AAA Tutorials

10. A complete system for AAA analysis

Grand Roman Joldes
Senior Research Fellow

Intelligent Systems for Medicine Lab. (ISML)
Vascular Engineering
Crawley, WA, 6009, AUSTRALIA

Phone: + (61) 8 6488 3125
Email: grand.joldes@uwa.edu.au

Software installation

Unzip all files from AAA_Analysis.zip in the folder where you want to keep all the analyzed AAA cases.

Software configuration

Modify the paths to Slicer.exe and pvpython.exe in AAA_Configure.bat according to your computer configuration.

All the other tools are accessed using relative paths and should be already correctly configured.

Running the software

Duplicate folder CaseID and rename it using your case ID (e.q. MA3RS1101). Change into this new folder and run AAA_AnalyseCase.bat. This will create the directory structure for you and will tell you the first step you need to complete.

Prepare the required input data and run AAA_AnalyseCase.bat again.

Required input data

.\1_Segmentation_CT\CT_cropped.nrrd
.\1_Segmentation_CT\CT_blood_label.nrrd
.\1_Segmentation_CT\CT_AAA_label.nrrd
.\2_Segmentation_MRI\MRI_cropped.nrrd
.\2_Segmentation_MRI\MRI_AAA_label.nrrd (run AAA_AnalyseCase.bat after this to register MRI to CT, so you can use both to extract thickness)
.\3_Thickness\M*.acsv (Slicer files containing thickness measurements)

Expected outputs

Complete analysis of the AAA, including geometry extraction, meshing, Abaqus input files, Abaqus analysis, stress results and rupture potential indexes (RPI) for constant/variable wall thickness and 3 different loading scenarios:

- Blood pressure applied on the interior ILT surface;
- Blood pressure applied on the interior wall surface;
- Blood pressure applied on the interior wall surface and no ILT included.

Advice regarding input data:

- Make sure the CT segmentations (blood, AAA) run over the entire height of the cropped CT image (check especially the top and bottom slice). This is needed in order for the AAA surface to be properly extracted.
- If you cannot segment properly the top and bottom slices (e.g. because you selected a ROI that is too large), you can:
    - Crop the CT_cropped.nrrd volume, using a smaller ROI and Voxel based cropping. Save as CT_cropped.nrrd;
    - Use the Transforms module to create a new Identity transform;
    - Use Registration->Resample Image (BRAINS) to resample the label maps (blood, AAA) to the size of the new CT_cropped.nrrd (select Image to Warp: CT_AAA_label (or CT_blood_label); Reference Image: CT_cropped; Output Image: same as Image to Warp; Transform file: The identity transform previously created; Interpolation Mode: NearestNeighbor).

Thank You !

grand.joldes@uwa.edu.au