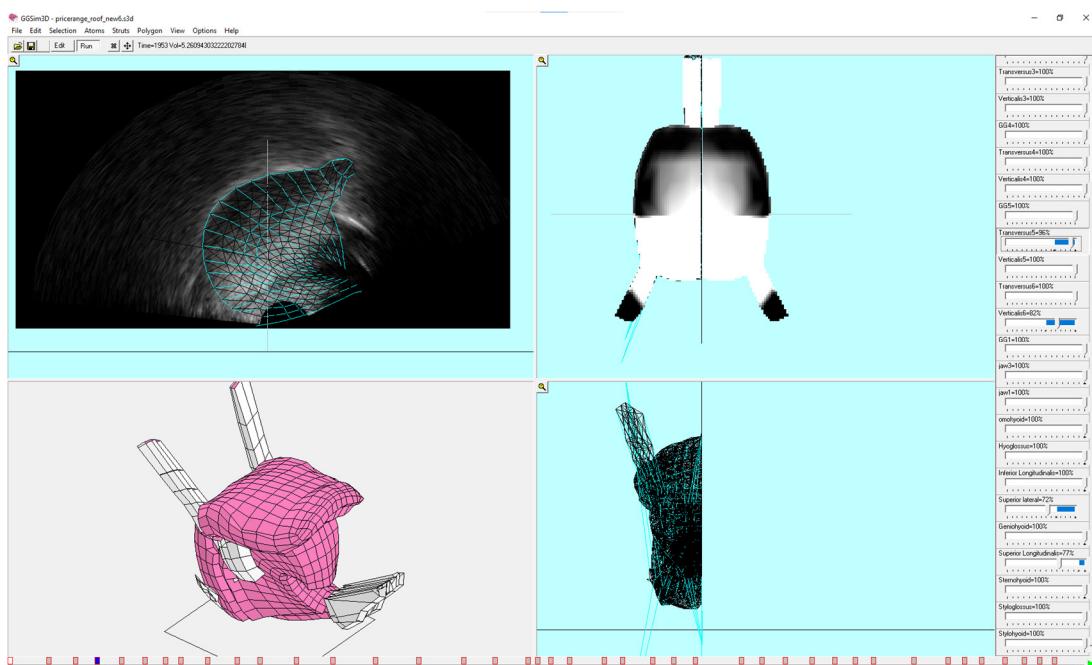


MyoSim3D User Guide

Version 1.00 Massless model

Address:
Articulate Instruments Limited
Queen Margaret Campus, Queen Margaret University Drive
Musselburgh EH21 6UU
UK

Phone:0131 474 0000
Email:support@articulateinstruments.com



Written by Peter Balch and Alan Wrench

Information in this document is subject to change without notice and does not represent a commitment on the part of Articulate Instruments Ltd. The software described in this document is furnished under a GNU Lesser General Public License v2.1 and may be used and copied only in accordance with the terms of that license agreement.

Contents

1	Introduction	3
1.1	Hot keys	3
1.2	Force and pressure calculations	3
1.2.1	Incompressibility of tissue.....	3
1.2.2	Muscle force.....	4
1.2.3	Balancing the forces.....	4
1.2.4	Force propagation	4
1.2.5	Force and pressure display	4
2	Creating and editing a hexahedral mesh	4
2.1	Model file format	4
2.2	Creating and editing a model	5
2.2.1	Creating/loading a model.....	5
2.2.2	General options.....	6
2.2.3	Setting the model physics parameters.....	7
2.2.4	Setting model colours and 3D view	7
2.2.5	Creating a mesh grid	8
2.2.6	Positioning a grid.....	9
2.2.7	Setting a symmetry plane	10
2.2.8	Viewing a single plane.....	11
2.2.9	Deleting atoms	11
2.2.10	Moving and rotating atoms	12
2.2.11	Zooming, moving and centring the model.....	12
2.2.12	Selecting, moving and adding atoms.....	12
2.2.13	Selecting and adding struts	14
2.2.14	Adding layers	14
2.2.15	Neglecting parts of the model.....	15
2.2.16	Rigid bodies	16
2.2.17	Merging atoms	16
2.2.18	Model statistics	17
3	Assigning muscles	18
4	Fitting model to image sequence.....	19
4.1	Importing image sequence as keyframes.....	19
4.1.1	Keyframe file format	19
4.1.2	Scaling and translating background image relative to model	19
4.2	Keyframes	20
4.2.1	Significance	20
4.2.2	Copy and paste	21
4.2.3	Delete and add keyframes.....	21
4.2.4	Adding images to keyframes	21
4.2.5	Muscle chart.....	21
5	Making a movie	22
6	Importing/exporting ANSYS meshes	23
7	Constraints – graphing EPG type data	24
8	Exporting atom kinematics (virtual EMA sensors).....	25
9	A tongue model.....	26
10	Bugs	27

1 Introduction

MyoSim3D enables the following functions:

- Create hexahedron grid consisting of atoms (nodes) and struts
- Up to 0.5 million atoms
- Select one or more atoms and drag to shape the grid
- Assign rigid groups of atoms
- Assign groups of struts as muscle fibres
- Control nominal muscle length as a fraction of rest length
- Define a hard palate or other boundary and measure distance to that boundary.
- Assign markers to atoms (like EMA sensors) and export their movement over time as muscle length assignments change.
- Import and export mesh in ANSYS format.
- Make dynamic 2D or 3D movie of model as it changes over time.
- Import and scale a 2D MRI or ultrasound movie and display as a background to the model so that the model can be adjusted to fit the movie images.

1.1 Hot keys

LeftClick an atom to select it

LeftClick a strut to select it

LeftDrag an atom to move selected atoms

LeftDrag (not on an atom or strut) to make selection box

LeftDrag selection to move selected atoms and struts (if selection visible)

Ctrl-LeftClick an atom or strut to remove from selections

Ctrl-LeftDrag to make a deselection box

Shift-LeftClick an atom or strut to add to selections

Shift-LeftDrag to add atoms and struts in selection box to selections

'A'-LeftClick to make an atom

'S'-LeftDrag to make a strut between atoms

'C'-LeftDrag an atom at the end of a row of selected atoms to reduce or increase the spacing. The farthest selected atom will remain fixed.

Ctrl-Z will undo the last operation. (only the last state is remembered)

1.2 Force and pressure calculations

1.2.1 Incompressibility of tissue

Skeletal muscle is most often attached to bones that are able to rotate about a joint. Those muscles operate in antagonistic groups to adjust the angle of the bones about the joint. For muscular hydrostats such as tongues, trunks and tentacles, "skeletal" muscles still operate in antagonistic groups but instead of a skeleton, they rely on the incompressible nature of the tissue to prevent the structure from collapsing as muscles contract. Incompressibility allows these muscles to operate to change the shape of the structure without changing its volume.

In this version of the simulator, incompressibility is represented by a gas pressure applied to walls of each polyhedron that makes up the model. If muscle contraction causes a polyhedron to shrink in volume, a pressure force is generated to try to restore the volume back to the rest state volume. A gas pressure variable can be set high (e.g. 3000) to represent near incompressibility.

1.2.2 Muscle force

In this version of the simulator, muscle contraction force is controlled by setting a nominal muscle length, expressed as a percentage of the length at rest. Force is proportional to the difference between the actual length of the muscle and the nominal control length. If the nominal length is shorter than the actual length, then a force is generated. This is a greatly simplified representation of what happens in a stretch reflex. Force applied by every strut is determined by Stiffness parameters defined for the muscle at rest and fully contracted.

1.2.3 Balancing the forces

Muscle force is greater if there are many parallel muscle struts contracting in a similar direction. If two muscles are intended to supply the same contraction force but one is represented by 2 parallel sets of struts and the other by 3, then the Stiffness can be adjusted to compensate.

The muscle force and the gas pressure force must be of a similar order otherwise at each incremental step one will dominate the other and the model will not converge to a stable equilibrium. A gas pressure force limiting (force clip) value can be lowered if the model is unstable.

1.2.4 Force propagation

The forces are applied in small incremental steps. Atom positions closest to the activated muscle(s) will change fastest. Volume preserving forces take longer to propagate out from the activated muscles to adjust the position of more distant parts of the model. The user sees this propagation play out in real time as the muscle controls change but this is not representative of the kinematics of real structures.

1.2.5 Force and pressure display

2 Creating and editing a hexahedral mesh

2.1 Model file format

Models are stored in *.s3d files . They contain the following:

'P': LoadAtom;
'S': LoadStrut;
'M': LoadMuscle;
'O': LoadOptions;
'K': LoadKeyframe;
'G': LoadPolygon;
'H': LoadPolyhedron;
'Y': LoadSymmetry;
'R': LoadRoof;
'E': dlgEMA.LoadEMA(line);

Atom parameters

P<atom index>:<x-co-ord>,<y-co-ord>,<z-co-ord>,<mass>,<Fixing type>,<rigid group index>

Strut parameters

S<Strut index>:<Atom 1 index>,<Atom 2 index>,<rest length>,<Stiffness at rest>,<Stiffness contracted>,<axis assignment>,<muscle assignment>,<colour>,<pen width>

Muscle parameters

M<Muscle index>:<Show in chart>,<top of muscle slider in pixels>,<Name>
Slider height is 47 pixels
Show in chart 0=Don't show 1= Show

Options

O:

There are no options parameters stored in this version of MyoSim3D

Keyframe parameters

K<keyframe index>:<time in ms>,"<x-y plane image file>","<x-z plane image file>","<y-z plane image file>",<significance>,<M0 slider %>,<significant>,<M1 slider %>,<significant>, etc
Significance 0= All muscle sliders control model 1= no muscles are controlled 2= selected muscles control model – list follows.
Significant 0=ignore 1= apply

4 sided Polygon parameters

G<polygon index>:<number of atoms>,<Atom 1 index>,<Atom 2 index>,<Atom 3 index>,<Atom 4 index>,<visible side>,<colour>
Number of atoms = 4 or 0
Visible side 0.000 = both sides.

Polyhedron parameters

H<polyhedron index>:<positive face polygon 1 index>,<positive face polygon 2 index>,<positive face polygon 3 index>,<positive face polygon 4 index>,<negative face polygon 1 index>,<negative face polygon 2 index>,<negative face polygon 3 index>,<negative face polygon 4 index>

Symmetry parameters

Y:<symmetry axis>,<co-ordinate in orthogonal axis>
Symmetry axis 0=XY 1= XZ 2=YZ

Roof boundary (constraint) parameters

R:<constraint axes index>=<1st axis grid index>,<2nd axis grid index>:<size of constraint grid>,<indexed grid node 'height'>,<grid is active>
Constraint axes: 0=Z-upper limit (Zpos), 1=Y forward limit (Ypos), 2=X left limit (Xneg), 3=X right limit (Xpos), 4=Z lower limit (Zneg), 5=Y rear limit (Yneg)
Note: Zpos is the one used for palatal constraint
<1st and 2nd axis grid index> e.g. x and y indices if Axis is Zpos
<size of constraint grid (N)> an NxN square grid of atoms forms the constraint. Each node of the grid can be moved in one dimension.
<indexed grid node height> variable position of the node in the one adjustable dimension.
<grid is active> 0= inactive 1 = active Note only the value assigned to the final node is used.

EMA tracking parameters.

E:L:<atom index>,<EMA channel> <ID>
<ID> = text shown in EMA dialog list box

Existing *s3d models can be loaded using the File|Open... dialog.

2.2 Creating and editing a model

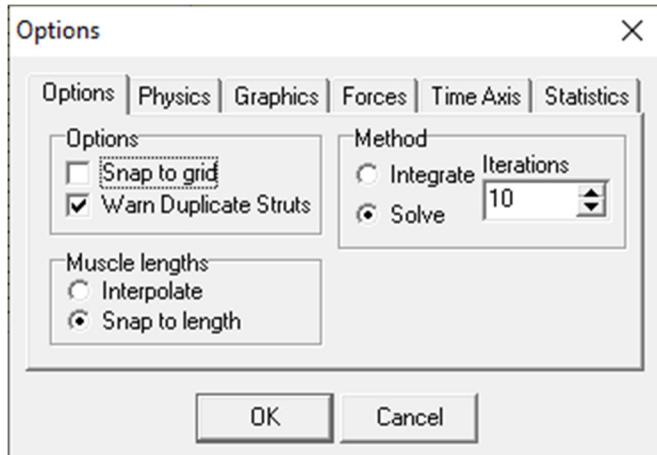
2.2.1 Creating/loading a model

A new blank model is created using the File|New... dialog.

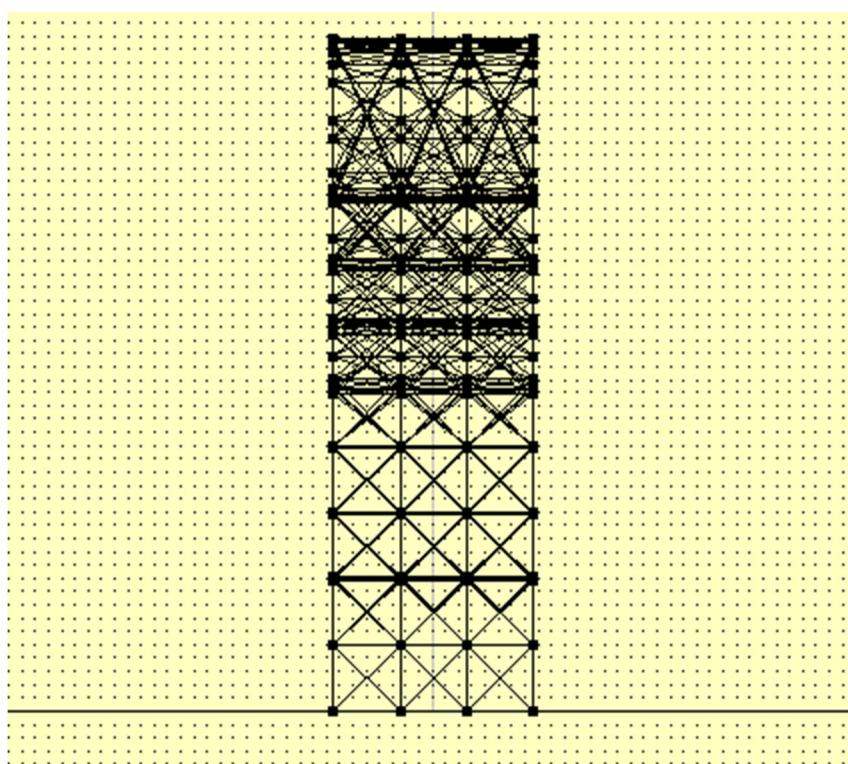
An existing model can be opened using the File|Open... dialog

2.2.2 General options

Select Options|Options... and chose the “Options” tab



The “Snap to grid” checkbox displays a fine grid (8 unit spacing). If set, then atoms will be constrained to lie on one of the grid points. By default this is unchecked.



“Method”:

Integrate – in the current version the integration method of calculating model deformation including mass and inertia is not properly implemented and should not be selected.

Solve – An iterative process of updating hexahedron pressure and stretch reflex force along struts. **This must be selected in this version of the software.**

Iterations – number of force and positional recalculations between redrawing. This does not limit the total number of iterations which in fact continue indefinitely while in run mode

Muscle lengths – these parameters relate to keyframes which are discussed in a later section of this manual.

2.2.3 Setting the model physics parameters

The model is named using the **File|Save...** or **File|Save As...** dialogs.

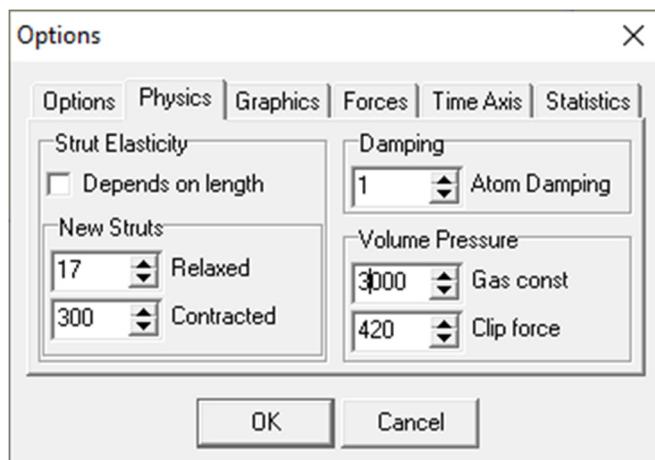
In the **Options|Options...** dialog select the “Physics” tab

Leave “Depends on length” unchecked.

Set the default stiffness for any newly generated strut in its “relaxed” (100% length) state and its “contracted” (<100% length) state.

Leave “Atom damping” at 1

Set Gas constant and Clip force for all hexahedrons (new and existing). If clip force is set too high then model will not converge but will oscillate.



2.2.4 Setting model colours and 3D view

Select **Options|Options...** and the “Graphics” tab.

Colours are:

Default – colour of Atom or strut not in one of the following four states

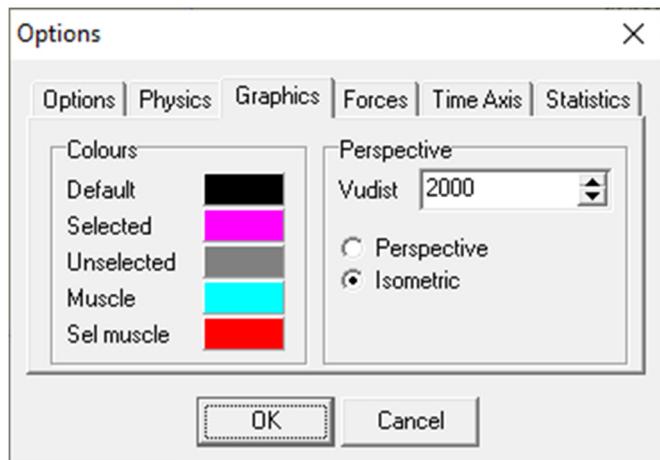
Selected - colour of and atom or strut that is selected for editing

Unselected – colour of unselected atoms and struts. Indicates that a selection is active somewhere in the model.

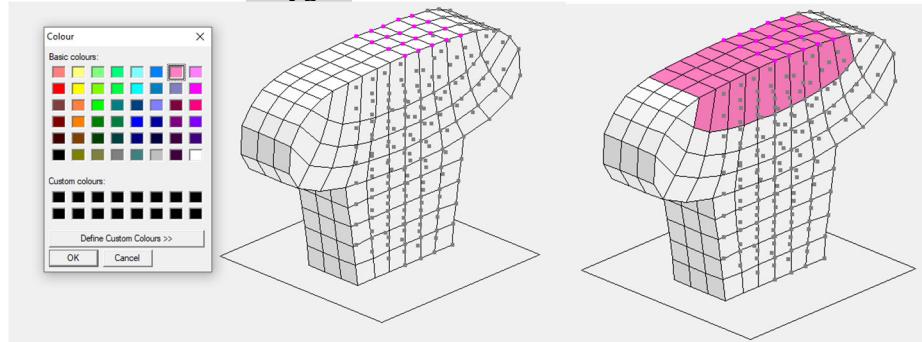
Muscle – colour of struts that have been assigned to a muscle

Sel Muscle – colour of the struts corresponding to the currently selected muscle.

The 3D model can be drawn in perspective from a camera viewpoint set “Vudist” units from the axes origin. Or it can be drawn isometrically.

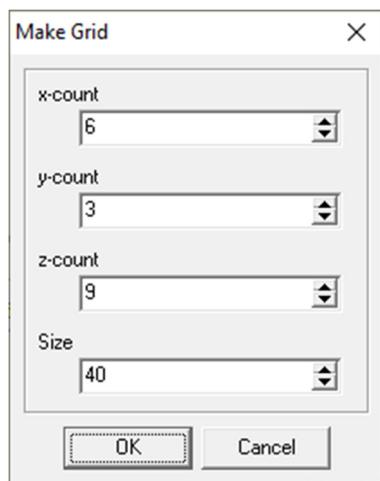


Colour (shown in the 3D view) of a selection of polygons can be changed using **Polygon** menu. If the 4 atoms that define a polygon are selected then the colour of all the faces of the hexahedron to which that polygon belongs is set by clicking on the “colour” in the **Polygon** menu.



2.2.5 Creating a mesh grid

To start a mesh it is usual to create a grid of $L \times M \times N$ cubic hexahedrons with “Size” (side length) of all hexahedrons in the grid measured in base units. The units are internally consistent but unspecified.



When the grid is created, struts lying along each axis have their axis noted and this assignment is preserved even if the strut is rotated so that it ends up aligned with a

different axis. This assignment forms an easy way of selecting, isolating and moving groups of atoms.

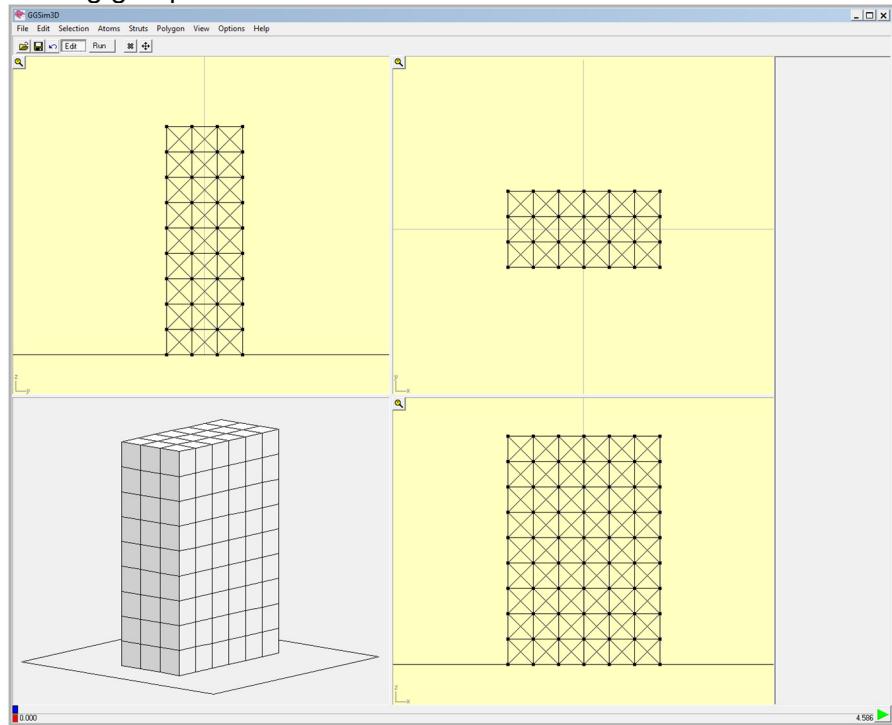


Figure An initial 6x3x9 grid of hexahedrons

2.2.6 Positioning a grid

The grid can be moved relative to the axes (the light and dark grey lines in the three orthogonal views and the plane in the 3D view indicate zero on these axes). To move the grid, select all the pixels, click and drag in one of the views until all the atoms are pink (default selection colour). Then click on one of the atoms and drag.

Here we drag the grid in the x/y plane and drag it so that its side is aligned with $x=0$.

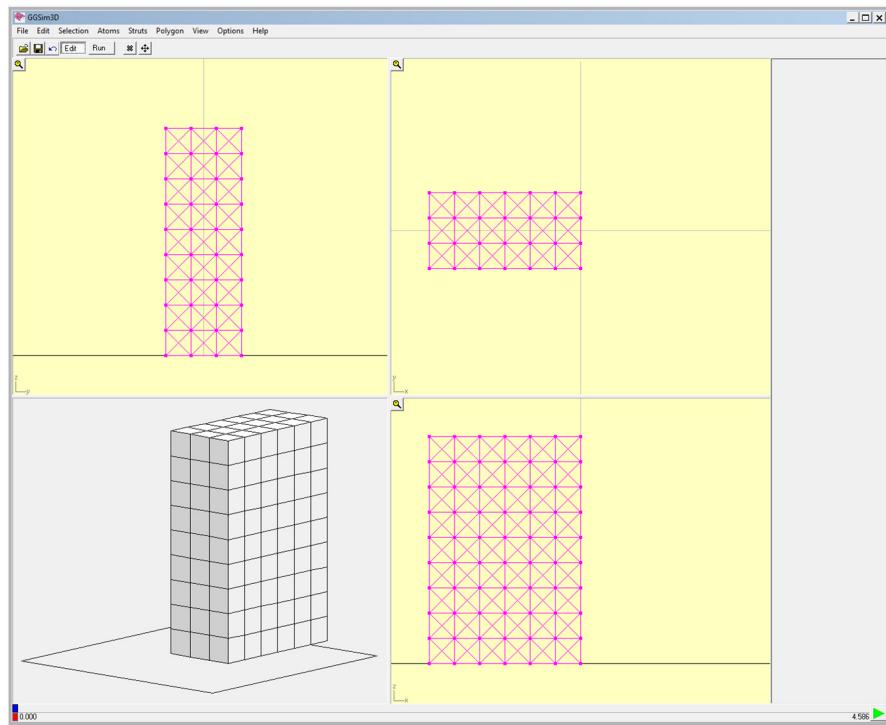
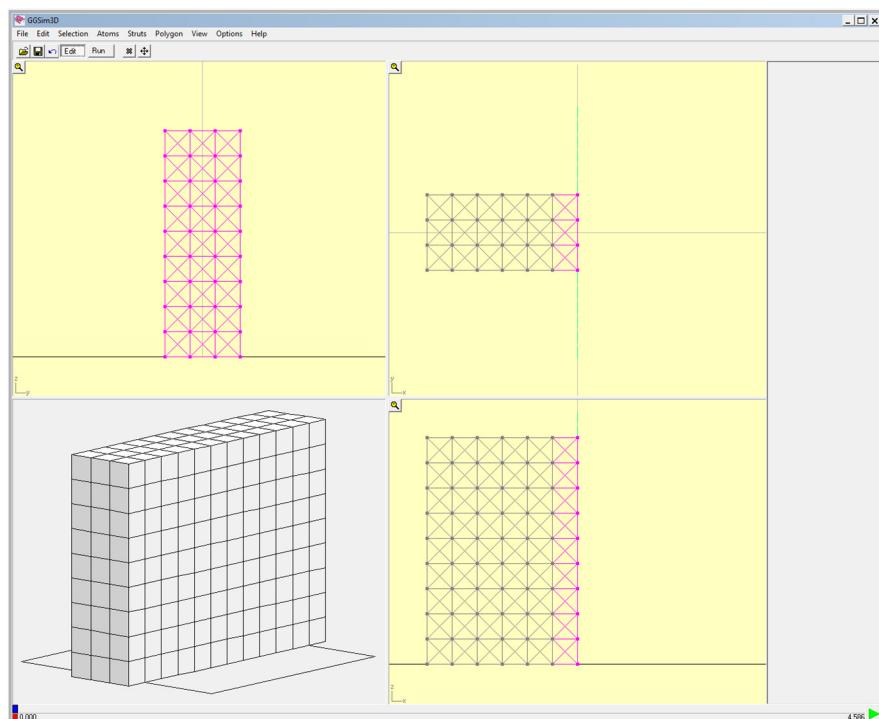


Figure Grid selected by clicking and dragging

2.2.7 Setting a symmetry plane

We can then set a symmetry axis by selecting the atoms on the $x=0$. Then from **Atoms|Fixing...** select “symmetry plane”. The symmetry plane can be in XY, YZ or XZ planes and does not need to be at zero on an axis.

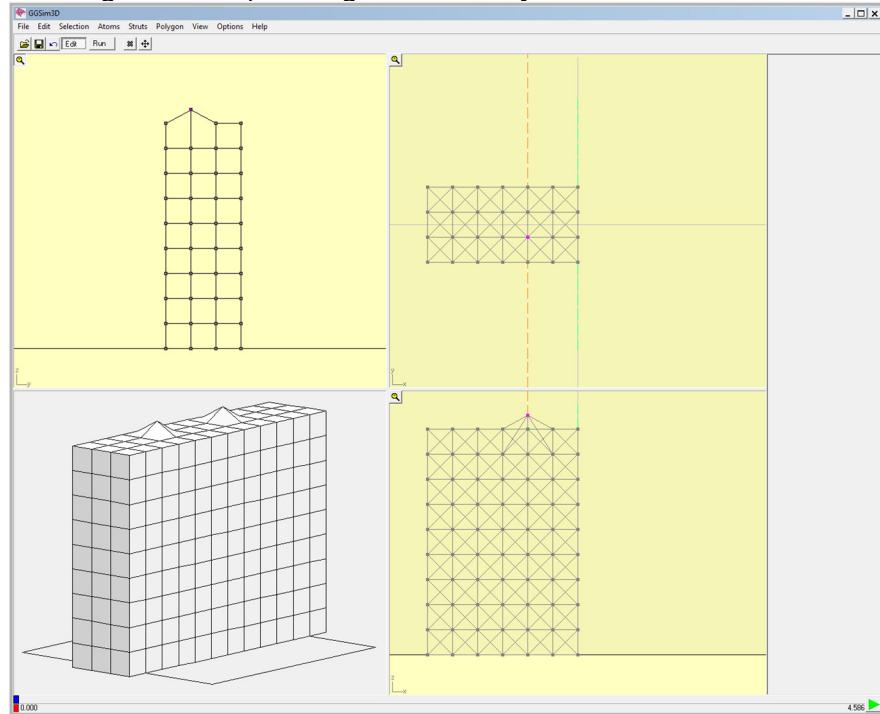


A mirror image can be added to the 3D view. This can be switched off by unchecking “Show symmetry” in **View>Edit**. If symmetry view is to be used then the model should lie on only one side of the symmetry plane, otherwise it will overlap with the

mirror image. **WARNING** If a symmetry plane is defined in the middle of a model then all atoms and struts below (negative to) the symmetry plane are deleted.

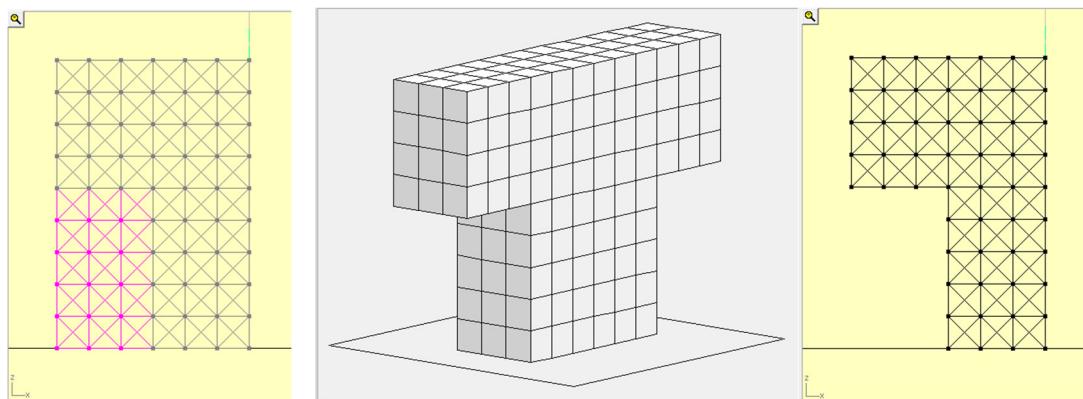
2.2.8 Viewing a single plane

Each plane view shows the atoms throughout the entire grid. To view the atoms lying in a single plane, click the  button in the corner of one of the 2D viewing windows. A red dashed line will appear in the other two 2D windows. Click and drag the red dotted line to select the single plane for viewing and so atoms in that plane can be moved by clicking and dragging them or they can be deleted by selecting and then pressing <delete> key.



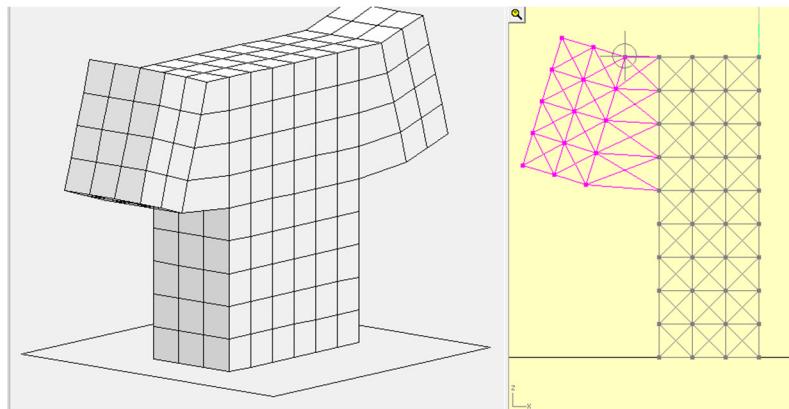
2.2.9 Deleting atoms

In planar or full view, a subset of hexagons can be deleted by selecting their associated atoms and struts and pressing the <delete> key



2.2.10 Moving and rotating atoms

A group of atoms can be rotated by first selecting them. Then right-click popup menu option “rotate” moving the cursor to the right will rotate the atoms anticlockwise and to the left – clockwise. The origin of rotation will be the position of the mouse when right-clicked. When a satisfactory rotation has been achieved, click the left mouse button to stop rotation. This process can be repeated if necessary.



2.2.11 Zooming, moving and centring the model

It is sometimes useful to zoom in to a 2D or 3D view in order to make it easier to select atoms and struts.

To zoom in on a region of the model in a particular view, right-click in the chosen window and select “Zoom”. Then moving the cursor left zooms in and moving the cursor right zooms out. The right-click position defines the origin of the zoom.

Clicking the left or right mouse again, terminates the zoom function. Alternatively , if you have a mouse with a wheel , it can be used to zoom in and out.

To move the model position within a window, hold the <shift> and <Ctrl> keys and left-click and drag the cursor to grab and move the axes (and thus the model) within that window.

Note that zooming and moving will also zoom and move the view in the other windows.

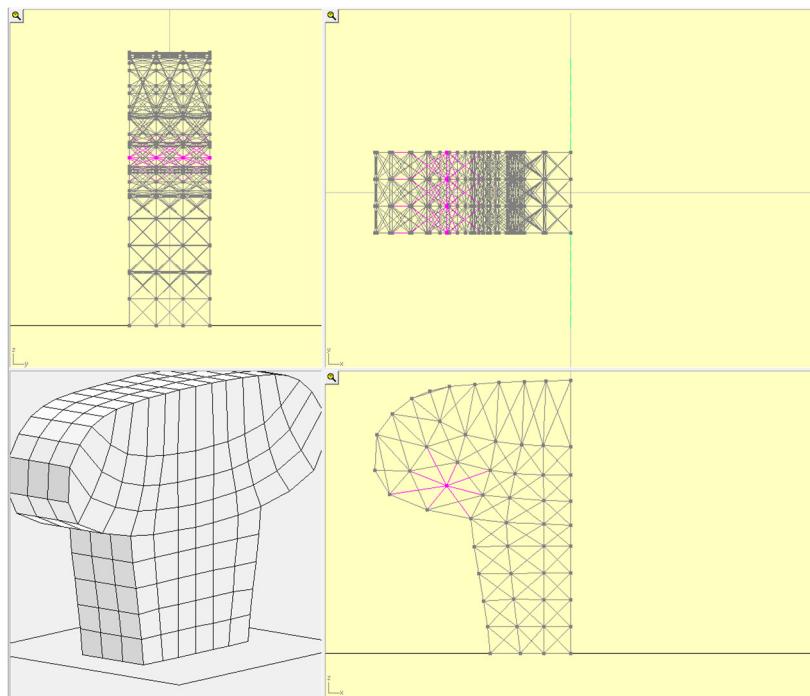
If Zooming or moving results in the model disappearing from view then the position is centred and scaling set to unity by clicking the  button at top of the application.

Or centred and rescaled to fit all axes in windows by clicking the  button.

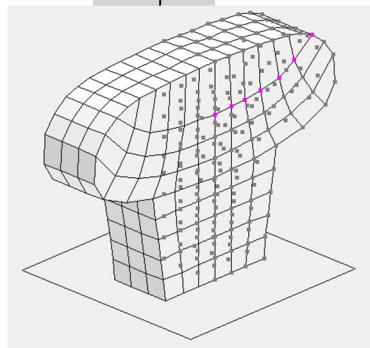
2.2.12 Selecting, moving and adding atoms

Groups of atoms can be moved and rotated to shape the grid. Selection can be done by clicking and dragging then holding the <shift> key and click and drag to append more atoms to the selection. Or hold the <Ctrl> key and click and drag to unselect atoms. When using click and drag to select a region of atoms and struts use **Sub-select|Atoms** to select only atoms within that region.

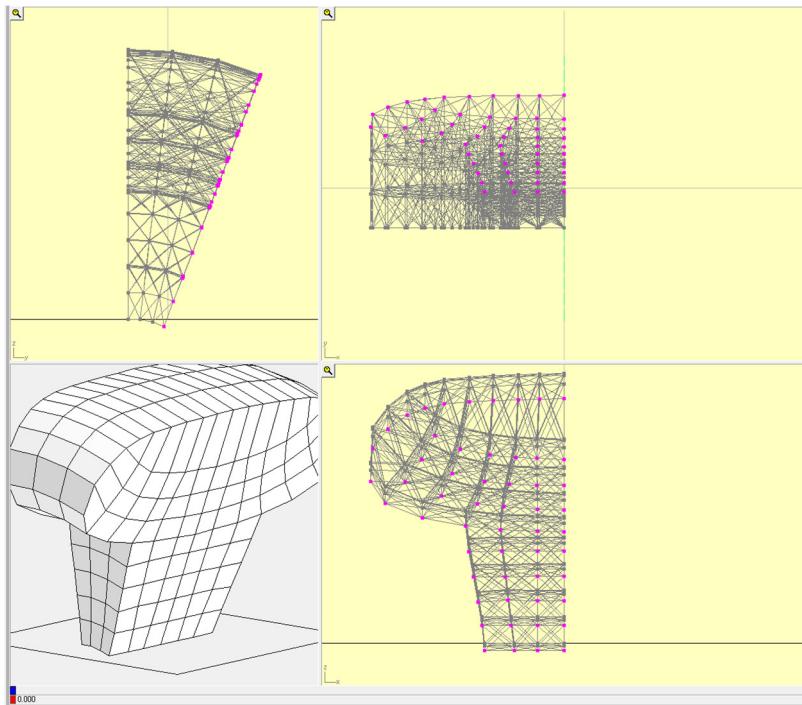
As an alternative to selecting a group by clicking and dragging, select one or two atoms then use **Selections|Extend Atoms** and select X-lines, Y-lines or Z-lines.



It is also possible to select individual atoms in the 3D view by clicking on them and holding the <shift> key to select more than one. To view atoms in the 3D viewer select View|Edit and click "Show 3D atoms"



Each plane can be rotated.



2.2.13 Selecting and adding struts

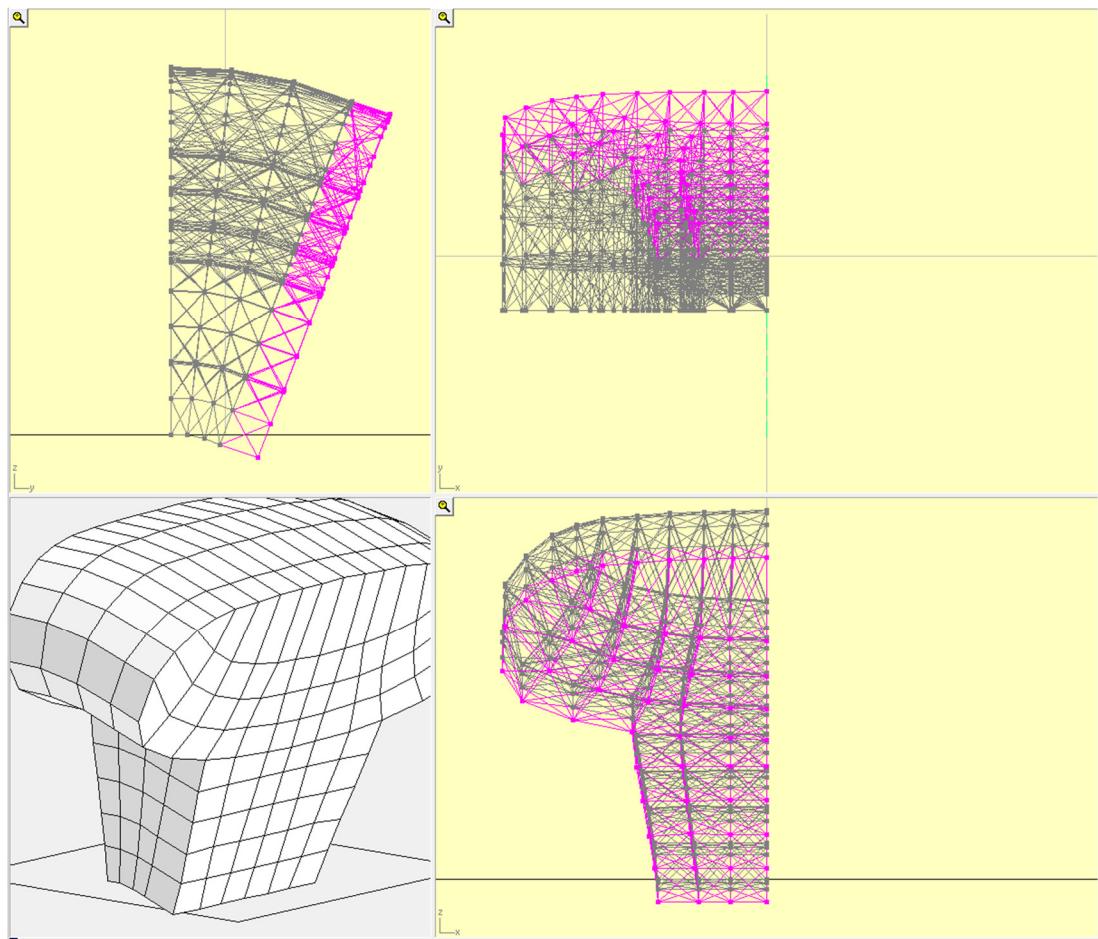
Struts may be selected in the same manner as atoms. Be aware that there are struts which connect opposing atoms across the face of every polygon. Use **Selection|Extend struts** to continue the selection of strut(s) along “x-lines”, “y-lines” and “z-lines”. When using click and drag to select a region of atoms and struts use **Sub-select|Struts** to select only struts within that region.

Struts may be added between existing atoms. Hold the ‘S’ key and left click close to one atom, then drag to a second atom and release the mouse button.

If by accident more than one strut is added between the same two atoms then a warning message will appear. To be certain that there are no duplicate struts, use **Struts| Delete duplicates...**

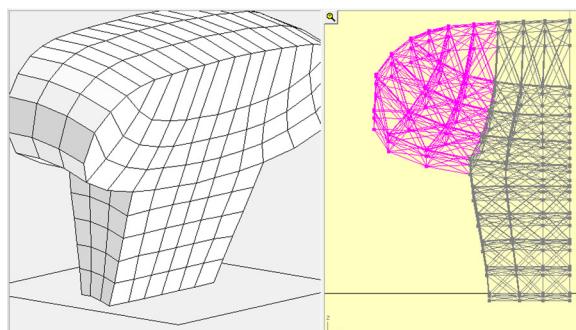
2.2.14 Adding layers

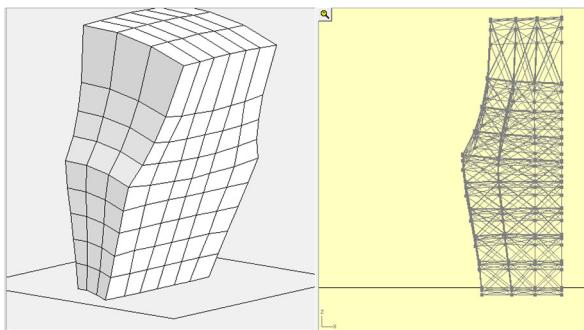
The grid can be extended a layer at a time by selecting one layer from the model and clicking **Edit|Add layer**



2.2.15 Neglecting parts of the model

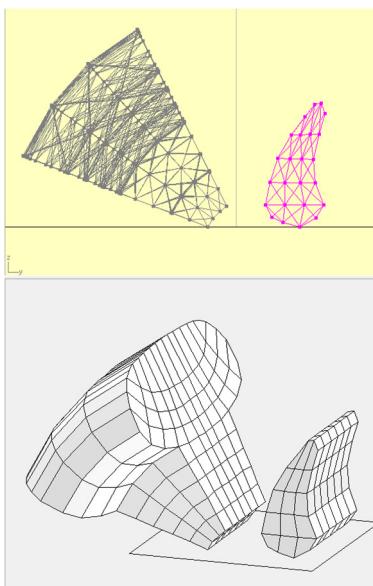
To make it easier to edit internal parts of the model, parts of it can be temporarily “neglected”. Neglected parts are invisible in Edit and Run mode and are ignored when atoms or struts are selected. Select a region then click either Selection|Atoms neglected|Selected or Selection|Atoms neglected|Unselected A flag is set in the software to effectively temporarily delete parts of the model. To restore the whole model click Selection|Atoms neglected|Heed all





2.2.16 Rigid bodies

If a symmetry plane has been defined then a set of atoms can be assigned to form a rigid body such that the distance between atoms is fixed but the set as a whole can rotate and translate in the plane of symmetry. Select a set of atoms. The click **Atoms|Rigid body...** and type in a rigid body number. If more atoms are to be added to the rigid body then the same number should be used. Rigid bodies are limited to rotate and translate about the symmetry plane. If a symmetry plane is not defined then a rigid body cannot operate.

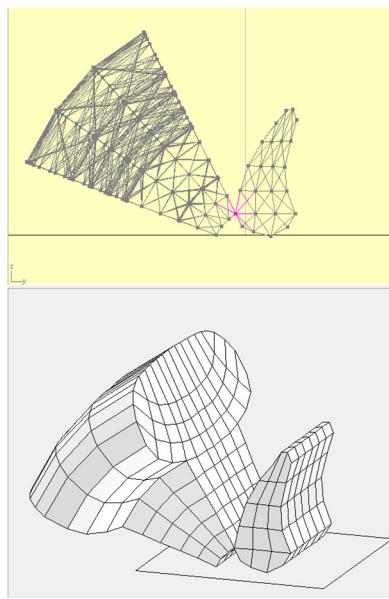


2.2.17 Merging atoms

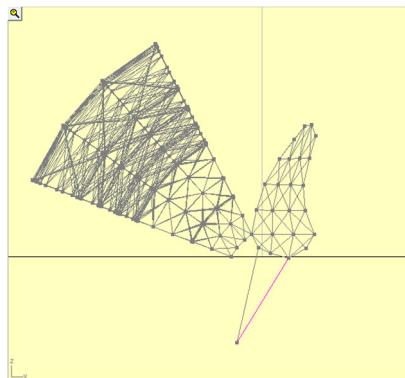
Separate grids can be linked by merging atoms. Move the two grid so that the points to be merged overlap and select them. Then select **Atoms|Merge** and click one of the following:

- “All selected” – will merge all the selected points to produce a single merged point.
 - “All close” - will merge any atoms closer than 8 units to each other.
 - “Close selected” - will merge selected atoms within 8 units to each other.
- The position of the merged atom will be half way between the two close atoms.

If the two grids are merged by one atom or a linear row of atoms perpendicular to the symmetry plane then this forms a hinge.



Atoms may be added by holding the ‘A’ key and left clicking in one of the 2D windows. Individual struts may be created by holding the ‘S’ key and clicking on one atom and dragging close to a second atom.

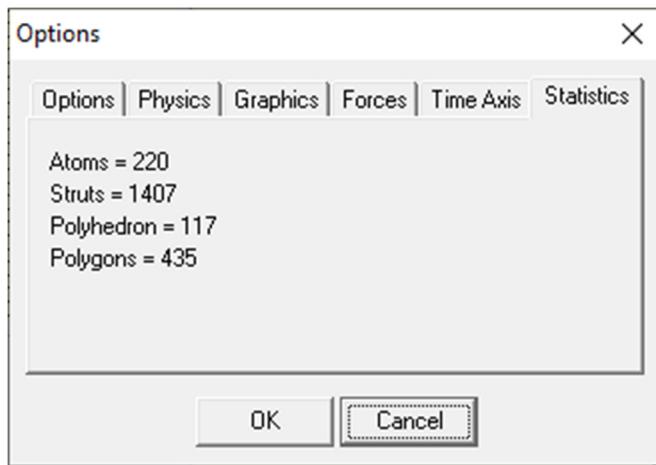


A selected atom or group of atoms may be fixed so they never move under any applied force by selecting [Atoms|Fixing](#) and selecting “Static”. Unfix them by selecting “Normal”

2.2.18 Model statistics

Select [Options|Options...](#) and choose the “Statistics” tab.

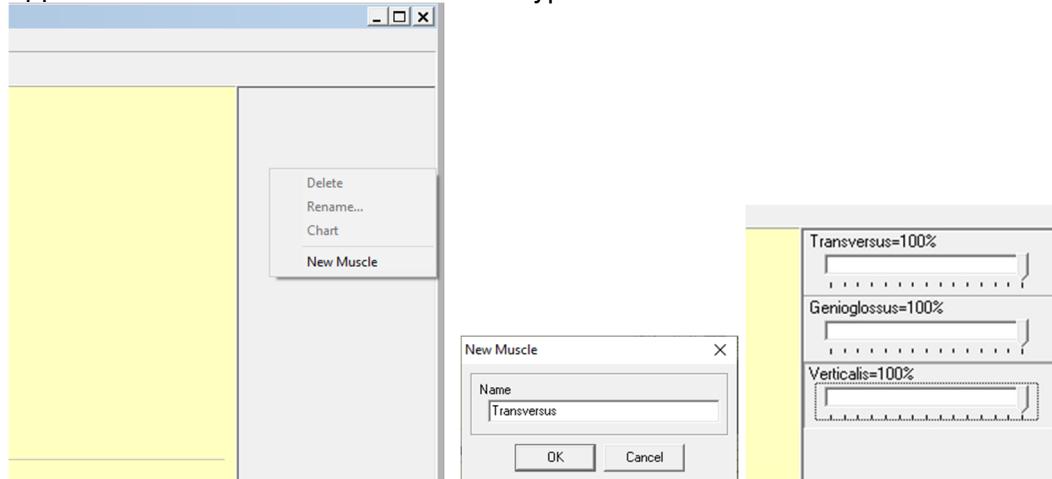
This shows the number of Atoms, Struts, Polyhedrons, and Polygons included in the model. [Note: This can also be determined by examining the *.s3d file]



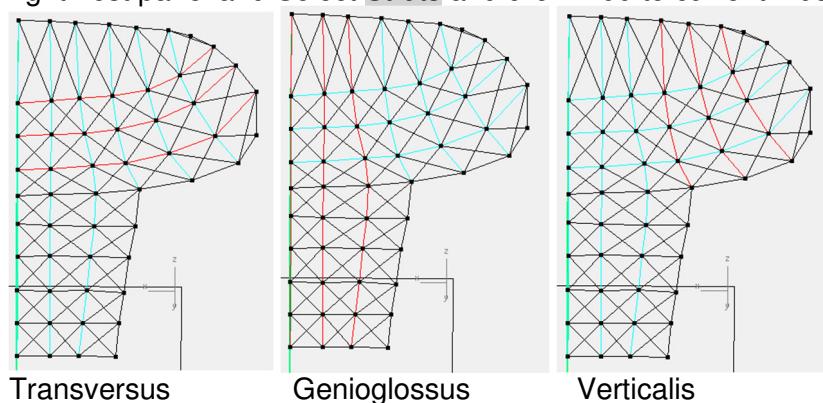
3 Assigning muscles

One or more struts may be assigned to a “Muscle”

If the Muscle does not exist then right-click in the Window on the far right of the application and click “New muscle” and type the name of the new muscle



Select a single row of atoms. Often it is easiest to select one and then use Selection|Extend atoms “X-lines” or “Y-lines” or “Z-lines”. Then use Selection|Extend atoms “Atoms to struts” to select the line of struts. Alternatively, select a strut and use Selection|Extend struts . Now select the muscle slider in the rightmost panel and Select Struts and click “Add to current muscle”.



Struts assigned to currently selected muscle are shown in RED.

4 Fitting model to image sequence

To assess the ability of a model to match deformation of the actual modelled structure, a means to fit the model to 2D images is included in the software.

4.1 Importing image sequence as keyframes

4.1.1 Keyframe file format

A sequence of images (e.g. movie frames from midsagittal ultrasound or MRI) can be imported and associated with a timeline. To do this, the path to each frame preceded by a time in seconds must be entered on separate lines of a text file. Such a file can be generated from Articulate Assistant Advanced software using **Export | Data**, selecting every frame of ultrasound or video in the “rows” tab and selecting ultrasound or video frame in the “columns” tab. The contents of the text file should look like this:

```
0.8067 C:\Users\Alan\Documents\MyoSim3D\the price_041215183623_36.png  
0.8252 C:\Users\Alan\Documents\MyoSim3D\the price_041215183623_37.png  
0.8437 C:\Users\Alan\Documents\MyoSim3D\the price_041215183623_38.png  
0.8622 C:\Users\Alan\Documents\MyoSim3D\the price_041215183623_39.png  
....
```

The software can load *.bmp or *.png format images.

To import, Select **File | Import keyframes** and click “Image to XY” or “Image to XZ” or “Image to YZ” which specifies the 2D view that the images will be displayed in. Then choose the text file using the browse dialog and click OK.

A series of white rectangles representing the keyframes will appear in the keyframe window at the bottom of the application.



After importing, right-click on the keyframe window and click Lock keyframes. This prevents accidental changes in the timing of the keyframes. They have a red border when locked .

4.1.2 Scaling and translating background image relative to model

To fit the model to the background image, select **View| move bg Image...**

Then edit:

size – scale of the image relative to the model

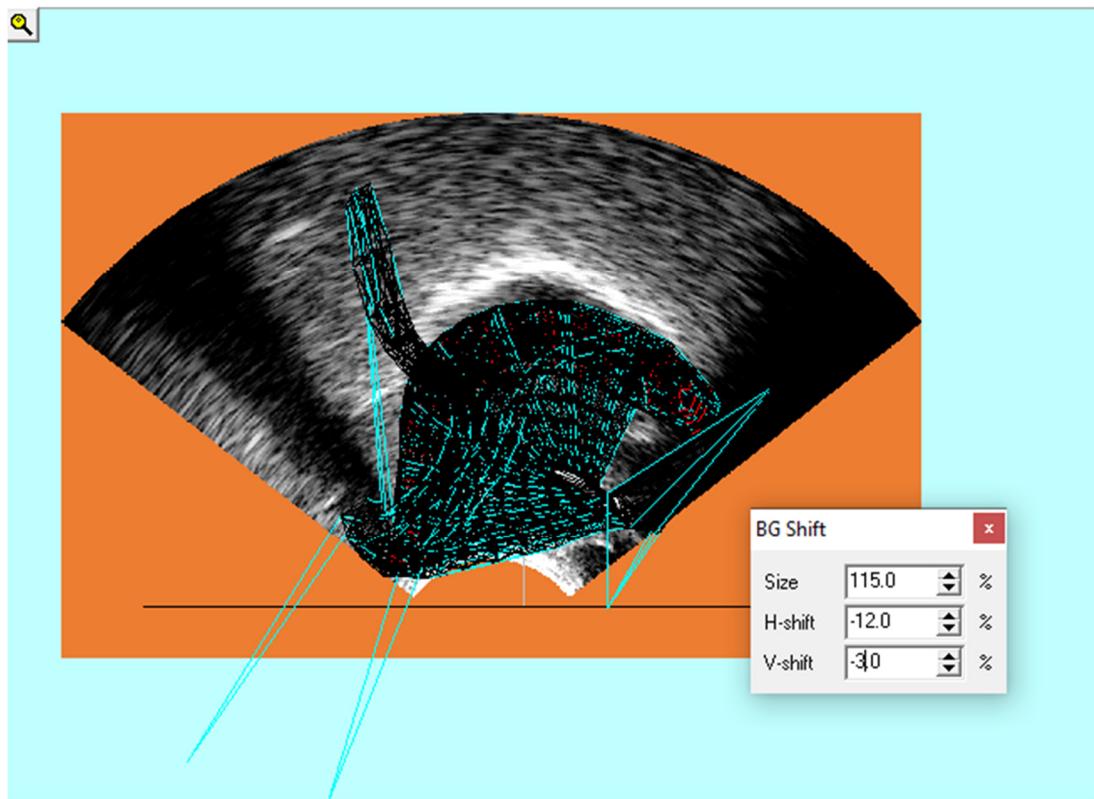
H-shift – the x position of the image relative to the model

V-shift – the y position of the image relative to the model

This scaling and translation applies to all the keyframe images.

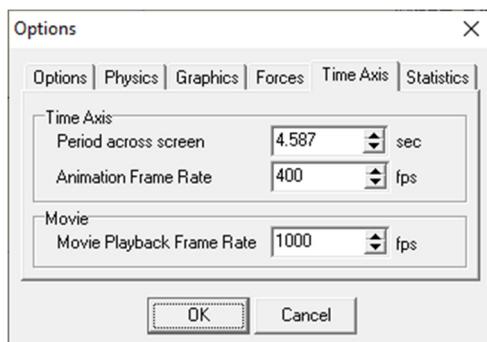
HINT: when fitting a tongue, first find a frame with a schwa, then move to fit the model in the rest position. Jaw and hyoid may need to be repositioned.

Rotation of the model relative to the image is carried out by selecting all the model points and rotating the model about its centre.



4.2 Keyframes

Each keyframe is associated with a time by its position along the timeline and is associated with muscle contraction values. In “Run” mode, when the button is clicked a timer starts to move a Red rectangle along the timeline. As it reaches each keyframe, the keyframe turns blue and the muscle length values associated with that keyframe are activated.



The time axis and rate of progress can be set by selecting Options|Options and choosing the “Time axis” tab.

Period across the screen – Sets max time in seconds.

Animation frame rate – Sets the amount of real world computation time. A value of 1000/fps * 200 is used as the real world interval in milliseconds. So for fps=400 there are 500ms of compute time per 1ms along the timeline.

Movie Playback frame rate – See the section on making movies.

4.2.1 Significance

Each frame has a significance which determines how it controls muscles.

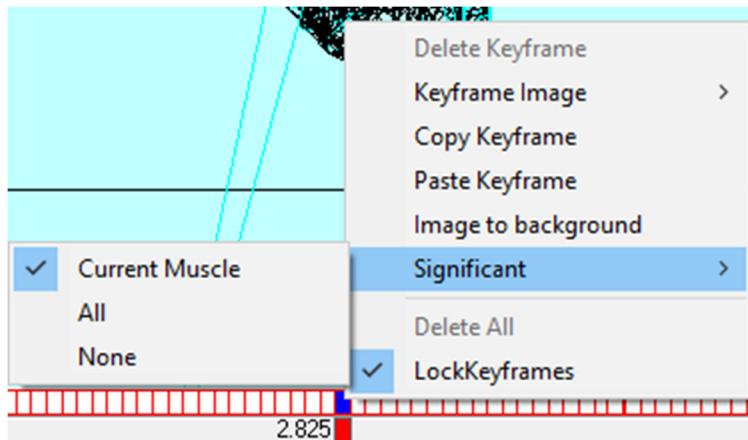
None – muscle slider settings are ignored for this keyframe. Ignored keyframes are shaded grey .

All – All muscle sliders are applied to the model for this keyframe

Current muscle – the keyframe applies the currently selected muscle slider.

Multiple individual muscles can be associated with the keyframe by selecting the muscle slider then setting the “Current muscle” menu option for each in turn.

If a muscle is selected and there is no tick next to any of the above then it means that one or more of the other muscles has been selected and you can choose to add this muscle or not, as required.



4.2.2 Copy and paste

The keyframe muscle slider and significance settings can be copied from one keyframe and pasted on to another. Right-click on the keyframe to be copied and select “Copy keyframe”. Then right-click on the keyframe that you wish to have the same properties and select “Paste keyframe”.

To create a new keyframe you must be in edit mode. It is disabled in run mode. Right-click at the timepoint where the new keyframe should appear and select “New keyframe”

4.2.3 Delete and add keyframes

To delete a keyframe you must be in Edit mode. Right-click on the keyframe to be deleted and click the “Delete keyframe” popup menu option. To delete all keyframes, right-click where there is no keyframe and a “Delete all” popup menu option appears.

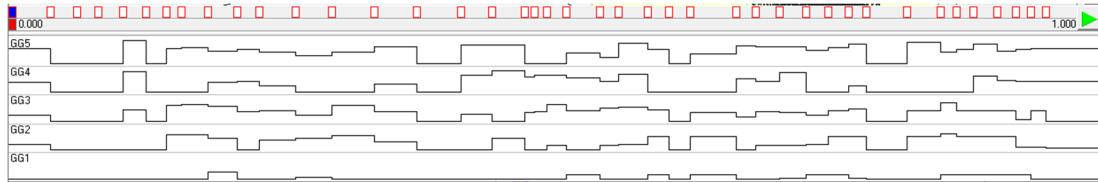
4.2.4 Adding images to keyframes

An image can be added to a keyframe to replace the existing one or to one of the other 2D planes. Right-click on the keyframe and select “Keyframe image” and either “XY...”, “XZ...” or “YZ...”. A browser dialog will then appear and a PNG or BMP can be selected to be shown in the associated 2D window.

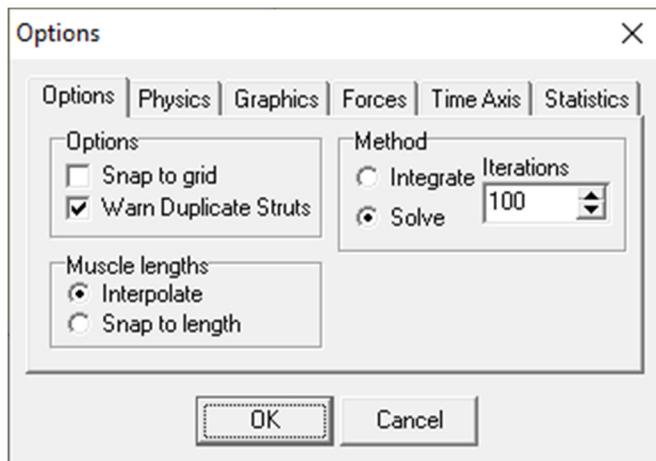
4.2.5 Muscle chart

Select **View|Muscle chart** to view a chart of muscle contraction levels. Muscles can be added to this chart by right-clicking on the muscle control at the righthand side of

the application and checking “Chart”. To remove a muscle from the chart uncheck “chart”.



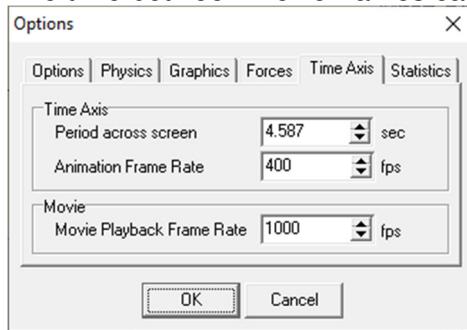
There is an option to linearly interpolate muscle length assignments across time between 2 keyframe settings. In this way, the muscle lengths change gradually over time between the keyframes rather than occurring suddenly as the keyframe is activated. To switch between these two modes select Options|Options and click the “Options” tab. Then select “interpolate” muscle lengths or “Snap to length”



5 Making a movie

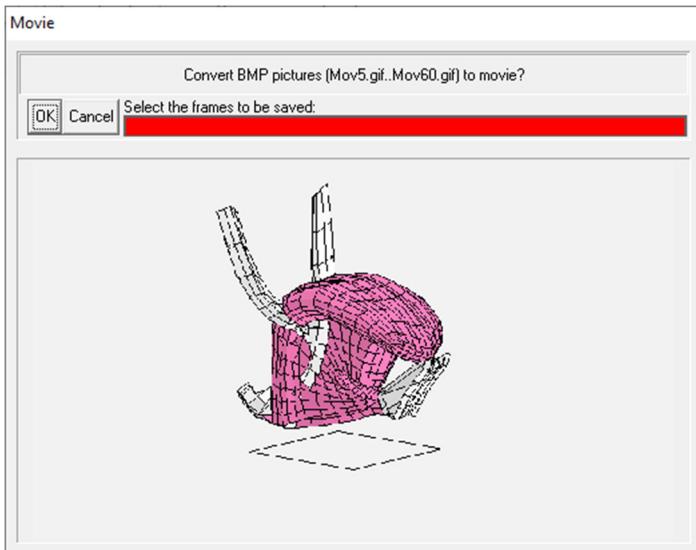
A movie of any of the 2D windows or the 3D window can be generated and stored as *.gif file.

The time between movie frames can be set independently of the fps for run mode.

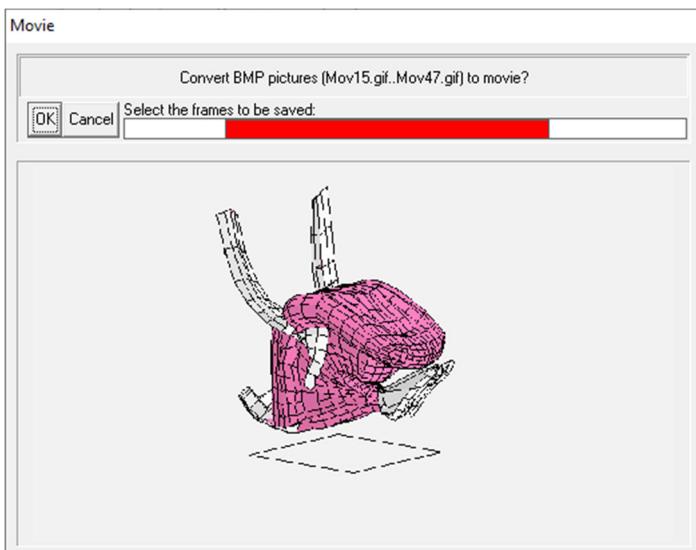


A higher **movie playback frame rate** will have the effect of speeding up the movie playback.

Select Options|Movie then click MovieXY or MovieXZ or MovieYZ or Movie3D. Images will start recording immediately. One image every time the image is redrawn, every N iterations as specified in section 2.2.2.



Click on the Red bar to see any of the images that have been recorded. Set the ends of the red section of the bar to define the first and last frames to be included in the exported GIF file. Then click “OK” to convert the selected range of images to one GIF file.



You can also manually rotate the 3D image while the movie is being recorded. Click and drag on the 3D Window.

6 Importing/exporting ANSYS meshes

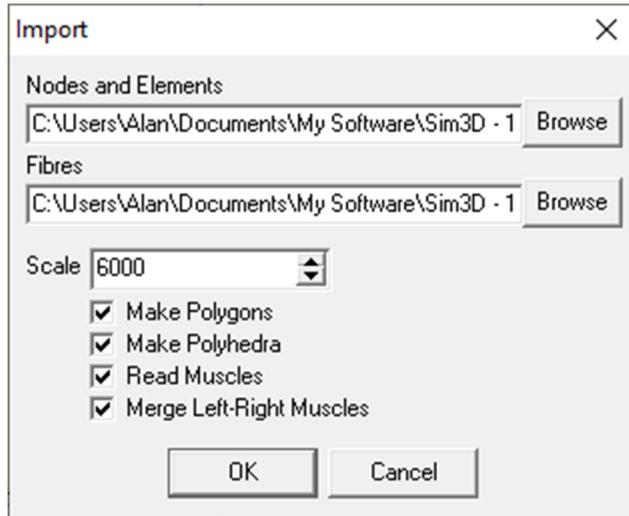
ANSYS is a company that provides commercial 3D model physics simulation software. They have a file formats for their model meshes. Myosim is able to import and export a 3D mesh in those formats. The information includes muscle fibre assignments so it may be possible to run MyoSim3D models in ANSYS.
Alternatively, MyoSim3D could be used to generate or edit a model for use in ANSYS.

They are:
<filestem>_fibers.mac

<filestem>.mac
<filestem>.elem
<filestem>.node

To export, select File|ANSYS and click “Export...”

To import, select File|ANSYS and click “Import...”
Then browse for the **node** file and browse for the **fibers** file



ANSYS files do not preserve polyhedron colours or the symmetry plane or (most importantly) whether the nodes are part of a rigid structure.

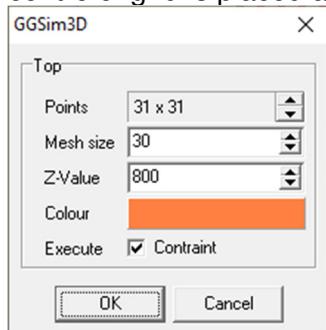
7 Constraints – graphing EPG type data

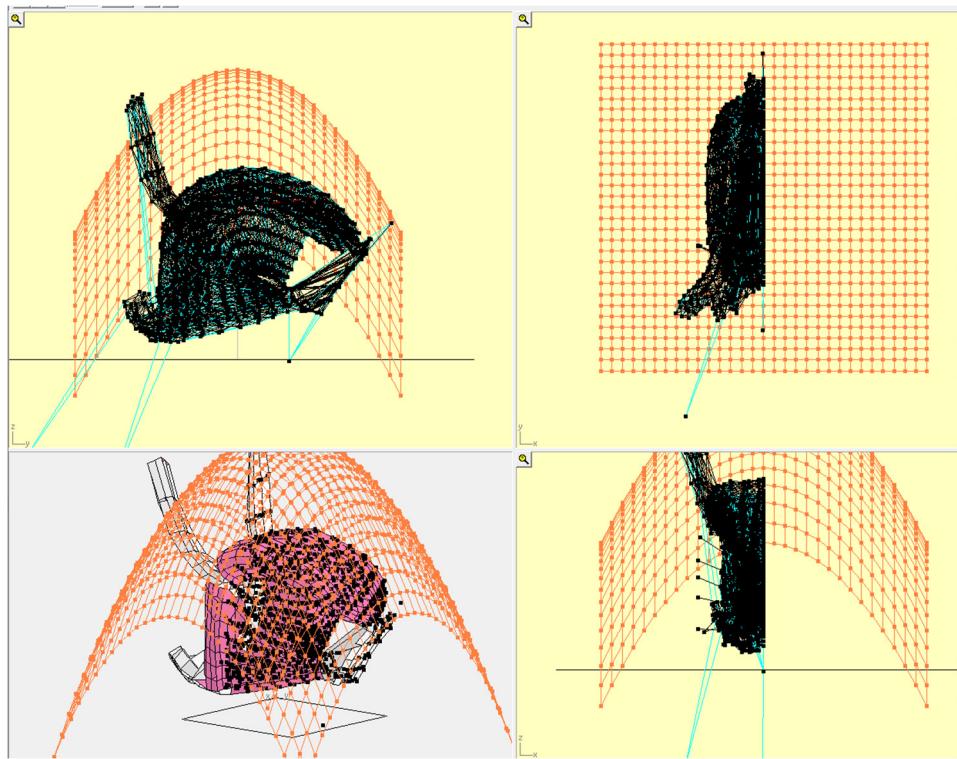
Constraints were conceived as a way of representing the hard palate in a tongue model. Their purpose is to measure the distance between the hard palate and the surface of the tongue model as it deforms. A constraint also acts as a boundary beyond which the model cannot move. However, the interaction between the constraint does not behave realistically. Contact between the constraint and the model should be avoided if possible.

This function is immature and may be rewritten in the future.

A constraint is an NxN x grid of nodes fixed in 2 dimensions. The grid nodes are spaced M units apart in those 2 dimensions. The ‘height’ of each node can be moved to any position in the 3rd dimension.

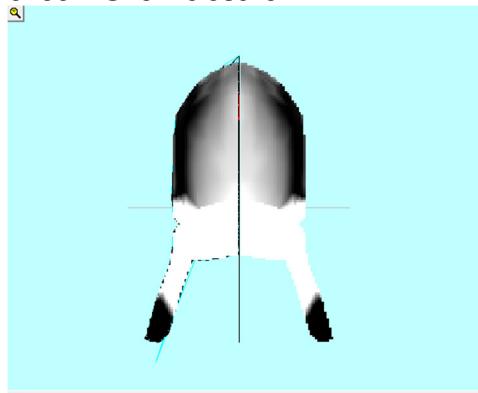
In the following example Xpos is selected N=31 (indexed -15 to +15) M=30 and centre of grid is placed at Z=800





Constraint grid nodes can be selected and moved in all the ways that model atoms can be selected except for extending x-lines, y-lines and z-lines, which are not parameterised for constraints. Grid nodes cannot be selected if model nodes are present in the same space. The software will default to selecting only model nodes if any are selected.

To display the distance between model and constraint grid , select `View|Run` and check “Show closure”



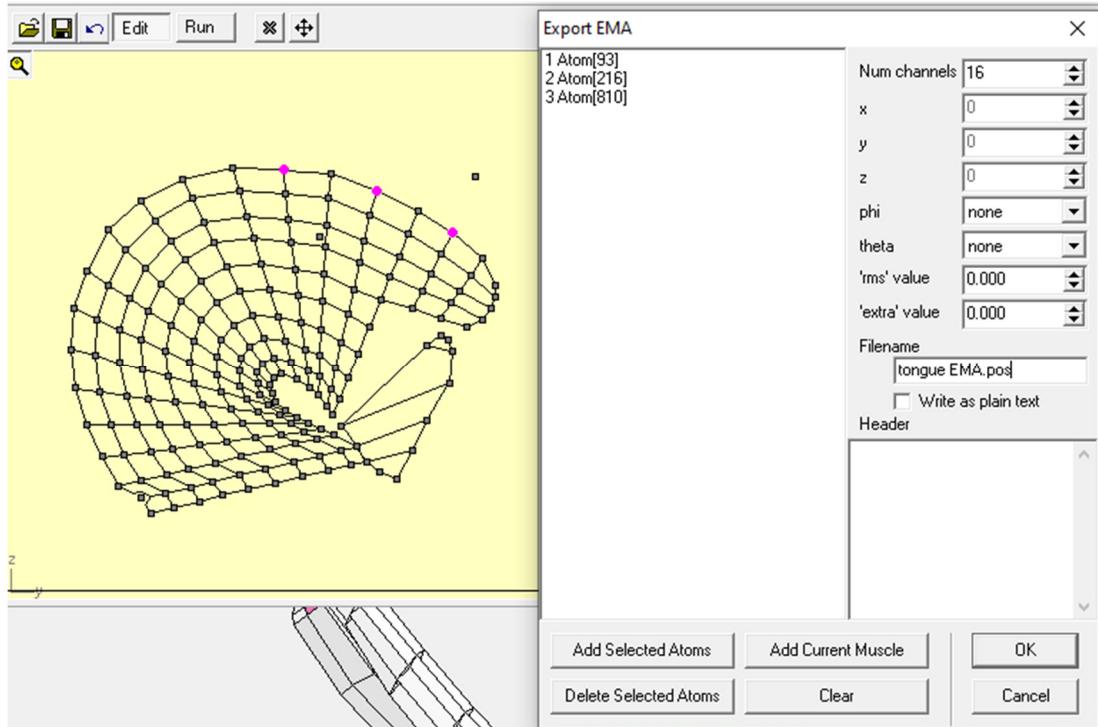
Constraint distance view.

8 Exporting atom kinematics (virtual EMA sensors)

This function allows the position of atoms to be recorded as the model deforms and exported in a *.pos file format compatible with the Carstens Electromagnetic Articulograph (EMA). In this way virtual EMA points can be recorded. MyoSim3D does not plot these data but the movements can be plotted in any other software that can read *.pos files (e.g. Articulate Assistant Advanced).

Note: Due to the slow propagation of pressure forces through the model and because mass is not modelled, kinematics of the hexahedral model in MyoSim3D are not realistic. However, the model can be run slowly so that the model reaches equilibrium when a snapshot is taken.

To enable the EMA, first select the atoms you wish to track. Then select **Atoms|EMA...** and click the “Add Selected Atoms” button. Then select a filename to store the recorded EMA values in



9 A tongue model

The provided tongue model “Tongue Model A – The price range.s3d” comprises of approximately 1400 hexahedrons with further hexahedrons modelling the hyoid, short tendon, and part of the mandible as rigid bodies. The tongue shape is controlled by the following muscle compartments:

5 genioglossus compartments

5 Transversus compartments

1 Verticalis

2 superior longitudinal compartments (lateral incorporating ceratoglossus and middle incorporating chondroglossus)

2 inferior longitudinal compartments (oblique and longitudinal)

1 styloglossus control (6 extrinsic compartments combined, lateral compartments along the tongue body are not yet specified.)

1 hyoglossus compartment (basioglossus)

Jaw rigid body (index 176) It includes two angled struts to simulate the mandible pivoting at the temporomandibular joint.

Short tendon rigid body (index 241)

Jaw and short tendon share atom 775 to form a hinge

Hyoid rigid body (index 122)

The model is far from perfect. Slight alterations to shape and muscle fibre assignments can make a significant difference to how it behaves. However, it does

show that by contracting one of the transversus compartments the tongue domes and by contracting the genioglossus compartment, it grooves. Five such compartmental sectors are modelled, controlling constrictions along the vocal tract.

10 Bugs

Cannot view keyframes beyond the optional max time or zoom in to the time axis.

Revision	Date	Notes
1.00	15/01/24	Initial manual

