

The aim of this document is twofold. In section 1, it details how to transform the CT and blueprint based subject/patient data to data that are readable for the shoulder and elbow musculoskeletal model (MSM). This will be explained in three different subsections associating to patients/subjects with anatomical glenohumeral joint (section 1-1), patients with anatomical total shoulder arthroplasty (aTSA) (section 1-2), and patients with reverse total shoulder arthroplasty (rTSA) (section 1-3). In section 2, it will be described how to transform the MSM predictions (output data) to data readable for the shoulder simulator test setup from LMAM.

## **1- From CT/Blueprint to MSM inputs:**

### **1-1 Patients/subjects with anatomical glenohumeral joint**

This section explains how to provide the input data for subject-specific tool of the MSM for replicating patients/subjects with no implant.

In order to replicate patients/subjects with no implant the following version of MSM must be used:

smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel

The README.txt file details the steps that should be followed in order to perform a simulation with the model.

The Subject-specific tool of this version of MSM takes as inputs the following data in order to adapt the generic model to each specific subject:

- Gender
- Weight [kg]
- Height [m]
- Glenoid orientation, including:
  - Glenoid version [degree]
  - Glenoid inclination [degree]
  - Glenoid fossa center in the scapula coordinate system<sup>1</sup> (<sup>S</sup>GC) [mm]
  - Implant/humeral head radius (Implant radius for patients with anatomical total shoulder arthroplasty and humeral head radius for subjects with not implant) [mm]
- Muscle PCSA [cm<sup>2</sup>]

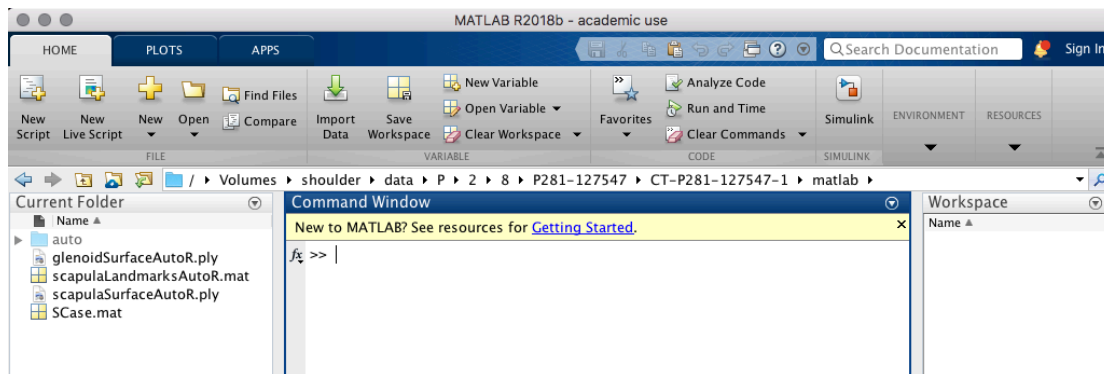
Take the following steps to define the input data for a subject with no implant:

- 1- Open MATLAB (must be a version later than 2015b)

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<sup>1</sup> The scapular coordinate system is defined according to "Terrier, A., et al. "Measurements of three-dimensional glenoid erosion when planning the prosthetic replacement of osteoarthritic shoulders." The bone & joint journal 96.4 (2014): 513-518." and is detailed in the Appendix. Note that this scapula coordinate is defined differently than the scapula coordinate system of the MSM that is defined according to ISB recommendations and used for defining the configuration of the scapula with respect to thorax.

- 2- Set the MATLAB path to the patient's directory from lbovenus/shoulder/data/P/.... For instance, for P281: lbovenus/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1<sup>1</sup>/matlab



- 3- Load the the SCase.mat file by the following command in the Command Window  
`>> load('SCase.mat')`
- 4- Use the following commands to obtain the patient's data build on the loaded SCase file:

Patient's gender → `SCase.patient.gender`  
 Patient's weight → `SCase.patient.weight`  
 Patient's height → `SCase.patient.height/100`  
 Patient's glenoid version → `SCase.shoulder.scapula.glenoid.version`  
 Patient's glenoid inclination → `SCase.shoulder.scapula.glenoid.inclination`  
 Patient's glenoid fossa center → `SCase.shoulder.scapula.glenoid.center`  
 Patient's humeral head radius → `SCase.shoulder.humerus.radius`

- 5- In order to adapt the PCSA of rotator cuff muscles take the following steps:

- I- Feed the MSM with the inputs obtained from the past 4 steps.
- II- Scale the MSM by going through the 9 initial steps of `smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel/README.txt`
- III- Explore to `smb://lbovenus/shoulder/data/Excel/ShoulderDataBaseDev.xlsx`.
- IV- In `ShoulderDataBaseDev.xlsx` find the patient and the associating PCSA. We call this value relative PCSA percentage ( $PCSA_r$ ). The  $PCSA_r$  is a measure of the remaining muscle cross section area with respect to its healthy situations.

<sup>1</sup> Always the folder that ends in "-1"

V- Take the associating PCSA value from the drop down menu of the subject-specific tool of MSM. We call this the scaled PCSA ( $PCSA_s$ ).

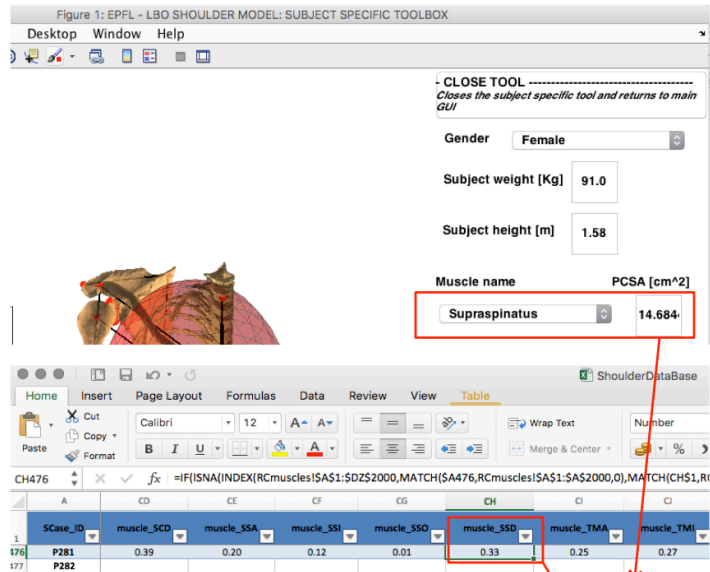
VI- Use the following equation to obtain the so-called absolute PCSA ( $PCSA_a$ ) that the MSM takes.

$$PCSA_a = (1 - PCSA_r) * PCSA_s$$

For instance, adaptation of PCSA of Supraspinatus is shown below for P281.

step 1: scaling

step 2: defining  
PCSA<sub>a</sub> Eq. 1



$$PCSA_a = (1 - 0.33) 14.68 = 13.90 \text{ cm}^2$$

## 1-2 Patients with anatomical total shoulder arthroplasty (aTSA)

This section explains how to provide the input data for subject-specific tool of the MSM for replicating patients with anatomical total shoulder arthroplasty (aTSA).

In order to replicate patients with aTSA the following version of MSM must be used:  
smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel

The README.txt file details the steps that should be followed in order to perform a simulation with the model.

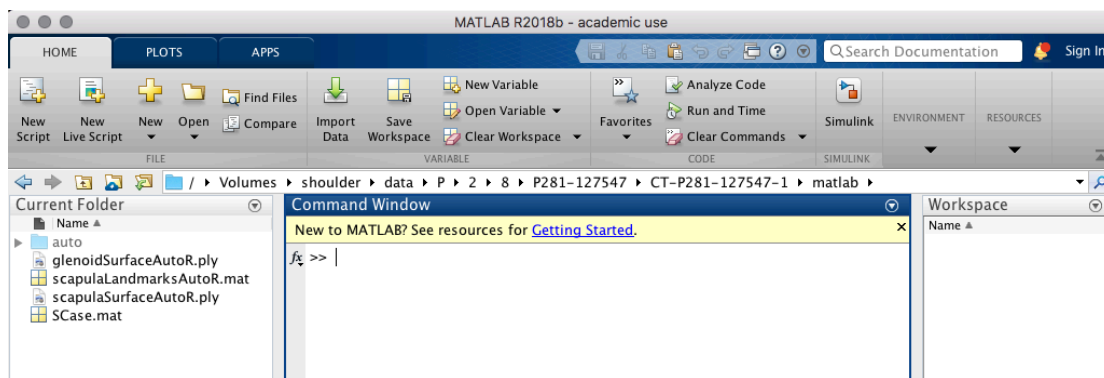
The Subject-specific tool of this version of MSM takes as inputs the following data in order to adapt the generic model to each specific subject:

- Gender
- Weight [kg]
- Height [m]
- Glenoid orientation, including:
  - Glenoid version [degree]
  - Glenoid inclination [degree]

- Glenoid fossa center in the scapula coordinate system<sup>1</sup> (<sup>S</sup>GC) [mm]
- Implant/humeral head radius (Implant radius for patients with anatomical total shoulder arthroplasty and humeral head radius for subjects with not implant) [mm]
- Muscle PCSA [cm<sup>2</sup>]

Take the following steps to define the input data for a patient with aTSA:

- 1- Open MATLAB (must be a version later than 2015b)
- 2- Set the MATLAB path to the patient's directory from lbovenus/shoulder/data/P/.... For instance, for P281: lbovenus/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1<sup>2</sup>/matlab



- 3- Load the the SCase.mat file by the following command in the Command Window  

```
>> load('SCase.mat')
```
- 4- Use the following commands to obtain the patient's data build on the loaded SCase file:
  - Patient's gender → SCase.patient.gender
  - Patient's weight → SCase.patient.weight
  - Patient's height → SCase.patient.height/100

- 5- The following steps are to follow to obtain implant radius, glenoid inclination, version, and fossa center using CT and Blueprint data.

Step 1: Obtain the scapula coordinate system {x<sub>s</sub>, y<sub>s</sub>, z<sub>s</sub>, SN}:

I. For the loaded SCase.mat file use the following commands in

<sup>1</sup> The scapular coordinate system is defined according to "Terrier, A., et al. "Measurements of three-dimensional glenoid erosion when planning the prosthetic replacement of osteoarthritic shoulders." The bone & joint journal 96.4 (2014): 513-518." and is detailed in the Appendix. Note that this scapula coordinate is defined differently than the scapula coordinate system of the MSM that is defined according to ISB recommendations and used for defining the configuration of the scapula with respect to thorax.

<sup>2</sup> Always the folder that ends in "-1"

the Command Window of MATLAB.

```
x_s = SCase.shoulder.scapula.coordSys.PA  
y_s = SCase.shoulder.scapula.coordSys.IS  
z_s = SCase.shoulder.scapula.coordSys.ML  
SN = SCase.shoulder.scapula.coordSys.origin
```

Step 2: Obtain implant planning from Blueprint:

I. Open patient's Blueprint file by exploring to the blueprint folder in patient's directory from Ibovenus/shoulder/data/P/.... For instance, for P281: Ibovenus/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1<sup>1</sup>/blueprint/P281-blueprint.txt.

II. Take "GlenoidImplant\_LateralAxis" and "GlenoidImplant\_Center" from the associating blueprint. Also, take the "HumerusImplant\_AnatHeadDiameter" as the implant diameter and divide it by 2 to obtain the implant radius.

GlenoidImplant\_LateralAxis is the normal vector of the glenoid implant surface in the lateral direction and in the CT coordinate system. GlenoidImplant\_Center is associated to the center of the glenoid implant in the CT coordinate system.

Step 3: Define the "image\_position" of patient's CTs using dicominfo of MATLAB:

I. Take the address of the most inferior CT of the patient from the dicom folder in patient's directory. For instance, for P281: /volumes/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1/dicom/P281-127547\_JN-bone.0001.dcm.

II. Use the following command in MATLAB command window.

```
allfields = dicominfo('/Volumes/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1/dicom/P281-127547_JN-bone.0001.dcm');
```

	1	2	3	4	5	6	7	8	9
1	-174.5000								
2	-75.7000								
3	-227.2000								
4									
5									
6									
7									

III. The image\_position obtains by:  
image\_position = allfields.magePositionPatient

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<sup>1</sup> Always the folder that ends in "-1"

Step 4: Use the MATLAB function “glenoid\_orientation\_preparation” in `smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel_pre_post_processing` to define version, inclination, and fossa center as the following:

```
[GC, GV, GI] = glenoid_orientation_preparation('aTSA', x_s,  
y_s, z_s, SN, GlenoidImplant_Center, image_position,  
GlenoidImplant_LateralAxis)
```

GV → glenoid version

GI → glenoid inclination

GC → glenoid fossa center

6- In order to adapt the PCSA of rotator cuff muscles take the following steps:

I- Feed the MSM with the inputs obtained from the past 4 steps.

II- Scale the MSM by going through the 9 initial steps of `smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel/README.txt`

III- Explore to `smb://lbovenus/shoulder/data/Excel/ShoulderDataBaseDev.xlsx`.

IV- In `ShoulderDataBaseDev.xlsx` find the patient and the associating PCSA. We call this value relative PCSA percentage ( $PCSA_r$ ). The  $PCSA_r$  is a measure of the remaining muscle cross section area with respect to its healthy situations.

V- Take the associating PCSA value from the drop down menu of the subject-specific tool of MSM. We call this the scaled PCSA ( $PCSA_s$ ).

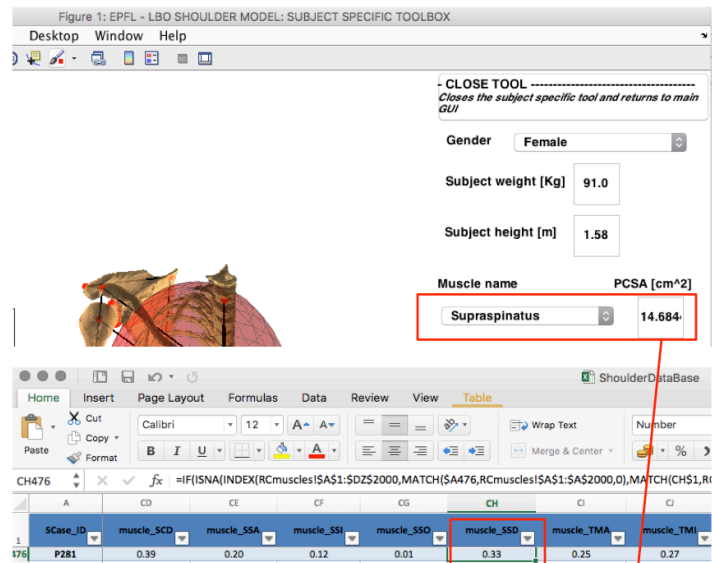
VI- Use the following equation to obtain the so-called absolute PCSA ( $PCSA_a$ ) that the MSM takes.

$$PCSA_a = (1 - PCSA_r) * PCSA_s$$

For instance, adaptation of PCSA of Supraspinatus is shown below for P281.

step 1: scaling

step 2: defining  
PCSA<sub>a</sub> Eq. 1



$$PCSA_a = (1-0.33)14.68=13.90 \text{ cm}^2$$

### 1-3 Patients with reverse total shoulder arthroplasty (rTSA)

This section explains how to provide the input data for subject-specific tool of the MSM for replicating patients with reverse total shoulder arthroplasty (rTSA).

In order to replicate patients with rTSA the following version of MSM must be used:  
smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel\_rTSA

The README.txt file details the steps that should be followed in order to perform a simulation with the model.

The Subject-specific tool of this version of MSM takes as inputs the following data in order to adapt the generic model to each specific subject:

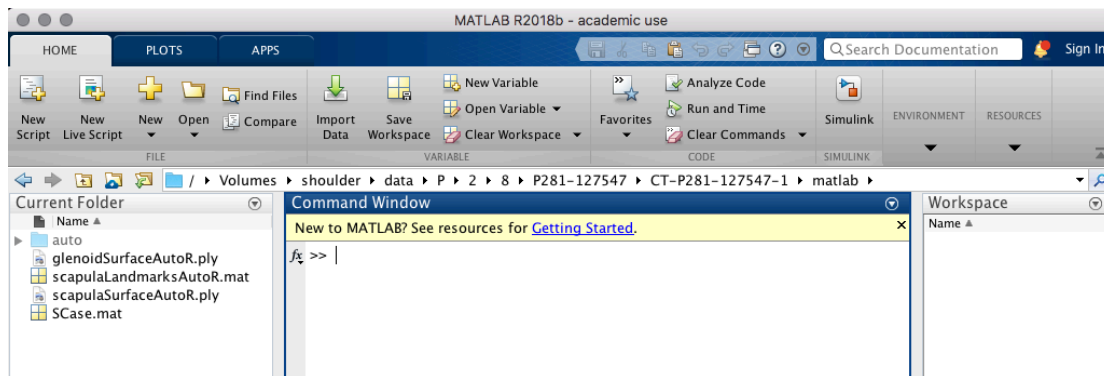
- Gender
- Weight [kg]
- Height [m]
- Glenohumeral joint morphology, including:
  - Humeral head lateralization
  - Humeral head anterization
  - Humeral head distalization
  - Glenoid fossa center in the scapula coordinate system<sup>1</sup> (<sup>S</sup>GC) [mm]

<sup>1</sup> The scapular coordinate system is defined according to "Terrier, A., et al. "Measurements of three-dimensional glenoid erosion when planning the prosthetic replacement of osteoarthritic shoulders." The bone & joint journal 96.4 (2014): 513-518." and is detailed in the Appendix. Note that this scapula coordinate is defined differently than the scapula coordinate system of the MSM

- Muscle PCSA [cm<sup>2</sup>]

Take the following steps to define the input data for a patient with aTSA:

- 1- Open MATLAB (must be a version later than 2015b)
- 2- Set the MATLAB path to the patient's directory from lbovenus/shoulder/data/P/.... For instance, for P281: lbovenus/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1<sup>1</sup>/matlab



- 3- Load the the SCase.mat file by the following command in the Command Window  
`>> load('SCase.mat')`
- 4- Use the following commands to obtain the patient's data build on the loaded SCase file:
  - Patient's gender → `SCase.patient.gender`
  - Patient's weight → `SCase.patient.weight`
  - Patient's height → `SCase.patient.height/100`
- 5- Open patient's Blueprint file by exploring to the blueprint folder in patient's directory from lbovenus/shoulder/data/P/.... And open the blueprint.txt file.
- 6- Take "Anteriorization", "Global lateralization", and "Distalization" values for the corresponding values in the subject-specific tool.
- 7- The following steps are to follow to obtain fossa center using CT and Blueprint data.

Step 1: Obtain the scapula coordinate system {x<sub>s</sub>, y<sub>s</sub>, z<sub>s</sub>, SN}:

- I. For the loaded SCase.mat file use the following commands in the Command Window of MATLAB.

```
x_s = SCase.shoulder.scapula.coordSys.PA
```

---

that is defined according to ISB recommendations and used for defining the configuration of the scapula with respect to thorax.

<sup>1</sup> Always the folder that ends in "-1"



```

y_s = SCase.shoulder.scapula.coordSys.IS
z_s = SCase.shoulder.scapula.coordSys.ML
SN = SCase.shoulder.scapula.coordSys.origin

```

Step 2: Obtain implant planning from Blueprint:

I. In the patient's blueprint file take "GlenoidImplant\_Center".

Step 3: Define the "image\_position" of patient's CTs using dicominfo of MATLAB:

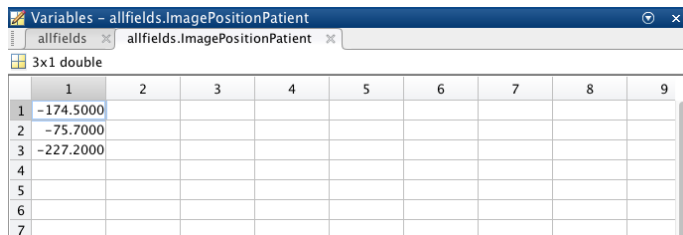
I. Take the address of the most inferior CT of the patient from the dicom folder in patient's directory. For instance, for P281: /volumes/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1/dicom/P281-127547\_JN-bone.0001.dcm.

II. Use the following command in MATLAB command window.

```

allfields = dicominfo('/Volumes/shoulder/data/P/2/8/P281-127547/CT-P281-127547-1/dicom/P281-127547_JN-bone.0001.dcm');

```



	1	2	3	4	5	6	7	8	9
1	-174.5000								
2	-75.7000								
3	-227.2000								
4									
5									
6									
7									

III. The image\_position obtains by:  
image\_position = allfields.magePositionPatient

Step 4: Use the MATLAB function "glenoid\_orientation\_preparation" in smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel\_pre\_post\_processing to define fossa center as the following:

```

GC = glenoid_orientation_preparation('rTSA, x_s, y_s, z_s, SN, GlenoidImplant_Center, image_position)

```

GC → glenoid fossa center

8- Rotator cuff muscles are often disabled in the rTSA. You can set their PCSA to zero. Otherwise, in order to adapt the PCSA of rotator cuff muscles to any other patient-specific value, take the following steps:

I- Feed the MSM with the inputs obtained from the past 4 steps.

II- Scale the MSM by going through the 9 initial steps of  
 smb://lbovenus/shoulder/methods/matlab/MSM/ShoulderModel/  
 README.txt

III- Explore to  
 smb://lbovenus/shoulder/data/Excel/ShoulderDataBaseDev.xlsx.

IV- In ShoulderDataBaseDev.xlsx find the patient and the associating  
 PCSA. We call this value relative PCSA percentage ( $PCSA_r$ ). The  
 $PCSA_r$  is a measure of the remaining muscle cross section area with  
 respect to its healthy situations.

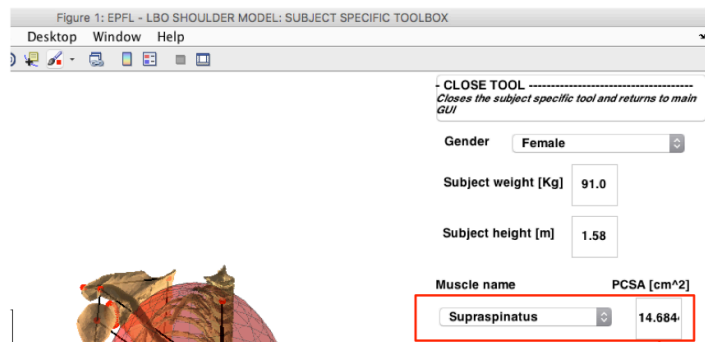
V- Take the associating PCSA value from the drop down menu of the  
 subject-specific tool of MSM. We call this the scaled PCSA ( $PCSA_s$ ).

VI- Use the following equation to obtain the so-called absolute PCSA  
 ( $PCSA_a$ ) that the MSM takes.

$$PCSA_a = (1 - PCSA_r) * PCSA_s$$

For instance, adaptation of PCSA of Supraspinatus is shown below for  
 P281.

step 1: scaling



step 2: defining  
 $PCSA_a$  Eq. 1

sCase_ID	muscle_SCD	muscle_SSA	muscle_SSI	muscle_SSD	muscle_SSD	muscle_TMA	muscle_TM
176 P281	0.39	0.20	0.12	0.01	0.33	0.25	0.27
177 P282							

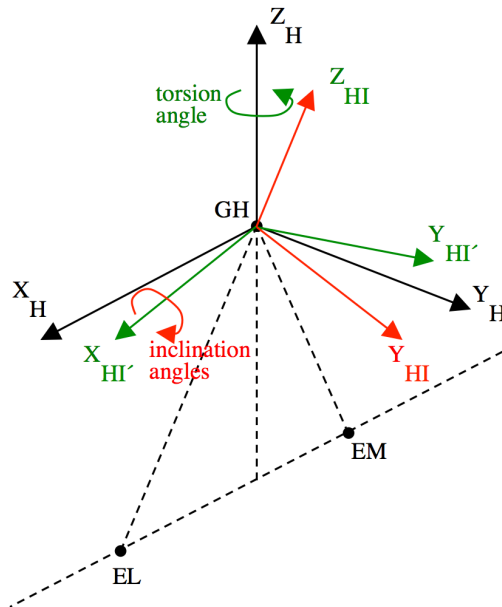
$$PCSA_a = (1 - 0.33) 14.68 = 13.90 \text{ cm}^2$$

## 2- From MSM to shoulder simulator:

All the necessary steps required for transforming the MSM outputs to readable inputs for the shoulder simulator were already implemented in the MSM. The only point that was brought up lately was the necessity of defining a coordinate system for the humeral head implant. In other words, the MSM provides the glenohumeral joint reaction force in the thorax frame. However, the shoulder simulator requires the force in the humerus implant coordinate. Therefore, the aim of this section is to define a coordinate system for the humerus implant and to provide its corresponding rotation matrices. In addition<sup>1</sup>, the shoulder simulator requires the kinematics from the glenoid implant to the humerus implant. To this end, it is also necessary to define the humerus implant. Equation (2) shows how to define the kinematics from the glenoid implant to the humerus implant.

$${}^{HI}R_{GI} = {}^{HI}R_H {}^H_T R \underbrace{{}^T_S R {}^S_{T_0} R_0 {}^{T_{cone}} R_0 {}^{cone}_{GI} R_0}_{{}^T_{GI} R} \quad (2)$$

Where,  ${}^{cone}_{GI} R_0$  is a rotation matrix from glenoid implant to the stability cone frame at the initial configuration (0 index) and it is defined as a rotation matrix around x axis with an angle ( $\Theta$ ) defined based on the positioning of the glenoid implant. In the current configuration of the shoulder simulator, it is tried to keep  $\Theta$  equal to zero.  ${}^S_{T_0} R_0$  and  ${}^{T_{cone}} R_0$  are rotation matrices from thorax to scapula and from glenoid cone to thorax in the initial configuration, respectively. These two rotation matrices are available in the MSM outputs (for details check the MSM readme.txt).  ${}^{HI}R_H$  and  ${}^H_T R$  are rotation matrices from humeral to humerus implant and from thorax to humerus frame, respectively. The definition of the humerus implant coordinate system is detailed in the followings.



<sup>1</sup> The shoulder simulator is an ongoing project that might face different changes during its development. The definition of all possible coordinate systems (e.g. for the humeral implant, glenoid implant, ...) helps to have the necessary information for any possible changes in the shoulder simulator project.

**Fig. 4:** Construction of the humerus implant coordinate system (red) from humeral coordinate system (black) through an intermediate coordinate system (green). EM and EL are two bonylandmarks on the the proximal end of the humerus used to construct the humeral coordinate system according to the ISB recommendations.

The humeral implant coordinate system can be obtained through two successive rotations from the humeral coordinate system. The two rotations are with two angles known as torsion ( $\tau$ ) and inclination ( $\iota$ )<sup>1</sup>. Inclination is typically 132°. Note that in Eq (3) it should be considered as  $\iota = -180^\circ + 132^\circ$ .

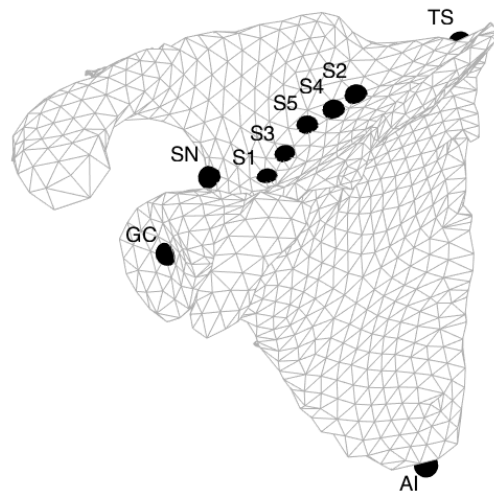
$${}^H_{HI}R = \underbrace{\begin{bmatrix} \cos \tau & -\sin \tau & 0 \\ \sin \tau & \cos \tau & 0 \\ 0 & 0 & 1 \end{bmatrix}}_{{}^H_{HI}R} \underbrace{\begin{bmatrix} 1 & 0 & 0 \\ 0 & \cos \iota & -\sin \iota \\ 0 & \sin \iota & \cos \iota \end{bmatrix}}_{{}^{HI'}_{HI}R} \quad (3)$$

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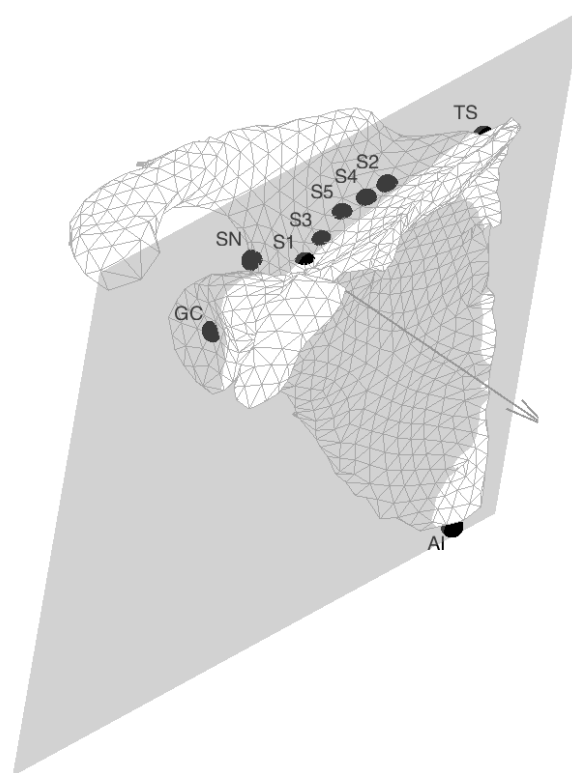
<sup>1</sup> Krahl, Vernon E. "The phylogeny and ontogeny of humeral torsion." American journal of physical anthropology 45.3 (1976): 595-599.

### Appendix (Scapula coordinate system):

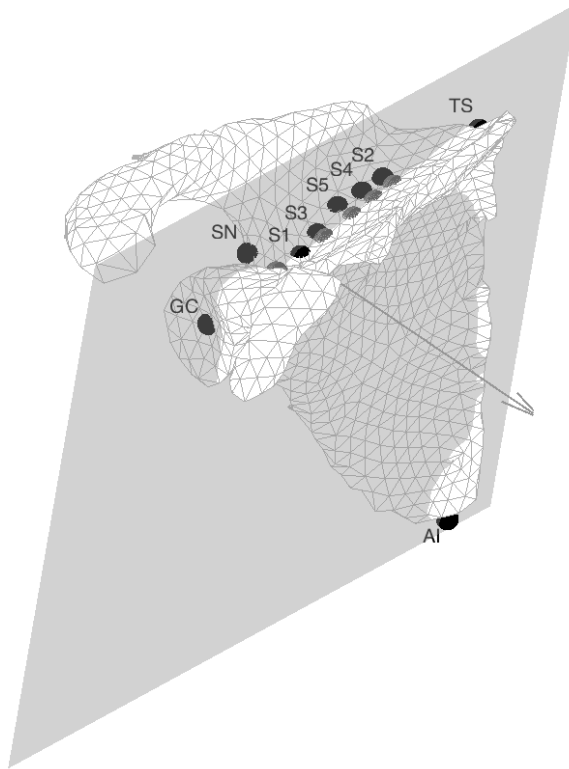
This appendix details the construction of the scapula coordinate system used to define the glenoid orientation. As mentioned earlier, the scapula coordinate system used to define the glenoid orientation is different than the one that is used in the MSM to define the scapula configuration with respect to thorax according to ISB recommendations. The scapula coordinate system is constructed following the steps below using the bony landmarks shown on the next figure.



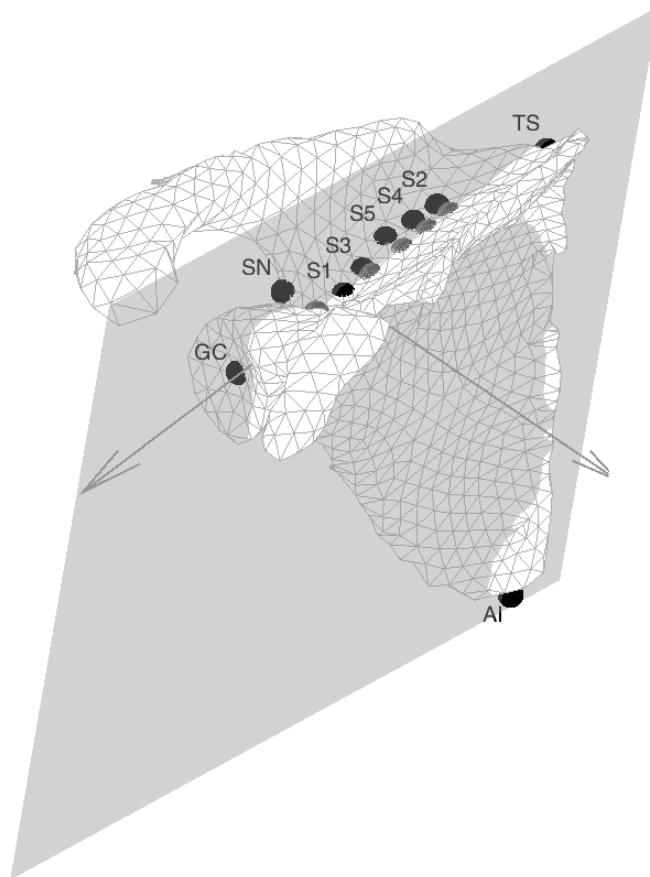
1. Define the scapula plane using the bony landmarks S1, TS, and AI, as shown in the next figure. Consider its normal vector in the posterior-anterior direction as the x direction axis of the scapula coordinate system.



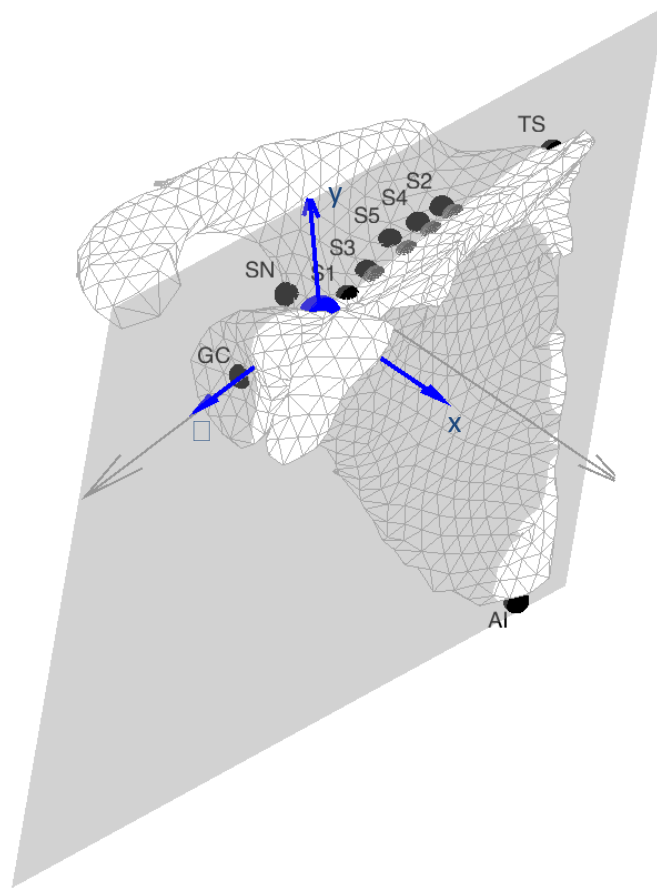
2. Project the five landmarks of the supraspinatus fossa (S1 to S5) and the scapula notch (SN) on the resulting scapula plane.



3. Fit a line through the resulting projected points and consider its medial-lateral direction as the direction of the z axis of the scapula coordinate system.



4. Construct a y axis by defining the common normal vector of the resulting x axis (step 3) and z axis (step 1) and construct the coordinate system on the project SN point.



All the steps are coded in the “scapula\_coordinate\_system.m”.