1 MATLABGUI MAYA-> LIGGGHTS

Script to run GUI for converting maya data to liggghts simulation scripts.

1.1 PRE-PROCESSING

If using joints, select all joints, otherwise place locators at proximal/distal ends of bones and select those. It helps to name these sensible things (e.g. TibiaDistalLocator). With all relevant objects selected, run the XROMM tools 'exp' shelf command. Select translation/rotation, do not pad frames with NaNs, and leave the frame number column on.

1.2 PROCESSING

1.2.1 Load data

Run the program, you should be presented with the following window:
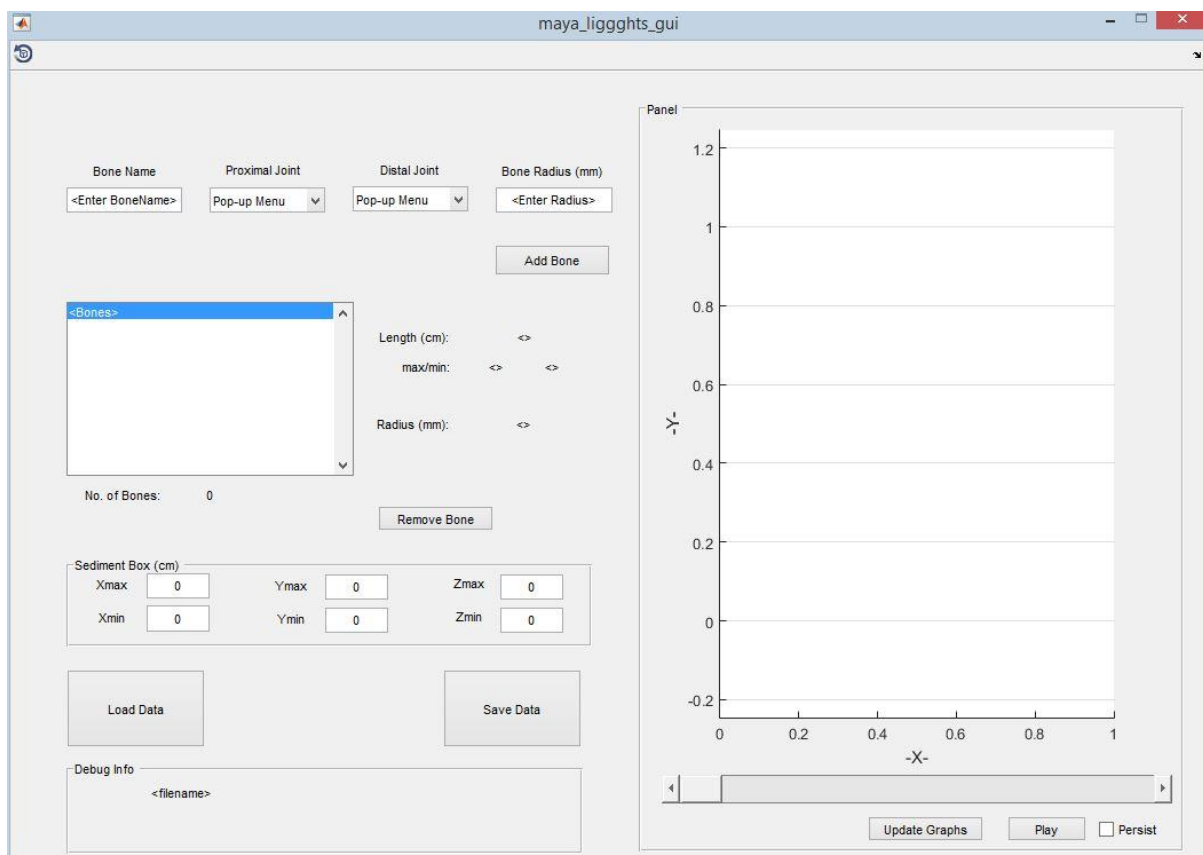
To begin, hit 'Load Data' and select the csv file as produced by maya. This will populate the drop-down menus for 'Proximal Joint' and 'Distal Joint' with the names of the exported objects.

1.2.2 Adding/removing bones

For each bone required, enter a name into the 'Bone name' box, select the proximal and distal joints/locators from the drop down menus, and enter a radius for the bone.
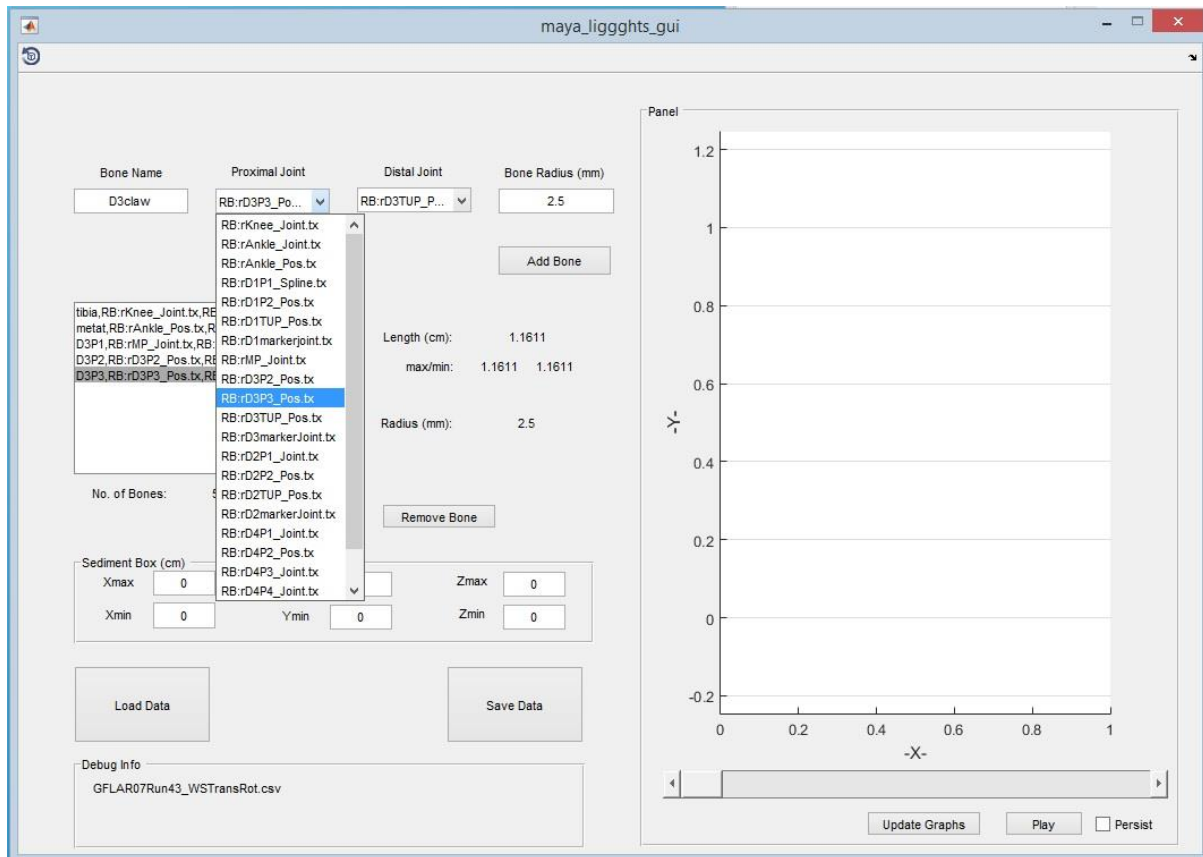
As you add bones, your program should look like the above. Each time you add a bone, it will be added to the visible list, showing name, proximal joint, and distal joint. Beside the list box is shown the length and radius. Length is calculated as the mean distance between proximal and distal joints/locators. Max/Min shows the maximum and minimum length for the bone over the entire exported animation – use this to see if the locators are moving correctly (significantly different max/min/mean indicate that the locators you have selected are not suitable for describing the motion of this bone and you should go back to the Maya file and check everything is correct).

If at any point you make a mistake, or wish to otherwise remove an already added bone, select the bone in the listbox and hit 'remove bone'

1.2.3   Viewing the constructed data

At any point you can hit 'Update Graphs' to visualize the currently added bones.
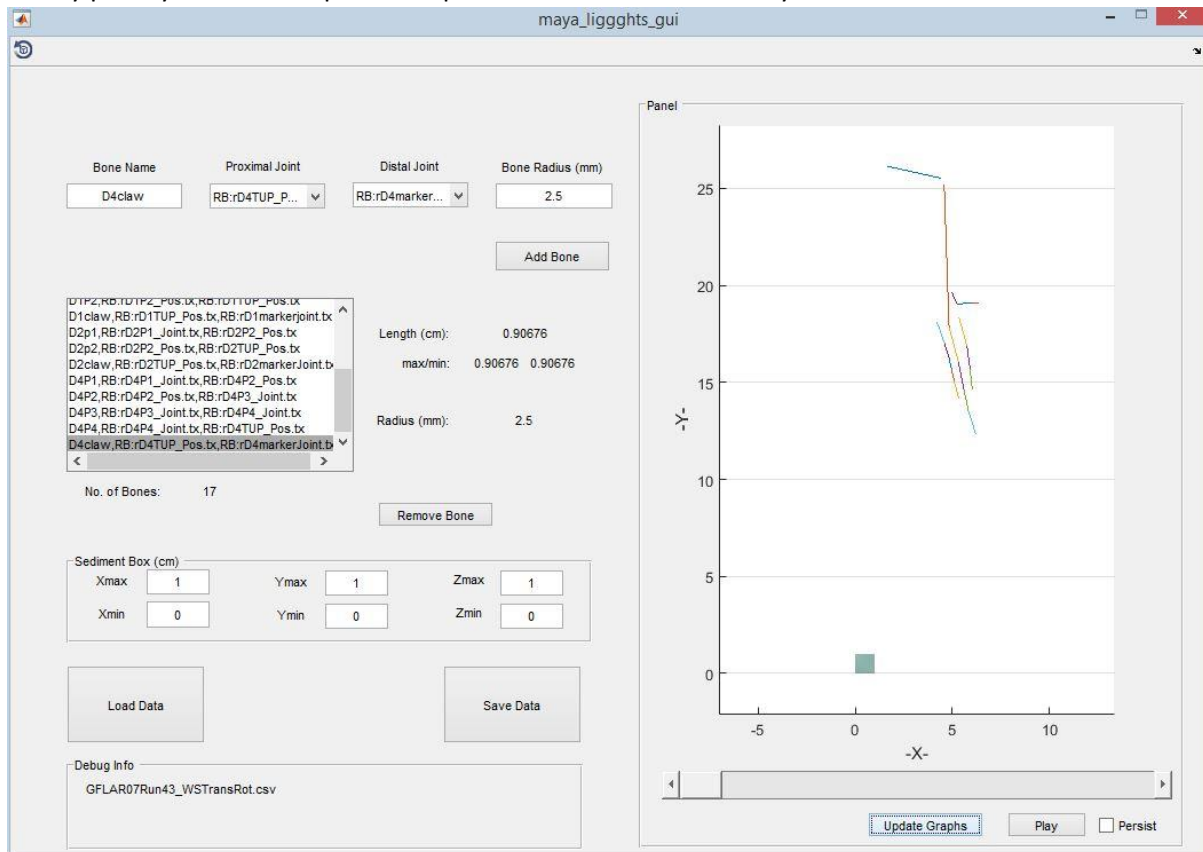
The green box is defined by the max/min x/y/z values in 'sediment box'. We will come back to this later.

Moving the slider beneath the graph will determine which frame is rendered when 'Update Graphs' is pressed – if you want to view the middle of the sequence for instance, drag the slider half way along and hit update.

You can animate the entire sequence by pressing the 'play' button beneath the graphs.

WARNING – currently the animation cannot be exited until it has completed 1 full cycle.
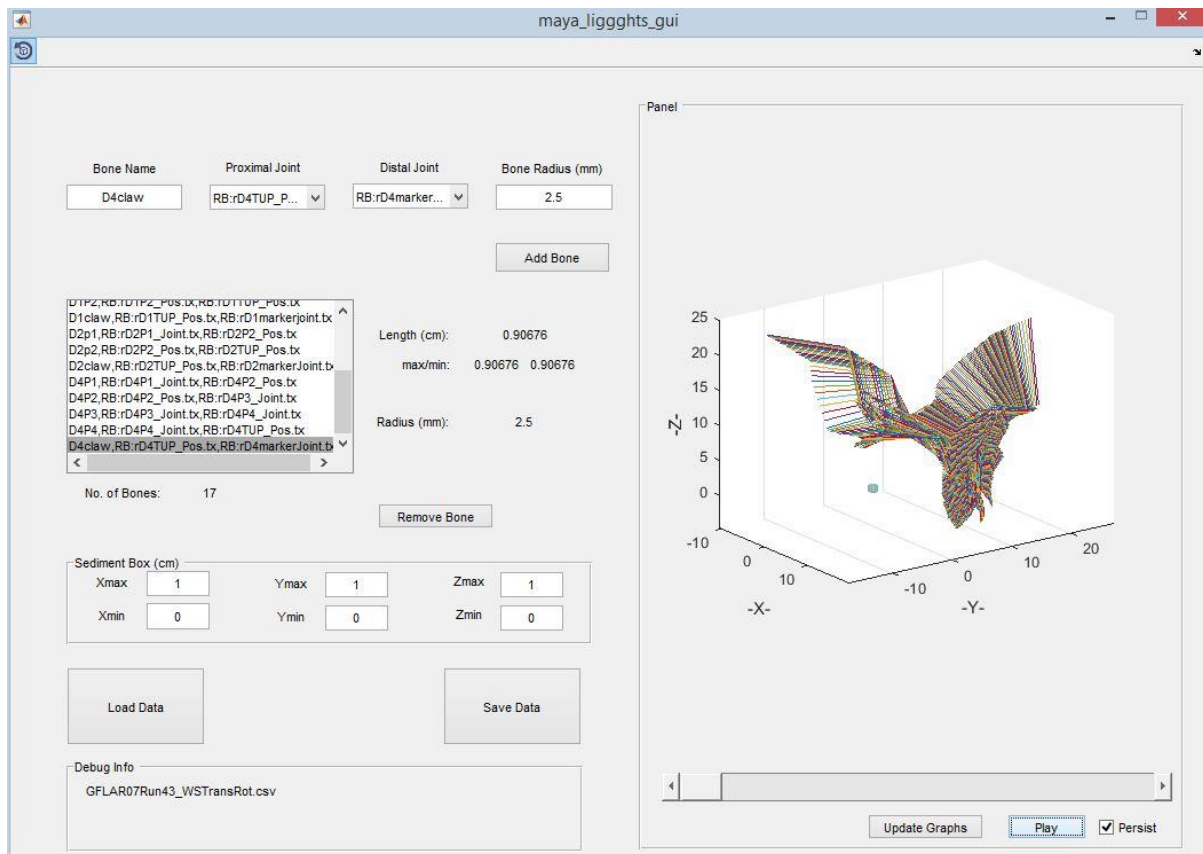
The default view is top-down (X-Y), but by selecting the rotate tool from the title bar you can rotate the axes in 3d:
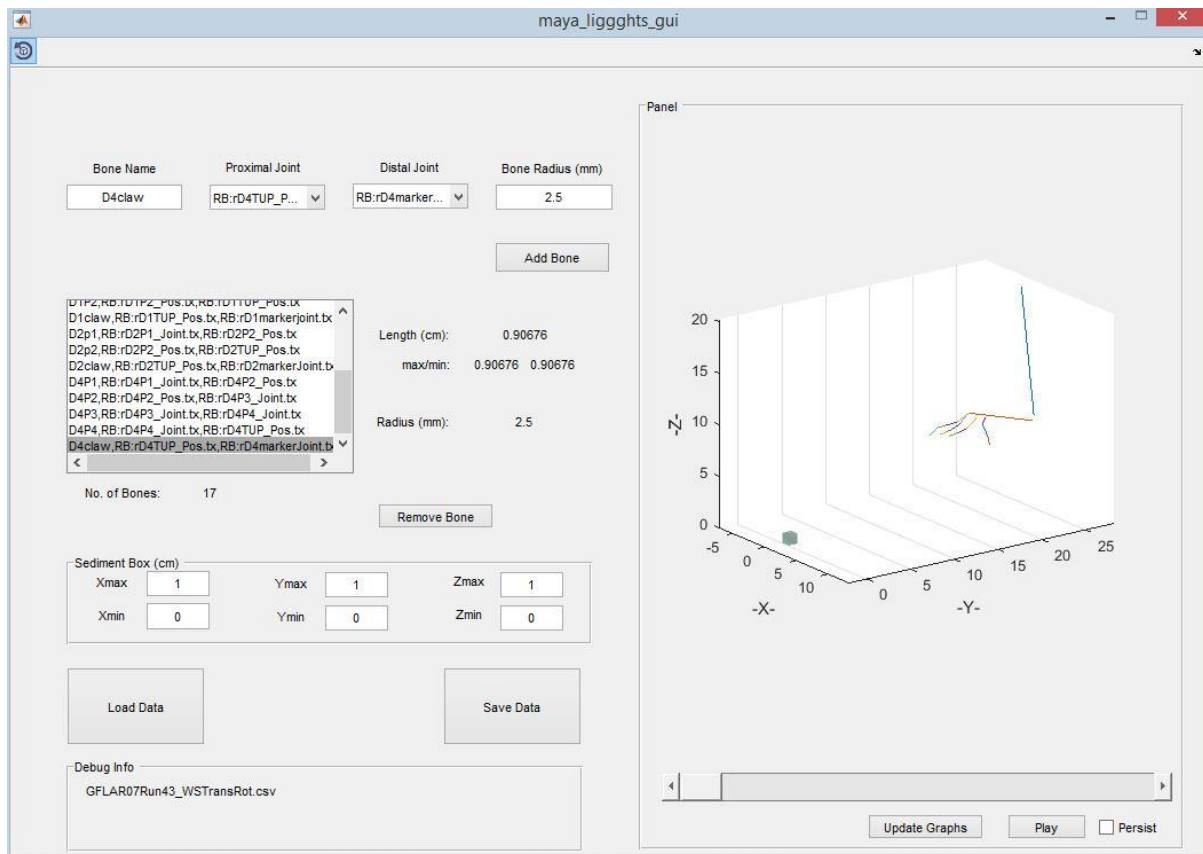
This provides a better view of the constructed bones, and of the sediment box.

1.2.4   Constructing the sediment box

In order to visualize the paths of the bones, ensure that the 'persist' checkbox is ticked, and hit the 'play' button.

This renders every 5th frame in the sequence to be visible at once, enabling you to view the full extents of the motion paths for each bone. To clear the axes, hit 'Update Graphs' at any point.

By viewing the entire motion paths, it is easier to construct a suitably sized sediment tray. Rotate the graph with the rotate tool to view the extents and create a sediment box based on where the foot travels (i.e. create a sediment box large enough to contain the footprint, but not so large as to make an unfeasibly long simulation. Enter the appropriate values into the text boxes under 'Sediment Box' and either hit 'Update Graphs' or 'Play'. Zmax should be the original ground surface as measured in cm in Maya.
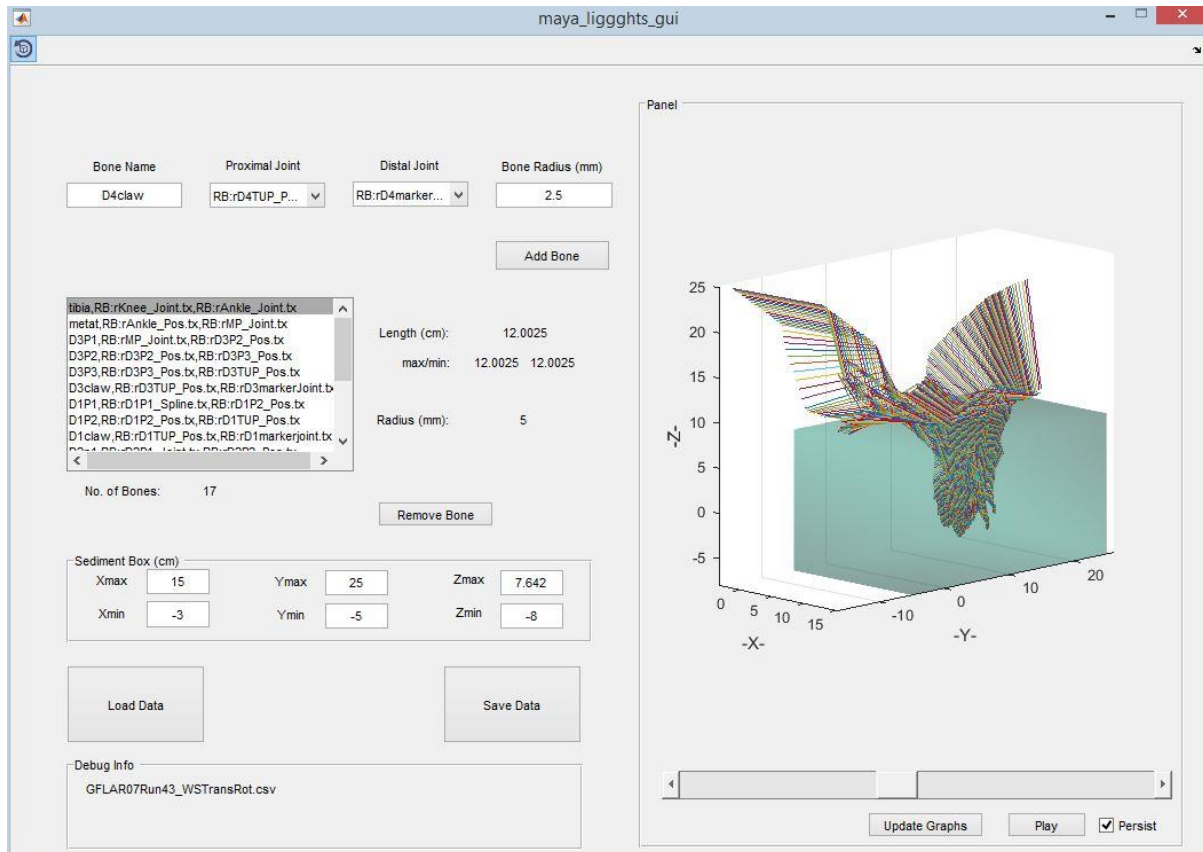
1.2.5   Saving data/Generating Liggghts input

Press the 'save data' button, and type in the name of the dataset. This will create a folder with that name, inside which will be individual stl files for each bone (named according to the name provided in 'Bone name'), and two liggghts input files; part.0 and part2. 'part.0' is an initialization file which will fill the sediment tray with particles upto twice the height specified by zmax. This is necessary as the particles settle under gravity and generally take up approximately half the volume they are inserted into. This file, when run with liggghts, creates an output file called 'restart.res' which is read by 'part2'.

'part2' reads the previous restart file, cuts all particles remaining above original ground surface, and then runs the bones through the sediment according to the prescribed motion.

In this way multiple runs can be made with different properties without having to carry out the time-consuming sediment insertion each time.

Particle properties by default are those used for poppy seed simulation in Falkingham and Gatesy 2014, but default particle size is 1 cm radius for debugging purposes. It is straightforward to open the input files part.0 and part2 and change the radius or other values (young's modulus/Poisson ratio etc) as these variables are declared near the start of each file.

1.3   RUNNING IN LIGGGHTS

Last tested with LIGGGHTS v3.2.0 on 9th Jun 2015. Run as follows:

Liggghts < part.0

Liggghts < part2