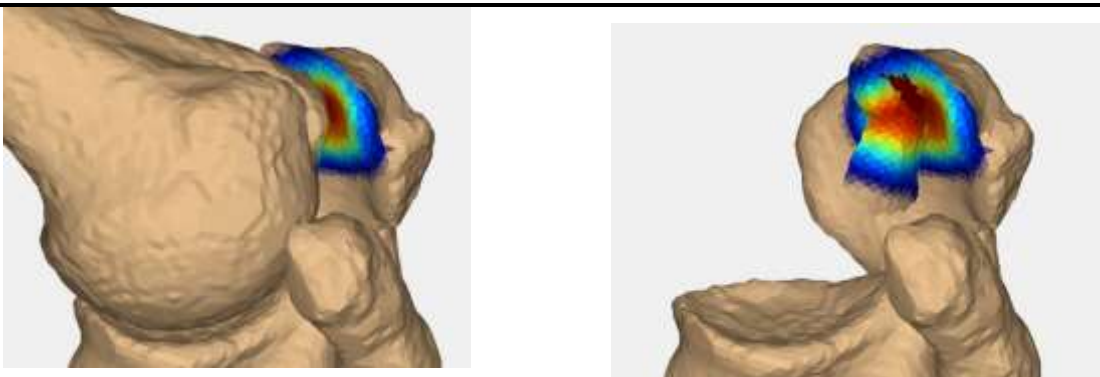
**Figure 3:** An example of when an angular constraint is useful. In this individual, abnormal colormapping occurred on the glenoid at higher angles. Upon closer inspection, this appears valid. From the glenoid's perspective, the closest point on the footprint is the very medial aspect of the articular margin. This vector does not penetrate the humeral head due to a relatively flat transition from the footprint to the articular surface. Therefore, with an unconstrained normal opposition angle, abnormal but valid colormapping occurred. Specifying a threshold angle of 60 degrees for the test for normal opposition resulted in more reasonable colormapping. Too low of an angle may result in invalidating good vectors when the surface is irregular.

#### Minimum Distance Calculation

1. Calculate point-to-point distances between all pairwise vertices on the 2 ROIs (variable: p2pDist).
2. Test whether the two ROIs are overlapping (variable: intersect). This test is conducted by determining whether any edge of one ROI intersects an edge of the other. It returns TRUE/FALSE for the entire structures and not *where* the intersection occurs.
3. Test normal opposition angle (if specified)
  - a. Calculate the opposition angle between all pairwise vertex normal vectors on the 2 ROIs (variable: oppAngle).
  - b. If the oppAngle > (180 – threshAng) (variable: validP2Pdist), then the corresponding pairwise distance is valid (value maintained in validP2Pdist).
  - c. If false, then make the corresponding pairwise distance invalid (set to 1000 in validP2Pdist for documentation) (Figure 1).
  - d. Note that this calculation may not catch all illogical minimum distance vectors as it does not account for the position of the pairwise vertices, only the angular distance (an example of an illogical but valid minimum distance vector is shown in Figure 2).
4. Test angular deviation (if specified)
  - a. Calculate the angle between all pairwise mindist vectors and the vertex normal vectors on the mapped surface (variable: ang). This constraint essentially creates a "cone" around the vertex normal with specified angular deviation such that only minimum distance vectors within the cone are valid. An example of when this constraint is useful is in Figure 3.

- b. If the  $\text{ang} < \text{coneAng}$ , then the corresponding pairwise distance is valid (value maintained in `validP2Pdist`).
  - c. If false, then make the corresponding pairwise distance invalid (set to 1002 in `validP2Pdist` for documentation).
- 5. Determine the smallest distance for each vertex of the mapped ROI (variable: `validMinDist`) and the corresponding vertex on the mapped ROI (variable: `distIndex`)
- 6. Test vector penetration (if specified)
  - a. Test whether the minimum distance vector from each vertex of the ROI penetrates the mapped and opposing segments. This test helps prevent a minimum distance vector off an ROI from intersecting (i.e., going through) its own segment, as is often the case at lower angles of humeral elevation when calculating the distance between the rotator cuff footprint and the glenoid.
  - b. If true, then the corresponding distance is invalid (value set to 1001 in `validMinDist` for documentation).
  - c. If false, then corresponding distance is valid (value maintained in `validMinDist`).
- 7. If the two ROIs are detected to intersect (step 2), then need to make sure that the distances for any vertex of the mapped surface inside the opposing surface is set to 0 (otherwise the distance value will be positive but will not reflect that the structures are in contact). This is done by checking the points defining the minimum distance vector to each vertex of the mapped ROI. This step involves more than just detecting intersection, it needs to detect when a point (or face) is entirely in the other ROI. This process is complicated when ROIs are not convex. Several (albeit imperfect) checks have been built in:
  - a. If the indexed point on the mapped ROI is detected to be within the opposing ROI, then set the minimum distance to 0. Importantly: this test may have false negatives when the ROIs are not convex. However, the test is done first because it is the simplest and if it is true, nothing else needs to be done.
  - b. If the indexed point on the mapped ROI is not detected to be within the opposing ROI (potentially a false negative) AND the `mindist` is *valid* (i.e.,  $< 1000$ ), then check if the indexed point on the mapped ROI is within the opposing *segment* AND if the corresponding indexed point on the opposing ROI is within the mapped *segment*. It is necessary to test in both directions to account for an issue that occurs when the mapped and opposing ROIs intersect AND a portion of the opposing segment that is not the opposing ROI is in contact with the mapped surface. In this case, the minimum distance to the faces on the mapped ROI that intersected the opposing segment (but not the ROI) were erroneously classified as being in contact (i.e., minimum distance set to 0). This issue was first identified when the footprint was contact with the glenoid rim and `inTest` also reflect contact between the glenoid and other surfaces of the humerus (e.g., articular surface). The faces of the glenoid ROI in contact with the articular surface were colored red (i.e., in contact) even though they may be distant from the footprint ROI. It is possible this solution may not detect intersection when only very slight contact has occurred (e.g., a single vertex on the mapped surface is within the opposing surface).
  - c. If the `mindist` is *invalid* (i.e.,  $\geq 1000$ ), then things get more complicated. This is because all `mindist` vectors failed the tests and when the `mindist` is calculated, the index on the opposing surface (`distIndex`) will be 1, which is illogical.

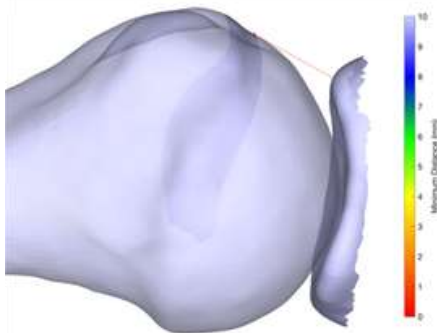
- i. If the mindist is *invalid* (i.e.,  $\geq 1000$ ) AND if the indexed point on the mapped ROI is detected to be within the opposing ROI AND the mapped ROI is inside the opposing segment, then the mindist is set to 0 and the index on the opposing surface (distIndex) is set to the face on the opposing surface closest to the mapped face. The second part of this check is necessary to help ensure the index on the opposing surface is valid (i.e., not 1 since all points on the mapped surface failed the tests). However, it may result in detecting contact with a different part of the opposing segment. For example, in Figure 4, the mapped surface is the acromion, which is in contact with the footprint. However, the check of whether specific points on the acromion are inside the humerus detects contact and assigns a minimum distance of 0 to those faces on the acromion even though they are not in contact with the footprint. This is a known issue.
- ii. If the mindist is *invalid* (i.e.,  $\geq 1000$ ) AND if the indexed point on the mapped ROI is not detected to be within the opposing ROI (potentially a false negative), then check how close the faces are. If they are within a tolerance (1 mm), then override the test results and set the distance and index on the opposing surface to the proximity calculated. This may result in mapped faces inside the opposing structure as having a positive value instead of 0 but it is as good as it's going to get with a non-convex ROI. Although the distance of a point inside the opposing surface will not be set to 0, it will ensure the distance is reasonably small to help prevent irregular colormapping (e.g., the distance of a point very close to surface being  $>1000$  and having irregular colormapping as a result). Furthermore, other locations of contact will be detected so the minimum distance across the whole ROI will still be valid (i.e., 0).
- iii. If the mindist is *invalid* (i.e.,  $\geq 1000$ ) AND if the index on the opposing surface is 1, then it is illogical and hasn't been fixed by previous logic. Therefore, just set the index to NaN to prevent an illogical minimum distance vector from displaying in the Proximity tab.



**Figure 4:** An example of the check for determining whether points on an ROI (acromion) are inside the opposing segment (humerus) returns values of TRUE even though the opposing points are not on the ROI.



8. Once the minimum distances to each vertex of the mapped ROI are validated, the minimum distance is identified on the mapped surface (variable: minDist)
9. Determine the coordinates of the minimum distance vector on both surfaces.
  - a. If contact occurred and one face was in contact: the face is the minimum distance location.
  - b. If contact occurred and more than one face were in contact: find the point closest to the minimum distance location on the previous frame. This is necessary because the min() function (which finds the minimum distance location) selects the first instance of the minimum value of there are multiple instances. This may result in the contact center coordinates jumping around. If the frame is the first frame and there is no previous frame from which to reference, the median coordinate is used.
10. Document the distances to each face of the ROI (later saved to "...\_FaceDistances.xlsx").
11. Determine the smallest minimum distance for each face for colormapping by calculating the smallest distance across the 3 vertices that define the face.
12. Steps 4-11 are conducted for each "direction". In other words, the steps are performed the first time when ROI1 is the mapped surface, and the second time when ROI2 is the mapped surface. The validPtPdist is valid for both directions but collapsing the matrix to determine the overall minimum distance depends on which ROI is mapped and opposing, as do all subsequent calculations.
13. Once steps 4-11 are conducted for each "direction", the minimum distances (and corresponding contact center coordinates) should be exactly the same. However, there are situations in which a vector which lays very close to the surface is detected to penetrate the surface when it does not (Figure 4). In this example, when the minimum distance vector was tested and the glenoid was the mapped ROI, penetration was detected. However, when the same minimum distance vector was tested when the glenoid was the mapped ROI, it was not detected. With more testing, it appears to only occur when the vector is very close to and aligned with the surface of a segment but not touching it.
14. Therefore, a subsequent test was employed after running the minimum distance validations from both perspectives: if the 2 minimum distances are different, take the smaller value as the actual minimum distance and convert the corresponding contact center coordinates (on both surfaces) into the appropriate local frames.
15. Note that the documented faceDistances will not be converted; therefore, the minimum distance magnitude will be accurate but the face's colormapping may be different. When this issue was detected in testing, it does not appear the colormapping was affected as long as the colorbar max value was large enough.



**Figure 5:** An example of a situation in which a vector which lies very close to the surface is detected to penetrate the surface when it does not. As a result, the minimum distances (and corresponding contact center coordinates) may not be the same in both "directions" of calculation (i.e., ROI1 -> ROI2 and ROI2 -> ROI1).



## Surface Area Calculation

Overview: Surface areas are calculated by assigning each face of the ROI to a distance bin (bin limits are specified in the Proximities sheet of the parameter file). Face surface areas are then summed within each bin.

1. The minimum distances on each face of the mapped surface (i.e., validMinDist) are binned twice: once for the minimum distance surface area calculation (based on the minimum distance bin limits) and again for the centroid surface area calculation (based the centroid bin limits).
2. If the bin limits are specified as "0,2,4,6,8,10" in the Proximities sheet of the parameter file, then there are a total of 5 bins, which are defined as follows: 0-2, 2-4, 4-6, 6-8, 8-10, >10.
3. The surface areas within each bin are calculated.

## Weighted Centroid Calculation

The calculation of the weighted centroid depends on the "Centroid type" specification in the parameter file (absolute or relative).

### Absolute Calculation

Overview: The absolute centroid calculation weights the centroid based on absolute minimum distance magnitudes deemed to be meaningful. The advantage to this approach is that centroid calculations across trials and/or subjects are on the same "scale". The disadvantage of this method is that some subjects may have further distances and centroid may not be calculated based on the specified bin limits. A valid centroid may not exist for a given frame if the minimum distance between surface is greater than the largest bin limit and that bin weight is 0.

1. The minimum distance to each face on the mapped surface is binned based on the "Centroid bins" specification in the parameter file.
2. Then, the coordinates of the face are duplicated based on the bin's weighting factor specified in the "Proximity Patterns" sheet of the parameter file.
3. The weighted centroid calculated as the geometric mean of these weighted (i.e., duplicated) coordinates (Anderst and Tashman. *J Biomech* 2003).
4. If the mapped surface is convex, the weighted centroid may lay within (i.e., under) the surface of the mapped ROI. Therefore, a final calculation is done to ensure the centroid coordinate lays on the surface of the ROI. This is done by determining which ROI vertex is closest to the weighted centroid coordinate. The weighted centroid coordinate is then updated to the coordinate of this closest vertex.
5. Finally, document the coordinates of the centroid in the global frame and transform the coordinates to appropriate local frame, including any user-specified transformation.

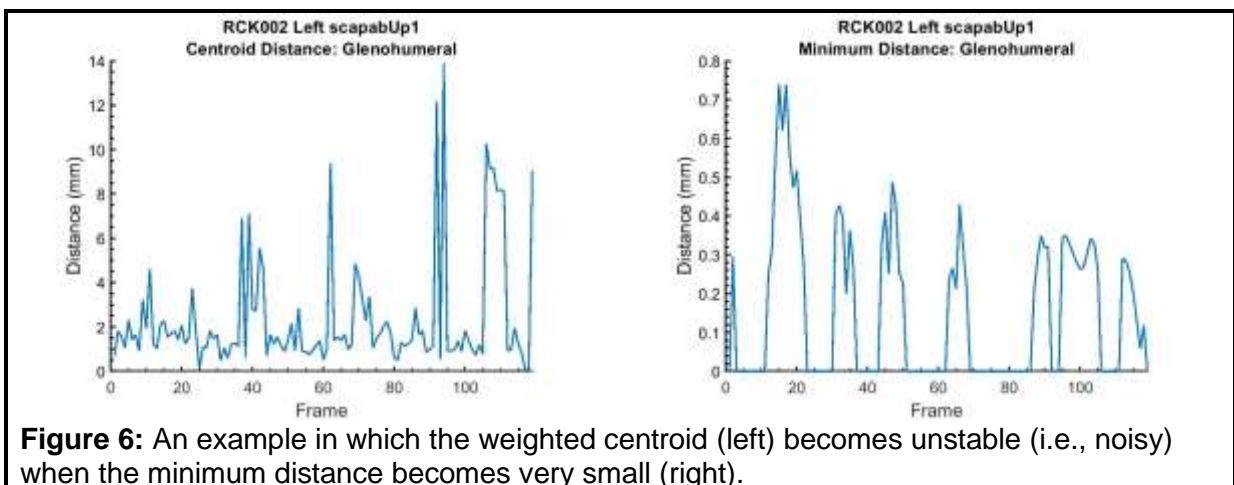
### Relative Calculation

Overview: The relative centroid calculation weights the centroid based on multiples of the minimum distance magnitude deemed to be meaningful. The advantage to this approach is that centroid calculations relative to the motion and anatomy of each individual subject/trial. The disadvantage of this method is that centroid calculations across trials and/or subjects are on different "scales". For example, if one subject's minimum distance is 4 mm and another is 1 mm, the difference is not accounted for in the weighted centroid calculation. Also, this calculation may be biased when the absolute minimum distance is very small. For

example, if the minimum distance is 0.5 mm and the bin limits are 1,2,3, then only the distances <1.5 mm will be included in the calculation. Compare this to a situation where the minimum distance is 2 mm and the bin limits are 1,2,3, then only the distances 6 mm will be included in the calculation, which may be a larger surface area.

1. The centroid bin limits are scaled to the absolute minimum distance. If the absolute minimum distance = 0 (i.e., contact between surfaces), the bin limits are scaled by a factor of 0.1 to ensure they are not all forced to be zero (i.e., bin limit \* 0 = 0).
2. The minimum distances to each face on the mapped surface are then binned based on the scaled bin limits.
3. Then, the coordinates of the face are duplicated based on the bin's weighting factor specified in the "Proximity Patterns" sheet of the parameter file.
4. If the mapped surface is convex, the weighted centroid may lay within (i.e., under) the surface of the mapped ROI. Therefore, a final calculation is done to ensure the centroid coordinate lays on the surface of the ROI. This is done by determining which ROI vertex is closest to the weighted centroid coordinate. The weighted centroid coordinate is then updated to the coordinate of this closest vertex.
5. Finally, document the coordinates of the centroid in the global frame and transform the coordinates to appropriate local frame, including any user-specified transformation.

Note: The weighted centroid calculation can become unstable (i.e., noisy) when the minimum distance becomes very small (**Figure 1**). This is because a multiple of a very small number remains very small, so the centroid becomes heavily biased towards the location of the minimum distance.



### Geodesic Path Coordinates

Overview: Contact paths defined by connecting contact center coordinates (i.e., Euclidean distance method) can result in the contact path penetrating the surface of the ROI depending on the distance between points and the curvature of the surface. Geodesic paths are constrained to follow the ROI surface and are therefore result in a more physiological path. There are many ways to estimate geodesic distances, most of which are extremely computationally intensive and difficult to implement in MATALB. The fast-marching method for calculating geodesic distance was used implemented by Gabriel Peyré. The geodesic distance calculation will increase the computation time several fold. Therefore, parallel processing is used to speed up processing time. The number of cores/workers used in the

parallel processing is limited to 75% of the total physical cores on the host computer to avoid overburdening the system and prohibiting other work from being executed.

1. A geodesic path requires a start and end frame (i.e., point1 to point2). These points were taken directly from the contact center coordinates.
2. The geodesic path was calculated using fastMarchingGeodesic, which was modified from the code referenced above.
3. This results in 1 or more coordinates for each frame interval to describe the path.

## Appendix D – Description of Range and Whole Motion Summary Calculations

Range and whole motion summaries are calculated by the CompilerModule. This includes summary statistics (mean, SD, median, min, max) for most variables. However, helical dispersion and contact path lengths cannot be calculated using summary statistics. The methods for summarizing these variables are described below.

### Helical Dispersion Parameters

An “optimal” helical pivot point and axis were calculated per Woltring 1990. The optimal pivot ( $sOpt$ ) was calculated as the point in space closest to all instantaneous helical axes using a least-squares approach:

$$sOpt = Q^{-1} \frac{1}{n} \sum_{i=1}^n Q_i s_i$$

where  $Q_i = I - \mathbf{n}_i \mathbf{n}_i^T$ ,  $Q = \frac{1}{n} \sum_{i=1}^n Q_i$ , and  $n$ =the number of frames of data during the motion trial. Similarly, the optimal direction vector ( $nOpt$ ) passing through ( $sOpt$ ) was calculated as the vector that was maximally coincident with all instantaneous helical axes. Together, the optimal helical pivot point and axis represent a single approximately mean helical axis for the motion trial.

Root-mean-square estimations of the mean angular ( $\chi_{eff}$ ) and positional ( $d_{eff}$ ) dispersions from the optimal helical axis and pivot point were calculated as:

$$\chi_{eff} = \sin^{-1} \sqrt{\frac{1}{n} \sum_{i=1}^n \sin^2 \chi_i}$$

$$d_{eff} = \sqrt{\frac{1}{n} \sum_{i=1}^n (\mathbf{s}_{opt} - \mathbf{s}_i)^T Q_i (\mathbf{s}_{opt} - \mathbf{s}_i)}$$

where  $\chi_i$ =the angle between  $\mathbf{n}_{opt}$  and  $\mathbf{n}_i$ .

Other parameters that were calculated include:

1. Ne: the average deviation from the optimal director vector ( $nOpt$ )
2. Se: the average deviation from the optimal pivot ( $sOpt$ )

**Important Note:** The coordinates of the optimal helical axis ( $nOpt$ ) and pivot ( $sOpt$ ) for left-sided data are NOT transformed to right-sided equivalence. This is to facilitate plotting, since the vector coordinates should plot directly onto the anatomy.

### Contact Center Path Length

The contact center path length was calculated using the contact center coordinates depending on the method specified by the “Path length distance method” parameter in the

CompilerModule parameter file (i.e., (Euclidean or geodesic). Once the correct coordinates were retrieved from the results file, the Euclidean distance was calculated between subsequent pairs of coordinates and summed over all frames to result in a total path length across the whole motion or limited range, as appropriate. Note that the “Path length distance method” parameter specifies which set of contact center coordinates to retrieve and that Euclidean distances were calculated across these coordinates.

## References

KinematicsToolbox utilizes several subroutines written by others and publically available via MATLAB File Exchange or elsewhere. Some required modified to be implemented within the program.

1. Holcombe, S. inpolyhedron (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/37856-inpolyhedron-are-points-inside-a-triangulated-volume?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/37856-inpolyhedron-are-points-inside-a-triangulated-volume?s_tid=srchtitle).
2. Jennings, A. sphereFit (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/34129-sphere-fit-least-squared?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/34129-sphere-fit-least-squared?s_tid=srchtitle).
3. Legland D. geom3d (library). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/24484-geom3d?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/24484-geom3d?s_tid=srchtitle).
4. Leygue, A. planeFit (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/43305-plane-fit?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/43305-plane-fit?s_tid=srchtitle).
5. Peyré G. Geodesic Distance Computation on 3-D Meshes. Available at:  
[http://www.numerical-tours.com/matlab/fastmarching\\_4bis\\_geodesic\\_mesh/](http://www.numerical-tours.com/matlab/fastmarching_4bis_geodesic_mesh/).
6. Ozturk, M. intersectPlaneSurf (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/22377-intersectplanesurf?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/22377-intersectplanesurf?s_tid=srchtitle).
7. Schmid, A. circle\_3D (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/44047-plot-a-circle-in-3d?s\\_tid=FX\\_rc3\\_behav](https://www.mathworks.com/matlabcentral/fileexchange/44047-plot-a-circle-in-3d?s_tid=FX_rc3_behav).
8. Simon, J. GetFullPath (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/28249-getfullpath?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/28249-getfullpath?s_tid=srchtitle).
9. Swiercz, W. cone (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/21951-cone?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/21951-cone?s_tid=srchtitle).
10. Tuszynski, J. TriangleRayIntersection (function). Available at:  
[https://www.mathworks.com/matlabcentral/fileexchange/33073-triangle-ray-intersection?s\\_tid=srchtitle](https://www.mathworks.com/matlabcentral/fileexchange/33073-triangle-ray-intersection?s_tid=srchtitle).
11. Veeger, D. afgnew3d, woltring3D, iha\_3D (functions). Obtained via personal communication (2018).