

# Knee Model Development Specification – DU02

## Site: University of Denver

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*This specification was developed for model development of Denver Knee DU02*

## 1. Summary of Raw Imaging Data

### 1.1 Overview

This section provides detail on the available imaging data for use in the model development phase of the KneeHub project.

### 1.2 Dataset for Denver Knee DU02

The dataset, identified as *Data for MD - DU02*, is available for download at:

[https://simtk.org/frs/?group\\_id=1061](https://simtk.org/frs/?group_id=1061)

Full details on imaging specifications:

[https://digitalcommons.du.edu/natural\\_knee\\_data/7/](https://digitalcommons.du.edu/natural_knee_data/7/)

*Stack 1: MRI: DU02\_fs\_SAG*

- Sequence: T2 fi3d\_fs\_SAG
- 112 slices
- In-plane resolution: 0.35 mm
- In-plane number of pixels: 512 x 432
- Slice thickness: 1.0 mm
- File format: DICOM

*Stack 2: CT: DU02\_knee\_06mm*

- 251 slices
- In-plane resolution: 0.39 mm
- In-plane number of pixels: 512 x 512
- Slice thickness: 0.6 mm
- File format: DICOM

## 2. Image Segmentation

### 2.1 Objective

The image segmentation section describes the process used to reconstruct bone, cartilage, and ligaments from the imaging data. Specifically, the process creates geometric representations of structures from a set of MRI and CT scans of the knee.

## Primary Tools

- Simpleware ScanIP (Version 7.0), Synopsys (Exeter, UK)

## Input(s)

- Data for MD - DU02: MRI and CT scans in DICOM file format (.dcm)

## Output

- .stl files of geometries for bone, cartilage, and ligaments

## 2.2 Image Formats

### *Procedure for DICOM format*

- For DU02, the downloaded MRI and CT scans are in DICOM format. DICOM format includes each slice of the scan in spatial order as separate .dcm files.
- The directory containing the DICOM scan deck can be opened directly by Simpleware ScanIP, so no further image converting will be necessary.

## 2.3 Segmentation Process

### *Loading DICOM files into ScanIP*

- Load DICOM files by selecting “Import DICOM” from the Getting Started Menu
- The user will then be prompted to select the folder containing the DICOM files. Hit “Okay” after viewing the preview of the images.
- The dialog box “Crop and resample” will allow the user to apply any image cropping or down-sampling across the image deck. Leave the number of pixels to skip in x, y, and z at 1, and do not apply any cropping of the image. Leave the “Pixel Rescaling” background type as 16-bit signed integer in order to ensure no changes to pixel depth are made.
- ScanIP will now display four distinct views of the scan. Three views are 2D reconstructions of the sagittal, coronal, and transverse planes. The fourth interactive image is a 3D voxel rendering of the scans.

### *Manual Image Segmentation*

- In the dataset browser, right click on the Masks tab and select “Create new mask.” This will create a new layer on top of the original scan in which the user can manually highlight specific regions of interest in each slice of the scan.
- ScanIP has different tools available to the user for manual image segmentation including paint, paint with threshold, and magnetic lasso. Each of these tools can be found under the “image processing” tab at the top of the window.
  - Paint: The paint tool is an easy to use and reliable tool, especially in low contrast images such as MRI scans. The user has the ability to control the size and shape of the brush, using point to point lines to outline a shape, and smoothing the edges of the lines based on grayscale values. If using paint to outline a region, the flood fill tool can be used to easily fill the enclosed area. The user has the option to paint the new layer on just the active slice, all slices, or a predefined set of slices.
  - Paint with Threshold: Paint with threshold is similar to the paint tool, in that you control the same parameters with the addition of a grayscale value threshold

control. The threshold control allows the user to set a range of grayscale values that will be painted by setting upper and lower greyscale boundaries. If the threshold is carefully set a larger brush can be used to quickly highlight the region of interest.

- Magnetic Lasso: The magnetic lasso enables the user to quickly trace the outline of the region of interest by latching onto edges defined by the gradient of grayscale values and adjusted by the sensitivity parameter. The user can vary this sensitivity while tracing the outline, as well as setting different control points along the boundary for greater edge control. Once the outline is defined, the lasso allows the user to highlight the region on the current slice and merge it with the current active mask. The outlines and control points defined on one slice can be propagated to subsequent slices, which can significantly speed up the segmentation process. When this operation is performed, the lasso will attempt to detect small changes in geometry from the previous slice based on the sensitivity and control points, however the user will usually have to make minor adjustments to the outline.
- Save your progress often during this process as any loss of data will be time consuming.

\*Note: During manual segmentation it is useful to see both the mask layer, as well as the MRI/CT scan below the mask. This can be done by selecting “Transparent masks” in the “2D slice views panel” under the “View” tab.

\*Note: Segmentation will not be performed on the lateral or medial menisci, as these will not be included in the model.

## 2.4 Segmentation Process for DU02

### *Segmentation of Bone Structures*

- Use Stack 2 - CT scan
- Segmented structures: femur, tibia, fibula, and patella
- Paint with threshold and the magnetic lasso will be used (Figure 1). The high contrast of the coronal CT scan allows for quick outlining and auto-propagation to the next slice.

### *Segmentation of Cartilage Structures*

- Use Stack 1 - MRI
- Segmented structures: femoral, medial tibial, lateral tibial, and patellar cartilage
- The magnetic lasso tool will work best for the manual segmentation process
- To help define bone-cartilage boundaries and to aid with the smoothing/filtering of the cartilage, some extra thickness is added to the inside boundary of the cartilage mask, which overlaps the bone (Figure 2). The extra thickness will help when applying smoothing filters to the cartilage, as these filters will often leave gaps in the shape of the cartilage since it is a very thin strip. A Boolean operation is then used to isolate the cartilage geometry by subtracting the bone geometry.

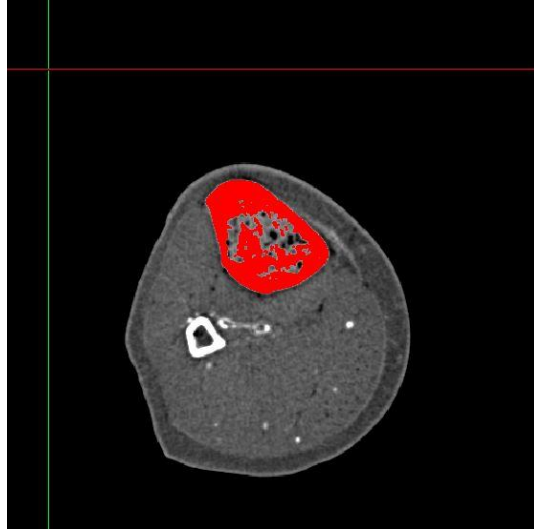


Figure 1. Segmentation of the tibia utilizing the paint with threshold tool will allow for quick definition of the bone's boundary.

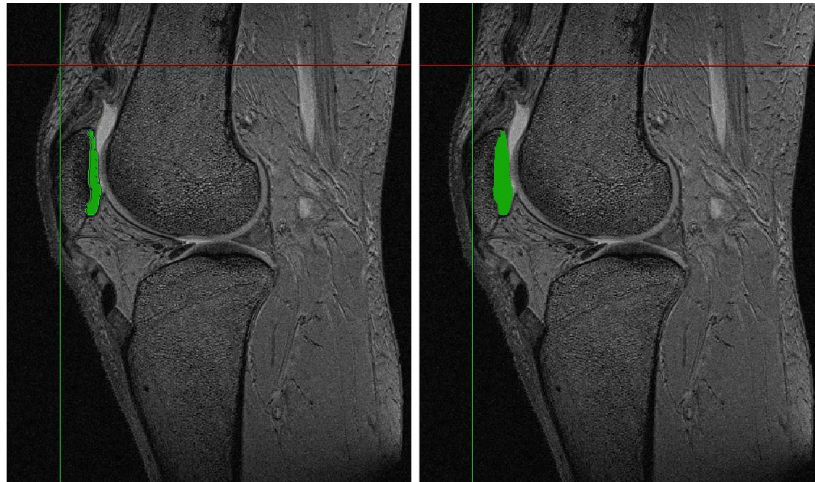


Figure 2. Segmentation of the patellar cartilage using the magnetic lasso (left), and with addition of overlap with the patellar bone (right).

#### *Segmentation of Ligaments and Tendons*

- Use Stack 1 - MRI
- Segmented structures: ACL, PCL, MCL, LCL, as well as patellar and quadriceps tendons
- The outlines of the ligaments are low-contrast and not easily defined, thus the paint tool with the 'point to point line' option selected is the best method for manual segmentation.
- The data set provides probed points for insertion points of ligaments and outlines of bone. These will be used to inform the reconstruction of the ligaments and other structures (Figure 3).

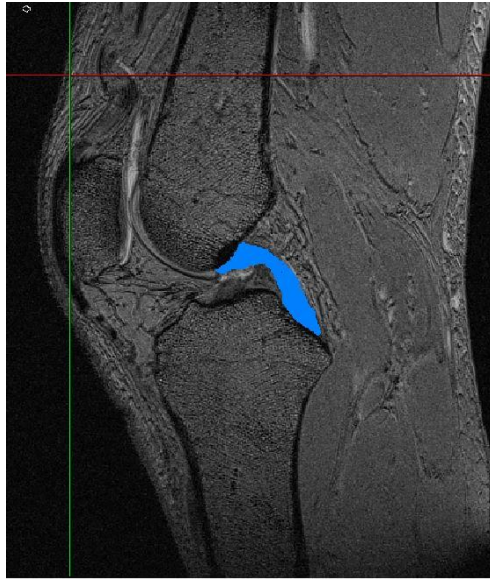


Figure 3. PCL segmentation using the paint tool. Insertion locations will be refined using probed point data.

## 2.5 General Processing of Segmented Structures - Filtering and Smoothing

During the noise reduction process, the goal should be applying the smallest amount of filtering and smoothing to the structure as possible. This will ensure minimal loss of geometric features from filtering and will result in a more accurate rendering of the surface. It should be noted, that the mesh as defined by ScanIP is quite fine at this point in the process, especially in comparison to the further discretization that will occur in the meshing stage. The average edge length of an STL model exported from ScanIP is approximately 0.4 mm (range: 0.12-0.94 mm).

It is important to save a copy of each mask geometry before applying filtering and smoothing in the next steps. This will ensure there is no loss of the original segmented data in the event further segmentation and refinement are needed. See the “Export” section below for how to export and save an STL file.

### *Generate Preview*

- After segmenting an entire structure, enter the interactive 3D view and select “Generate a fast preview.” This will render a 3D visualization of the segmentation process thus far.
- The 3D rendering of the bone may appear as a poor representation due to discretization of the surface and uncertainties during the segmentation process. See the “Smoothing - Recursive Gaussian” section for instructions on applying filters to eliminate the surface noise.

### *Hole Closure*

- Depending on the manual segmentation process performed, there may be voids within the cavity of the mask (especially if paint w/ threshold was used). It is important to remove these gaps before further filtering is performed.
- Select the morphological “close” function found under the “Image processing” tab. Make sure to select “Apply on active mask” to apply the function to the desired mask (Figure 4).
- In the “Structuring element” section, modify the x, y, and z pixel radius (selecting “Cubic values” usually will work well). Start with lower radius values and increase the radius to strengthen the close function to the desired level.

### *Island Removal*

- There may be small “islands” of voxels present above the surface of the mask. To remove these from the scan utilize the “Island removal” function found in the “Additional” section under the “Image processing” tab (Figure 5).
- Set the desired voxel threshold. The higher the threshold, the larger the “islands” of voxels the filter will remove. Find a value that eliminates the noise above the surface, while maintaining the geometry of the component.

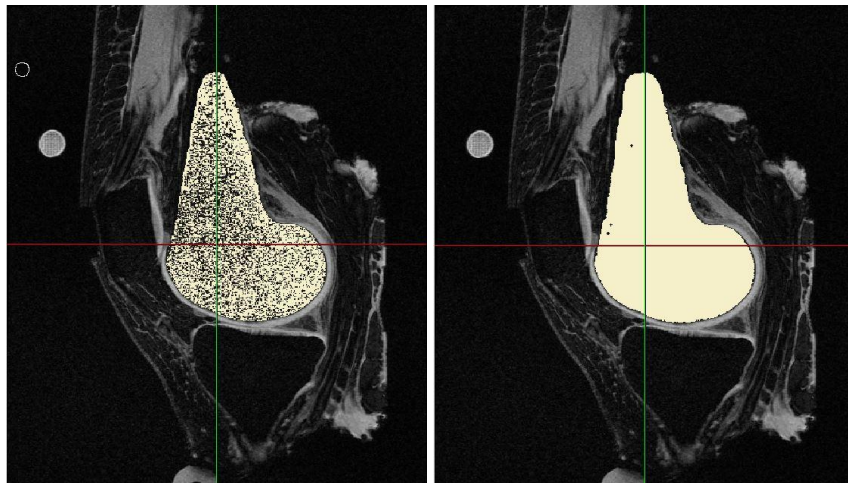


Figure 4. Before and after application of the ‘morphological close’ function to fill voids within the femur geometry

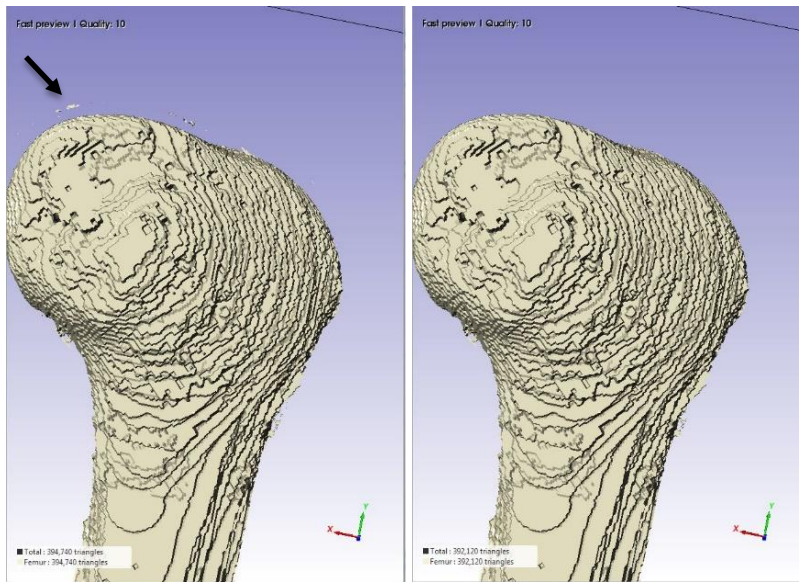


Figure 5. Before (left) and after (right) application of the “island removal” function to remove point clouds near the surface

#### *Smoothing - Recursive Gaussian*

- After closing any gaps in the volume and removing any additional noise, the recursive Gaussian filter will be used to smooth the surface of the geometry, by removing the unnatural noise from manual segmentation (Figure 6).
- Select the “Recursive Gaussian” button in the “Smoothing” panel, under the “Image processing” tab.
- Ensure the current mask being smoothed is chosen in the “Target Volume” field, and that “Apply on active mask” is selected.

#### *Settings/Considerations*

- Check the “Binarise” box to apply binarization to the background. This will help with maintaining volume and reducing surface noise.
- Under the “Gaussian sigma” section enter the number of nearest neighbors in each dimension the filter will consider. The higher the number, the stronger the filter will be for the given dimension. Selecting “cubic values” and beginning at 1 is a good starting point. Increase the filter to the desired level while maintaining the geometrical features of the structure.

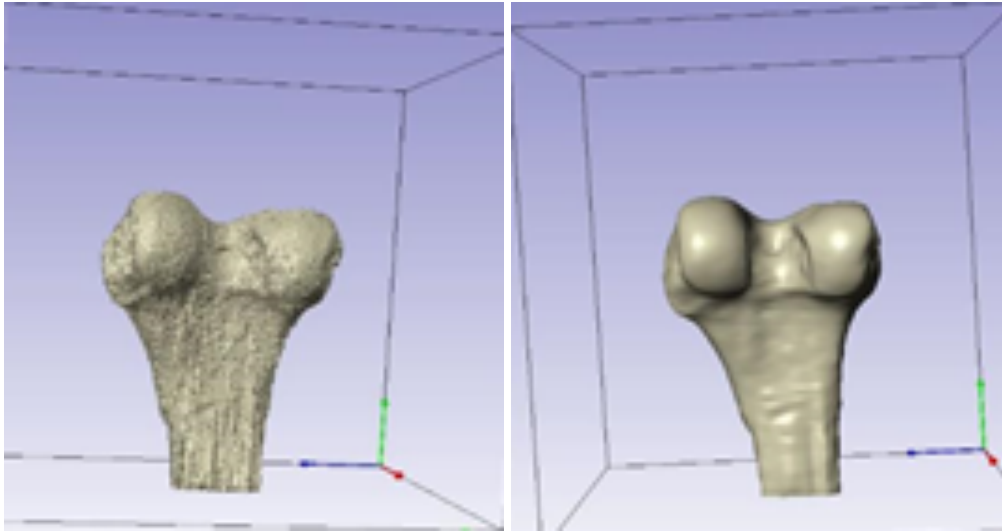


Figure 6. Femur before (left) and after (right) application of the Recursive Gaussian filter. Gaussian sigma parameters ( $\sigma_x$ ,  $\sigma_y$ , and  $\sigma_z$ ) were set at 3.

#### *Export*

- To export a .stl file of a surface, right click on the “Models” tab under the “Dataset browser” tab. Choose the option “Create a new surface model,” then drag the desired mask from the Masks tab into the Models tab.
- Double click on the model in the “Dataset browser” or select “Setup model” under the “Model setup” panel under the “Surface model” tab.
- Make sure “Surface” and “STL (RP)” are selected in the “Model type” and “Export type” tabs at the top of the dialogue box.
- Maintain default parameters under the “General” and “Surface settings” tabs, however it is important to make sure the global coordinate system is chosen under the “Export options” panel.
- Close the dialogue box, and select “Full model” in the “General” panel under the “Surface model” tab. Perform a visual inspection of the generated mesh, then click “Export” and select “Binary” for the file export type.



### **3. Registration of Available Probed Points**

#### 3.1 Objective

Digitized points were collected as part of the experiment to represent the articular surfaces and specific landmarks such as epicondyles, hip joint center, and attachment sites of ligaments. Points were also collected to describe the location of the rigid body marker arrays used for kinematic tracking. This section describes the process used to align the probed points from the experimental testing to the segmented geometry from the imaging (Section 2).

#### Primary Tool

- MATLAB (custom script), MathWorks (Natick, MA, USA)

#### Inputs

- Geometry bone, cartilage, and ligament (.stl)
- Probed point data (.txt) in testing space

#### Outputs

- Probed point data (.txt/.inp) in scan (model) space.

#### 3.2 Registration Process

- The segmented surfaces are reported in the scan space, and the probed points are reported in a coordinate system associated with the testing. It is necessary to register the data so that both bony geometry and probed points can be used to describe ligament, cartilage, and bony geometry when necessary.
- An iterative closest point (ICP) algorithm is used as part of a custom MATLAB script to develop a transformation between the two coordinate systems (scan and testing). The transformation matrix is a 4x4 which captures rotations and translations between the coordinate systems.
- Once the transformation matrix has been found, it will be multiplied by the probed point nodal geometry to relocate them into scan space. The resultant probed point data can be overlaid on the segmented geometry in the scan space (Figure 7)

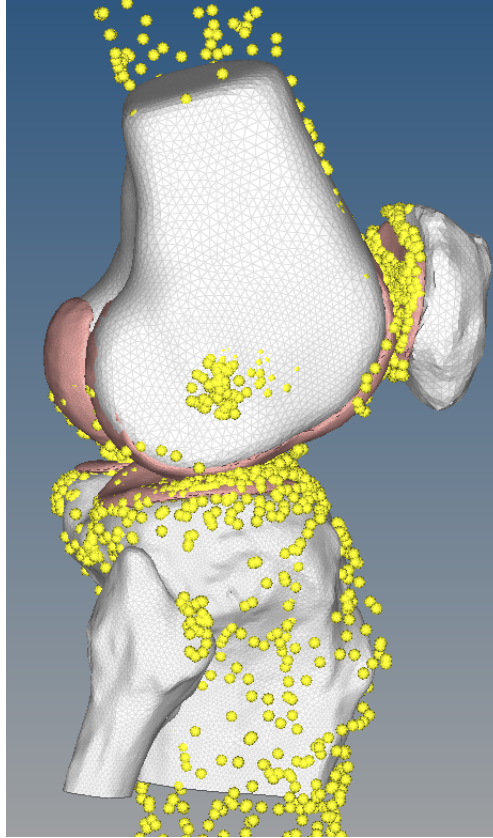


Figure 7. Registration of probed point data onto STL bone and cartilage geometry obtained from ScanIP. Image is shown in the scan space.

## 4. Meshing Structures

### 4.1 Objective

The meshing section describes the development of meshes to represent the segmented geometries from the previous section in a finite element model. In joint mechanics evaluations, the bones can often be modeled as rigid structures while cartilage and ligaments may be deformable. Accordingly, bones are defined by tri surface meshes, and cartilage is defined by hex solid meshes (Figure 8). Ligaments are defined by placing spring connectors representative of the 3D segmented geometry; attachment sites are defined by the structure's footprint from images and probed point data.

Finalizing the meshes through readiness and quality checks (e.g. surface overlays) ensures that the newly defined geometries are representative of the segmented structures. To support model development, a consistent numbering convention has been developed for nodes and elements of the various structures (Tables 1 and 2).

Lastly, the finite element modeling will be carried out in ABAQUS, Dassault Systems (Johnston RI, USA). Accordingly, the meshes are exported in the input (.inp) format that is utilized in Abaqus.

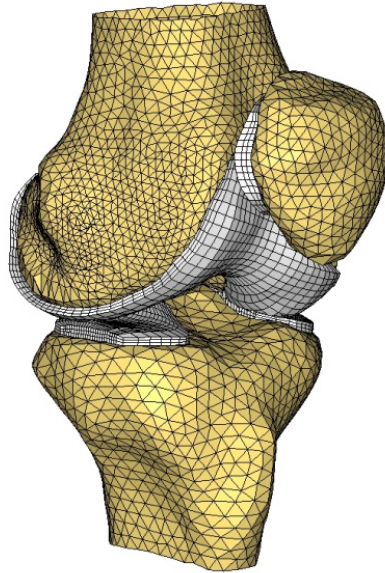


Figure 8. Representative mesh showing bone and cartilage structures of the knee. Bone meshes consist of tri elements and cartilage meshes consist of hex elements

#### 4.2 Meshing of Bones

This section describes the meshing of the bony structures with tri surface elements.

##### Primary Tool

- Hypermesh (v. 14.0), Altair (Troy, MI, USA)

##### Inputs

- Geometries for bone (.stl)

##### Outputs

- Finite element mesh (tri) in Abaqus format (.inp)

##### *Importing*

- Open Altair Hypermesh
- In the import tab, set the “File Type” to STL and browse to one of the STL files representing the geometry of the femur, tibia, or patella.
- Click Import. At this point the STL should become visible in the viewport.
- Repeat this process to load in the two remaining geometries.

##### *Mesh Building*

- At the bottom of the program, navigate into the 2D menu. Here we will find the automesh feature which allows for the remeshing of our currently dense mesh obtained

from Scan IP.

- Select a single element on the femur, it should turn white to indicate the selection.
- Click the yellow “elems” button, to bring up a sub menu and navigate to “by attached”. The entire femur bone should now be completely selected (white).
- Set the element size to between 1.5 and 2.0 mm and set the mesh type to “tri”.
- Before a new mesh is generated we must create a new component to store the generated mesh. In the model selector tab, right click on the Component heading and choose Create from the popup menu. You will be prompted to name the new component, type BONE-FEMUR, and click OK. The new component should be visible in the list. Right click on the newly created component and choose Make Current.
- In the menu to the right of the element size, set the drop down to “elems to current comp”. This prompts the newly created nodes/elements to be deposited into the new component.
- Automatic seeding of nodes along feature edges based on the defined element size often provides an excellent mesh. If instead you would prefer to update the seeds manually, switch the bottom left dropdown from automatic to interactive.
- Click Mesh and wait for Hypermesh to complete the meshing process. If you are satisfied with the mesh, repeat the same process for BONE-TIBIA and BONE-PATELLA.
- At this point, hide all other components except BONE-FEMUR, BONE-TIBIA, and BONE-PATELLA.

#### *Mesh Quality Assessment*

- The following are a short list of mesh quality and characteristic assessments which should be performed before model assembly.
  - Check to see that the surface normals of each bone are pointing outward. This is important for contact modeling using FEA. Navigate to Tool→Normals, and check to ensure the arrows point away from the bones. If not, they can be reversed using the tool.
  - Under Tool→Check Elms, click connectivity and duplicates to check for potential issues with mesh generation. As the meshing was performed in Hypermesh it is unlikely anything will come up but it’s a good check to perform. Results of each search will be displayed at the bottom left of the Hypermesh window.
  - Under Tool→Faces, select the elements of one bone and click preview equivalence. The results will be displayed at the bottom left. If anything is found click equivalence to equivalence the displayed co-located nodes. Perform this check on each bone.
  - As a final check, re-import the STLs of the femur, tibia, and patella output from ScanIP. Ensure that the remeshed geometry is a valid representation of the ScanIP geometry. Selecting a larger Element Size would likely affect the representation of each bone and ultimately the kinematic response.

#### *Save HM File*

- Save the current Hypermesh file.

### *Renumbering Nodes and Elements*

- Renumbering is not crucial for simple models, but for large multibody musculoskeletal models having a clear and predictable numbering system is very important. The node and element numbering convention is shown in Table 1. For example, nodes and elements for the femur start at 1,900,000, while nodes and elements for the tibia start at 1,200,000.
- As an example, this document will step through the process of renumbering the nodes and elements for the femur, but each bone should be updated before exporting the ABAQUS input files. The renumbering process must be carried out for the nodes and the elements, separately.
- Hide all components except the femur. FEMUR-BONE should be the only component visible in the viewport and via the component hierarchy on the left.
- Navigate to Tools-Renumber
- Click the dropdown next to the yellow box and select “nodes”.
- Click the yellow box and select “displayed”. The femur nodes should now be selected.
- Set the Start With field to 1900000, Increment by 1, and Offset 0.
- Click Renumber. The results of the renumbering will be displayed at the bottom left of the window. Check that the nodes started at 1900000 and that the start node + number of nodes-1 = last node. This is an important check as Hypermesh will not warn you if there are conflicting node/element numbers in the current workspace and it will just skip them. If this happens, remove any unnecessary components from the workspace and try again.
- Click the dropdown to left of the yellow box “nodes” and choose “elements”.
- Click the yellow box and select “displayed”. The femur elements should now be selected.
- Confirm that the Start With field to 1900000, Increment by 1, and Offset 0.
- Click renumber. Check the results of the renumbering make sense as described previously.
- Repeat this process for the tibia and the patella using the appropriate numbering of convention (Table 1).
- Save the HM file.

### *Exporting Input File for ABAQUS*

- After meshing and renumbering, export the geometries representing the femur, tibia, and patella as input (.inp) files for use in ABAQUS analyses.
- As an example, this document will step through exporting an input file for elements and nodes of the femur, but the process should be repeated for all three bones.
- Hide the Tibia and Patella in the Component Hierarchy.
- Navigate to File→Export→Solver Deck to bring up the Export tab on the left-hand side of the application.
- Set File Type to Abaqus and Template to Explicit.
- Set the file location as preferred and the filename to BONE-FEMUR.inp
- Under export options, set Export to “displayed”.
- Uncheck Hypermesh comments.

- Click Export
- Repeat this process for Tibia and Patella.
- Check the new input files for correct numbering and data. If there are any read/write issues or no selected elements Hypermesh will leave the file blank.

Table 1. Node and element numbering convention for bone and cartilage structures.

Structure	Mesh Type	Export Filename (.inp)	Starting Node Number	Starting Element Number
Femur	Tri	BONE-FEMUR	1900000	1900000
Tibia and Fibula	Tri	BONE-TIBIA	1200000	1200000
Patella	Tri	BONE-PATELLA	6400000	6400000
Femoral Cartilage	Hex	CART-FEMUR	1990000	1990000
Tibial Cartilage	Hex	CART-TIBIA	4990000	4990000
Patellar Cartilage	Hex	CART-PATELLA	3990000	3990000

#### 4.3 Meshing of Cartilage

This section describes the meshing of the cartilage structures with hex solid elements.

##### Primary Tool

- Custom GUI developed in Matlab, Mathworks (Natick, MA, USA)
- Hypermesh (v. 14.0), Altair (Troy, MI, USA)

##### Inputs

- Geometry of Cartilage (.stl)

##### Outputs

- Finite element mesh (hex) in Abaqus format (.inp)

##### *Meshing*

- The meshing of cartilage geometries is performed using a custom Matlab script with GUI which allows the user to morph a hexahedral template mesh onto the existing dense cartilage geometry (STL) exported from ScanIP (Figure 9). The methodology has been described in Baldwin et al. (2010) and Fitzpatrick et al. (2011).
  - The cartilage meshes were represented by hexahedral elements to support contact analyses. The template contained 3968, 2736, and 780 nodes for the femur, tibia, and patella, respectively.

- A subset of the surface nodes were designated as handles on the template mesh to facilitate a mesh-morphing process to generate subject-specific meshes using Hypermesh; 2030, 504 and 390 handles were identified for the femoral, tibial, and patellar cartilages, respectively
- User input is required to manually choose landmarks (features) on the cartilage surfaces as prompted by the GUI application. A custom algorithm divides the STL meshes into subsections based on landmark points and distributes handles to represent each structure.
- Morphing of the template to a subject-specific mesh was achieved by repositioning the template handles to the subject's corresponding handle coordinates. Surface and edge drafting is performed to improve contact analyses.
- The cartilage hex mesh is morphed by Hypermesh (Hypermorph) and displayed to the user.
- An FE readiness check is performed automatically through a dummy simulation which checks for small or negative-volume elements.
- If necessary, the final step performs a mesh refinement by splitting quad elements into smaller elements. These quads are then used to extrude 3D hex elements between the two major surfaces.
- Finally, the code exports ABAQUS input (.inp) files for each cartilage geometry. The node and element numbering of the exported cartilage meshes are based on the numbering convention (Table 1).
- Smoothing of the mesh is performed on the mesh handles as described previously. The amount of smoothing can be controlled by the user. To ensure that the smoothed hex mesh accurately represents the segmented geometry, both the input file from the hex mesh generation and the STL from ScanIP should be imported into Hypermesh for visual inspection.
- Inter-rater variability in cartilage registration using the GUI was evaluated between three raters. Each rater was familiar with knee anatomy and given basic GUI instructions. Error was quantified by the average 3D geometric distance between corresponding surface handles. Inter-rater variability was measured as  $0.25 \pm 0.16$  mm for average 3D geometric distance between corresponding handles, which resulted in 0.1 mm average thickness variation between corresponding handles of each rater's registered geometries.

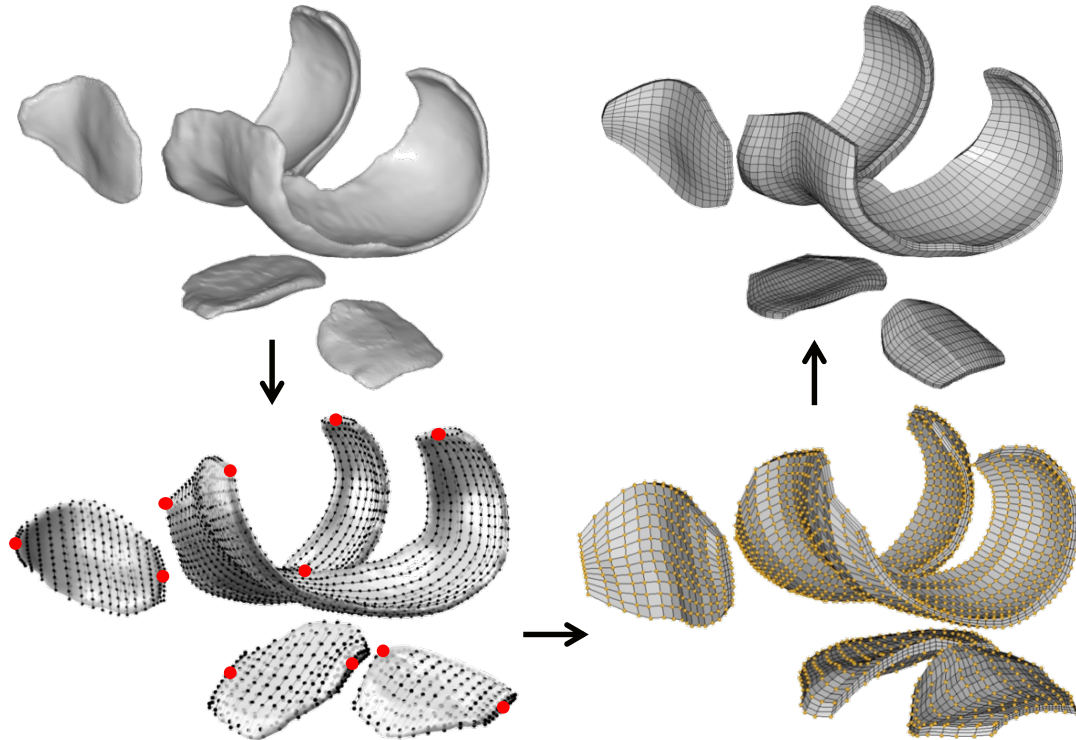


Figure 9. Process used for subject-specific morphing of cartilage. As segmented surfaces (top left), selection of landmarks (bottom left), automated determination of node handles (bottom right) and morphing of template to create the subject specific hex mesh.

#### 4.4 Meshing of Ligaments and Soft Tissues

This section describes the meshing of the ligaments and quadriceps extensor mechanism with 1D spring and fiber-reinforced membrane elements.

##### Primary Tool

- Hypermesh (v. 14.0), Altair (Troy, MI, USA)
- Matlab, Mathworks (Natick, MA, USA)

##### Inputs

- Geometry of ligaments and bones (.stl)

##### Outputs

- Finite element mesh in Abaqus format (.inp)

##### *Meshing*

- Development of ligament mesh geometry will be informed using a combination of data sources: (1) 3D representations exported from ScanIP as described above, (2) probed point data from the experiment (when available), (3) and descriptions from literature. Preference will be given to data sources (1) and (2) to describe the attachment regions, with information from the literature used to supplement as needed.



- The ligament representations of the anterior and posterior cruciate ligaments (ACL, PCL), the medial and lateral collateral ligaments (MCL, LCL), posterior oblique ligament (POL), popliteofibular ligament (PFL), and anterolateral structure (ALS) will be defined using 1D tension-only non-linear spring elements. Representation of the patellar and quadriceps tendons will be defined using fiber reinforced membrane elements (Figure 10)
- Identification of footprint geometry will be performed in Hypermesh. An appropriate shape (rectangle, ellipse) will be fit to the footprints of the ACL, PCL, MCL, LCL, POL, PCAP, PFL, and ALS when possible. In instances where the ligament is not reliably digitized from the MRI or using probed point data the bounding region will be defined based on literature descriptions of the ligament. These regions will define boundaries of each ligament and inform perturbations made during the calibration phase. Initial ligament geometry is described below along with number of fibers and ligament bundle descriptions (Table 2).
- For example, the ACL will be represented by 2 bundles (anteromedial and posterolateral) composed of 2 fibers each, resulting in 4 total fibers (Table 2). Each of the 2 fibers representing a bundle will be placed based on anatomical descriptions and within the boundary of the footprint geometry.
- Patellar Tendon: The patellar tendon will be represented using a series of reinforced membrane elements. The membrane will be formed by morphing a template mesh onto the 3D representation of the patellar tendon exported from Scan IP.
- Quadriceps Tendon: The quadriceps tendons will be represented using a series of fiber reinforced membrane elements. Four quadriceps tendons will be formed by morphing a template mesh onto the 3D representations of the quadriceps tendons exported from ScanIP. If the muscles are visible in the MRI, they will be digitized to inform the direction and orientation of the quadriceps tendons where appropriate.
- As with previous meshing or morphing based on segmented STLs from ScanIP, as a final check the spring and membrane elements will be imported into Hypermesh and overlaid on the segmented STLs to check for proper alignment.

Table 2. Description of ligament representation including number of bundles and fibers, and the node and element numbering convention.

Ligament Name	Bundles	Total Fibers	Starting Node Number	Starting Element Number
ACL	2	4	2400	20000
PCL	2	4	7400	70000
MCL	2	6	5400	50000
POL	1	2	5412	50012
LCL	1	3	4400	40000
ALS	1	3	3400	30000
PFL	1	3	8400	80000
PCAP	2	8	6400	60000

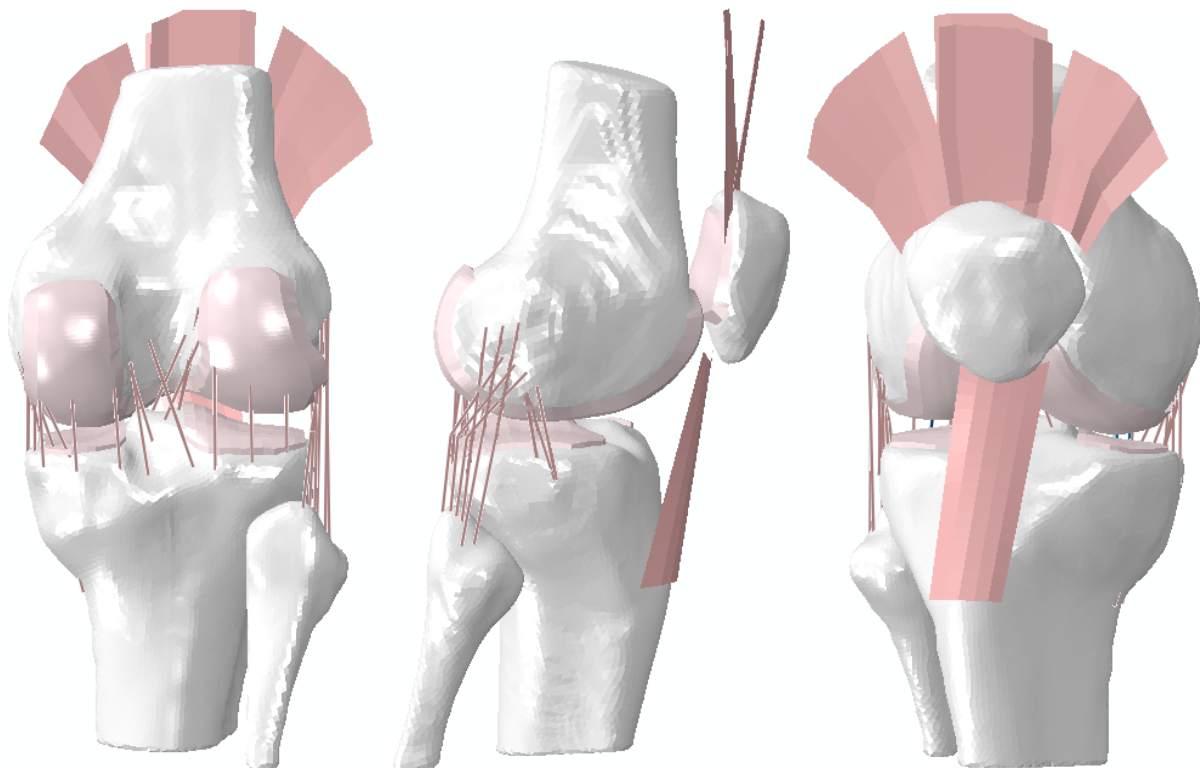


Figure 10. Mesh of bone, cartilage, and ligament structures for a representative subject.

## 5. Creation of Coordinate Systems

### 5.1 Objective

This section creates local coordinate systems for each of the bony structures. The coordinate systems are based on anatomical landmarks. Subsequent reporting of tibiofemoral and patellofemoral coordinate kinematics will be described relative to these coordinate systems.

### Primary Tool

- Hypermesh (v. 14.0), Altair (Troy, MI, USA)
- Matlab, Mathworks (Natick, MA, USA)

### Inputs

- Geometry of bone (.stl)

### Outputs

- Files with landmark locations used to create coordinate systems for each bone

### 5.2 Building Local Coordinate Systems

- Anatomical coordinate systems are based on the descriptions provided by Grood and Suntay (1983) and modified in cases where hip joint center and ankle joint center are not available using methods described by Lenz et al. (2008). In the current work, the femoral coordinate system for DU02 will be defined using available data on the hip joint center.
- The coordinate system consists of an origin with x, y, z coordinates and then three orthogonal axes representing the superior-inferior (SI), anterior-posterior (AP) and flexion-extension (FE) axes.
- Import the STL geometries obtained from segmentation of the femur, tibia, and patella into Hypermesh using the steps described previously. Using the STLs from segmentation allows for better point placement as the mesh is much finer (0.5 mm) than the mesh which will be used in the Abaqus analyses (1.5 to 2 mm).
- Node numbering for points defining the local coordinate systems are described in Table 3 based on Grood and Suntay (1983).
- Axis definitions for local coordinate systems
  - Femoral coordinate system
    - Origin: 196001
    - SI axis (mechanical): The vector from 196001 to 196002 where 196002 corresponds to the hip joint center.
    - AP axis: Take the cross product of the SI axis with the axis defined by a vector which originates at 196003 and travels through 196004.
    - FE axis: Take the cross product of the AP axis and the SI axis.
    - Correction: If the SI axis was defined using the anatomical method, the femoral coordinate system will be rotated by the varus angle about the AP axis.

Table 3. Node numbering convention for the local coordinate systems.

Structure	Anatomical Landmark	Node
Femur	Most distal point on posterior trochlear groove	196001
Femur	Hip Joint center	196002
Femur	Most posterior point on the medial epicondyle	196003
Femur	Most posterior point on the lateral epicondyle	196004
Tibia	Midpoint between the center of the lateral plateau and the medial plateaus as determined by the centroid of an ellipse fit to each region	396001
Tibia	Centroid of an ellipse fit to the medial plateau	396002
Tibia	Centroid of an ellipse fit to the lateral plateau	396003
Tibia	Centroid of distal tibia cut	396004
Tibia	Proximal tip of the medial spine of tibial eminence	396005
Patella	The centroid of an ellipse fit to the articular surface	496001
Patella	The most distal point on the patellar ridge	496002
Patella	The most proximal point on the patellar ridge	496003
Patella	The most lateral point on the articular surface	496004

- Tibial coordinate system
  - Origin: 396001
  - FE Axis: The vector which originates at 396002 and passes through 396003.
  - AP Axis: Define a temporary SI axis as a vector which originates at 396004 and passes through 396005. AP axis is defined by crossing this temporary vector with the FE axis.
  - SI Axis: Cross the FE axis with the AP axis.
- Patellar coordinate system
  - Origin: 496001
  - SI Axis: The vector which originates at 496002 and passes through 496003.

- AP Axis: Take the cross product of the SI axis with the vector which originates at 496004 and passes through the midpoint of 496002 and 496003.
  - FE Axis: Take the cross product of the AP axis and the SI axis.
- Once the nodes used to describe the local coordinate systems for femur, tibia, and patella have been defined in Hypermesh they will be exported as a node set to an ABAQUS input file. Node numbering for nodes that define the local coordinate systems also have a numbering convention (Table 3).
- The origin of the coordinate systems serves as the rigid body reference node. The local coordinate systems use beam elements to connect the other points to the rigid body reference node for each bone in the knee model.

## 6. References

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