## Information for the Exercise

202.064 Computational Biomaterials and Biomechanics

#### Motivation

The goal of this exercise is to learn how to create an FE simulation model from a CT dataset as it was presented during the lecture.

Calculations are done using medtool (www.medtool.at) and the visualisation can be done with Paraview (www.paraview.org).

## Organizational aspects and grading

- Each student will do an exercise using an individual dataset and document their work in a report.
- You can find your dataset ID in TUWEL in "Grades", Column "Feedback", "SXX".
- A list of the parameters for each dataset ID is found at the end of this document.
- On January 10<sup>th</sup>, 14:00 to 15:30, there is a question hour.
- The report (pdf) has to be uploaded to TUWEL.
- The deadline for submission is January 17<sup>th</sup> 23:59.
- There will be an interview/exam on January 24<sup>th</sup>, 13:00 to 16:00.
- The interview is focussed on the report but includes background information from the lecture.

### Recommendations

- Go through the content of the lecture first.
- Install medtool and Paraview and read the "getting started".
- Watch the exercise videos and try to reproduce the steps of the video.
- Work through the following medtool examples by yourself (www.dr-pahr.at/html/04.html):
  - Image Processing
  - Image Calibration
  - Image to FEA
- Read the exercise instructions carefully.
- Talk to other students and build groups.
- Download the data and start with the exercise.
- If questions emerge, write them down and come to the question hour.
- Go through the report guidelines before you start writing.

### Exercise

The dataset for the exercise is a 3D medical image of a proximal femur obtained from a CT scanner (see Figure 1).

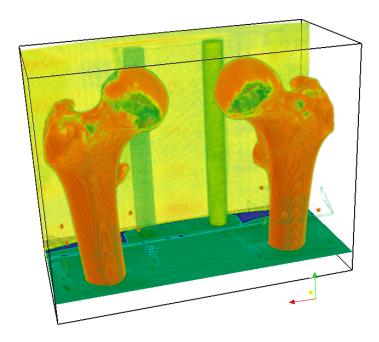


Figure 1: QCT Dataset with 2 femurs and a calibration phantom

The dataset includes 2 femora and one calibration phantom and is provided as:

- ASCII meta data file (\*.mhd) which contains informations about the image, together with a
- binary data file (\*.raw format) which holds the gray values.

Each student has to process one dataset and generate a FE model which shows linear elastic, bone density dependent material behavior, a voxel mesh, and loads the femur in stance configuration.

The model should be used to display and interpret the stress distribution of the femur under loading. Additionally, the spring stiffness of the whole femur and the displacement of the femoral head in x- and y-directions should be evaluated.

## Step-by-step instructions

- Create a working directory structure.
- Download and explore the dataset with Paraview and medtool's viewer. Hints:
  - Use a projected output in medtool (mic:-proj) and adjust the contrast in the medtool viewer using the respective slider
- Use the cut option of medtool (mic:-cut) to obtain two images: one image containing only the phantom and one image containing only one of the two bones (according to your dataset). Hints:
  - Use medtool's viewer to selected the approriate region of interest (ROI).
  - Cut off a few mm of the femoral shaft (there should be no empty space left at the distal end), but leave enough empty space around the rest of the bone for further processing (e.g. embedding).
  - Think about the output data format (mic:-form). How can you save memory capacity?
- Calibrate the bone image using Image Calibrator. Hints:
  - There is a medtool example showing this procedure step by step (see www.dr-pahr.at/html/04.html#image-calibration).
  - Establish the calibration law using the image that only contains the phantom.
  - The phantom chambers have the same densities as in the example (0, 100 and 200 mgHA/ccm). Pay attention to a proper assignment of the chamber labels to these densities.
  - Make sure that the min/max densities are set to 0/1060 mgHA/ccm.
  - To apply your calibration to any given image, you can use the ctcal:-inc option
     (e.g. the image containing only the bone) and save it using the ctcal:-out option.
- Change the resolution of the bone image to around 3 mm with mic:-resf. In addition, scale the image to 0-250 (from 0-1060) to prepare it for the FE model generation.
- Create a mask of the previous bone image (outside = 0, inside = 1) with mic. Hints:
  - Using the viewer, try to find an approriate gray-value threshold that separates the bone from the background.
  - Use (mic:-fill) option with a relatively low threshold to create a segmented image of the bone (it is fine if it is not perfect). Leave all the other parameters unchanged.
  - Delete artifacts with (mic:-clean).
  - Use the viewer's overlay option to check the mask.
  - Scale the mask to 0-1 afterwards (mic:-scale).
- Mask the bone image mic:-mask

- Embed the bone image mic:-embed at the femoral head such that only the head is embedded (not the rest of the bone)
- Generate a CalculiX input file by using Image Converter FEA. Hints:
  - Study the Image to FEA example carefully (http://www.dr-pahr.at/html/04.html#image-to-fea).
  - Use a power law to model the bone material properties using the parameters according to your instructions and a standard elastic material for the embedding (E=2200 MPa,  $\nu$ =0.3).
  - Define displacement boundary conditions as follows:
    - \* Fix the distal end of the femoral shaft (no displacement at the bottom layer, nodeset ALL\_NODES\_B).
    - \* Apply a displacement in z-direction according to your instructions to the embedding of the femoral head (all nodes of the top layer, nodeset ALL\_NODES\_T).
  - Use the imgToFe:-nodedat option to define result variables to be put in a text file as needed for further calculations (see below).
  - Check the generated \*.inp file with a text editor e.g. gvim.
- Analyze your model with CalculiX (medtool Solve Calculix ccx). Activate the ccxRun:-vtk option to obtain an additional VTK output file for Paraview. Hints:
  - In case CalculiX crashes, try to use the absolute path to your \*.inp file and make sure that there are no blanks in your file path.
- Post-process your model in Paraview to visualize the displacement field (DISP) and von Mises stress distribution (STRESS\_Mises). Hints:
  - Use the clip function in Paraview to have a look inside the bone.
  - Think about the displacement field: Does it look as expected for the given loadcase?
  - Think about the von Mises stress distribution: Where do you observe the highest stresses? Are the absolute values and the distribution of the stresses plausible?
- Calculate the spring stiffness (force over displacement) of the whole femur in z-direction. Hints:
  - Try to compare the spring stiffness to that in literature. Are your results plausible?
- Determine the displacements of the femoral head in x- and y-directions.

## Report guidelines

The report should include the following sections:

#### • Introduction

- Brief background to the subject (why is it important?)
- Motivation (why are you performing this FE analysis?)
- Goals (what are the specific goals?)

### • Methods

- Describe the methods you used to achieve your goal
- Provide enough information such that others could reproduce your results
- Document your method step by step, illustrate them with figures

#### • Results

- Put all requested results in here (including figures, tables)
- Results are presented but not discussed in this section

### • Discussion

- Briefly restate the goal and the main results
- Discuss your results (e.g. are the results plausible? what are the limitations?)
- End your report with a brief conclusion

Finally, note that you are supposed to write a scientific report rather than an essay. This means that you should use concise and objective language, provide captions for all figures and tables, and include references to figures, tables and literature.

# Individual data and parameter sets

In the following table you find a list of individual data and parameter sets. This includes the data (specimens 1-5), the side of the femur you should choose (left or right according to the medtool-view), the E-modulus  $E_0$  of the bone material (for BV/TV=1), the exponent k of the material law of the bone (power-law) and the applied displacement in z-direction.

number	data	side	$ m E_0~(MPa)$	k (-)	z-displ. (mm)
S1	specimen1	left	5000	1.5	-0.1
S2	specimen1	right	6000	2	-0.15
S3	specimen2	left	7000	2.5	-0.2
S4	specimen2	right	8000	1.5	-0.25
S5	specimen3	left	5000	2	-0.3
S6	specimen3	right	6000	2.5	-0.1
S7	specimen4	left	7000	1.5	-0.15
S8	specimen4	right	8000	2	-0.2
S9	specimen5	left	5000	2.5	-0.25
S10	specimen5	right	6000	1.5	-0.3
S11	specimen1	left	7000	2	-0.1
S12	specimen1	right	8000	2.5	-0.15
S13	specimen2	left	5000	1.5	-0.2
S14	specimen2	right	6000	2	-0.25
S15	specimen3	left	7000	2.5	-0.3
S16	specimen3	right	8000	1.5	-0.1
S17	specimen4	left	5000	2	-0.15
S18	specimen4	right	6000	2.5	-0.2
S19	specimen5	left	7000	1.5	-0.25
S20	specimen5	right	8000	2	-0.3
S21	specimen1	left	5000	2.5	-0.1
S22	specimen1	right	6000	1.5	-0.15
S23	specimen2	left	7000	2	-0.2
S24	specimen2	right	8000	2.5	-0.25
S25	specimen3	left	5000	1.5	-0.3
S26	specimen3	right	6000	2	-0.1
S27	specimen4	left	7000	2.5	-0.15
S28	specimen4	right	8000	1.5	-0.2
S29	specimen5	left	5000	2	-0.25
S30	specimen5	right	6000	2.5	-0.3

number	data	side	$ brack { m E_0~(MPa)}$	k (-)	z-displ. (mm)
S31	specimen1	left	7000	1.5	-0.1
S32	specimen1	right	8000	2	-0.15
S33	specimen2	left	5000	2.5	-0.2
S34	specimen2	right	6000	1.5	-0.25
S35	specimen3	left	7000	2	-0.3
S36	specimen3	right	8000	2.5	-0.1
S37	specimen4	left	5000	1.5	-0.15
S38	specimen4	right	6000	2	-0.2
S39	specimen5	left	7000	2.5	-0.25
S40	specimen5	right	8000	1.5	-0.3
S41	specimen1	left	5000	2	-0.1
S42	specimen1	right	6000	2.5	-0.15
S43	specimen2	left	7000	1.5	-0.2
S44	specimen2	right	8000	2	-0.25
S45	specimen3	left	5000	2.5	-0.3
S46	specimen3	right	6000	1.5	-0.1
S47	specimen4	left	7000	2	-0.15
S48	specimen4	right	8000	2.5	-0.2
S49	specimen5	left	5000	1.5	-0.25
S50	specimen5	right	6000	2	-0.3
S51	specimen1	left	7000	2.5	-0.1
S52	specimen1	right	8000	1.5	-0.15
S53	specimen2	left	5000	2	-0.2
S54	specimen2	right	6000	2.5	-0.25
S55	specimen3	left	7000	1.5	-0.3
S56	specimen3	right	8000	2	-0.15
S57	specimen4	left	5000	2.5	-0.2
S58	specimen4	right	6000	1.5	-0.25
S59	specimen5	left	7000	2	-0.3
S60	specimen5	right	8000	2.5	-0.15
S61	specimen1	left	7000	2	-0.2
S62	specimen1	right	8000	2	-0.25
S63	specimen2	left	5000	2	-0.3
S64	specimen3	right	5000	2.5	-0.3
S65	specimen3	left	5000	2	-0.2
S66	specimen3	right	6000	2.5	-0.25
S67	specimen4	left	7000	1.5	-0.3
S68	specimen4	right	8000	2	-0.15
S69	specimen5	left	5000	2.5	-0.2
S70	specimen5	right	6000	1.5	-0.25
S71	specimen1	left	7000	2	-0.3
S72	specimen1	right	8000	2.5	-0.15
S73	specimen2	left	5000	1.5	-0.2
S74	specimen2	right	6000	2	-0.25
S75	specimen3	left	7000	2.5	-0.3