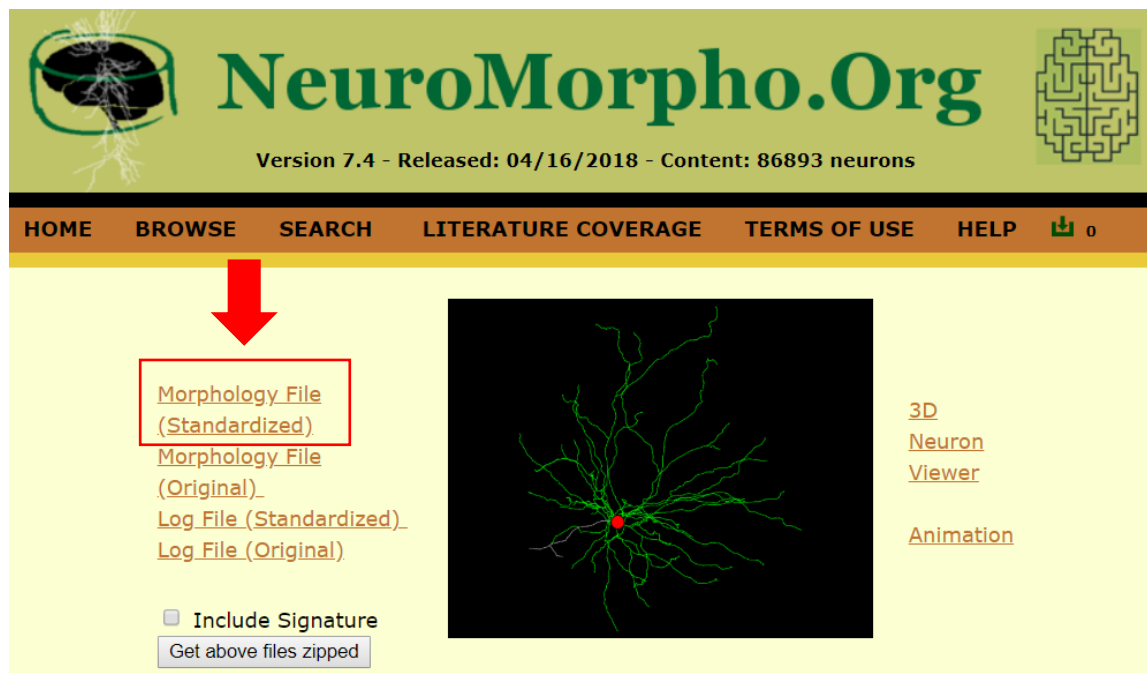


How to create a morphologically realistic neuron model using Cell Builder

Ben Latimer – based on the tutorial at
<https://www.neuron.yale.edu/neuron/static/docs/cbtut/pt3d/outline.html>

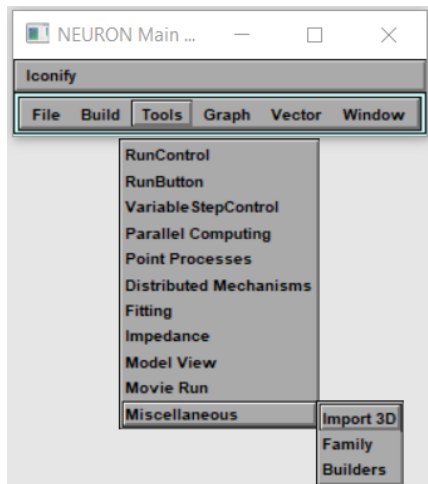
Step 1 – Download your cell from NeuroMorpho.org

Go to neuromorpho.org and browse the many available cells that have been reconstructed. They are arranged by species, brain region, etc. Once you find one you like, right click on the link as shown below and click “save link as”. This will save an “.swc” file to your computer.

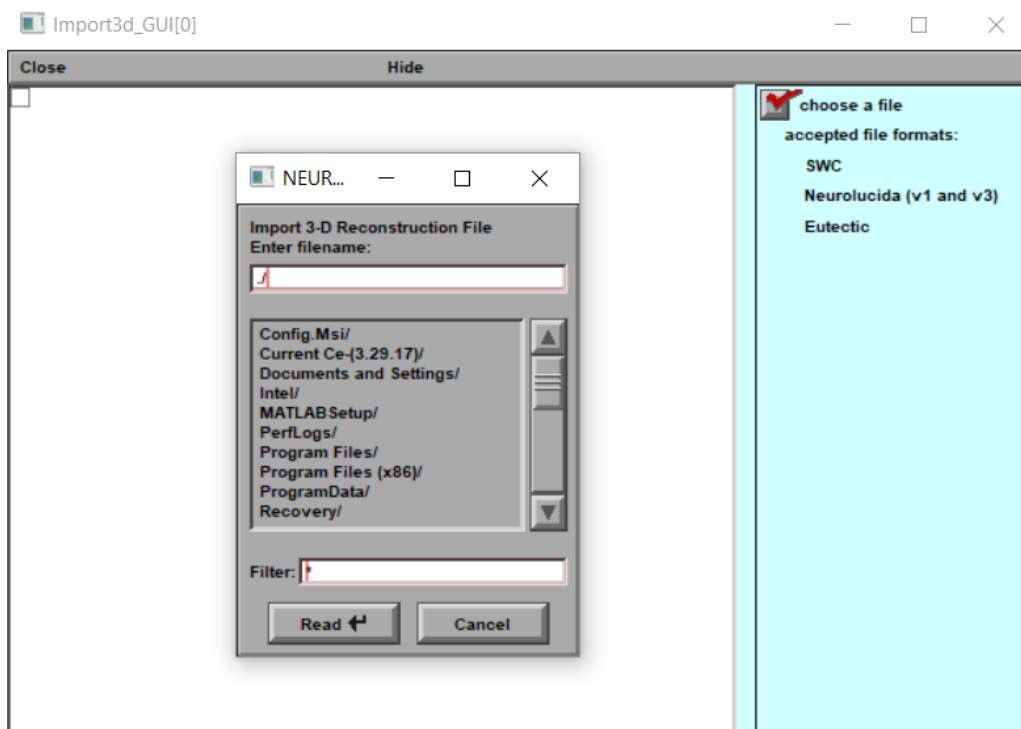


Step 2 – Import the cell geometry into NEURON

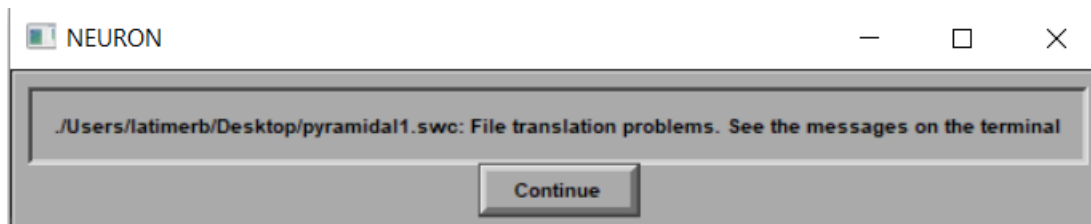
Open NEURON (note these instructions are for NEURON 7.5) by typing *nrngui* at the command prompt (Mac OS/Linux) or bash shell (Windows). You'll see the familiar NEURON GUI. Click Tools > Miscellaneous > Import 3D.



Click the box that says “choose a file” and navigate to where you stored the .swc file.

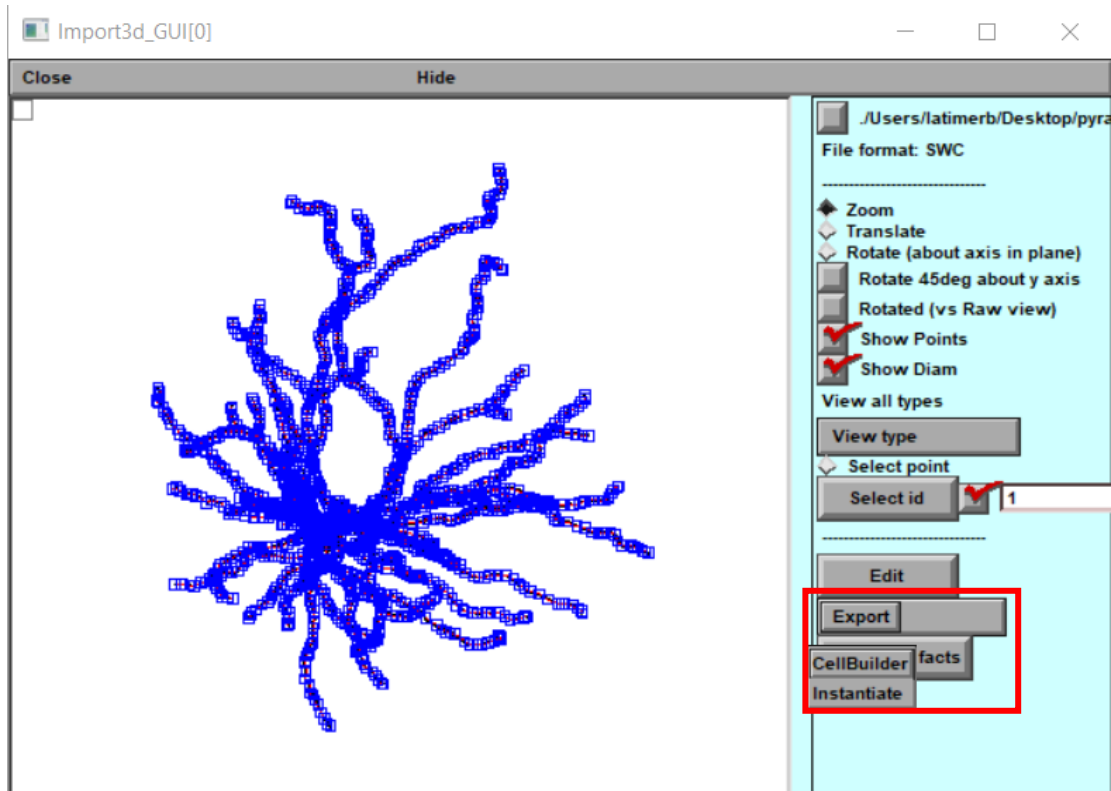


You may see this message:



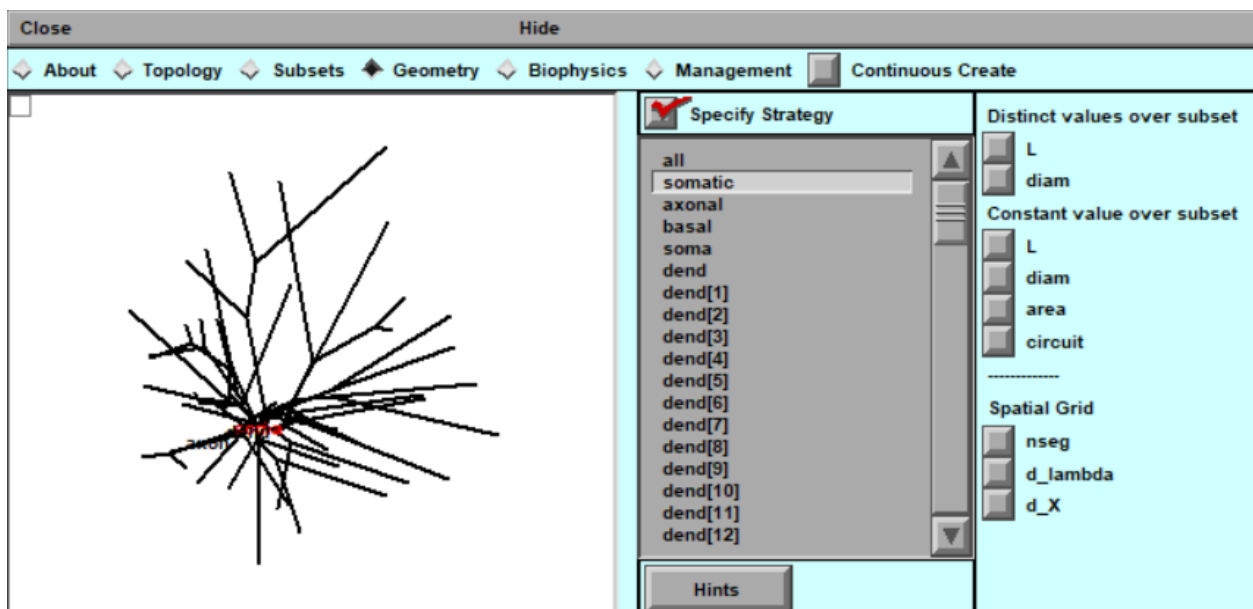
Typically, this is just because there are some comments in the .swc file that couldn't be interpreted. No need to worry but check out the messages in the terminal anyway.

Now you've got a cell! Click Export > CellBuilder

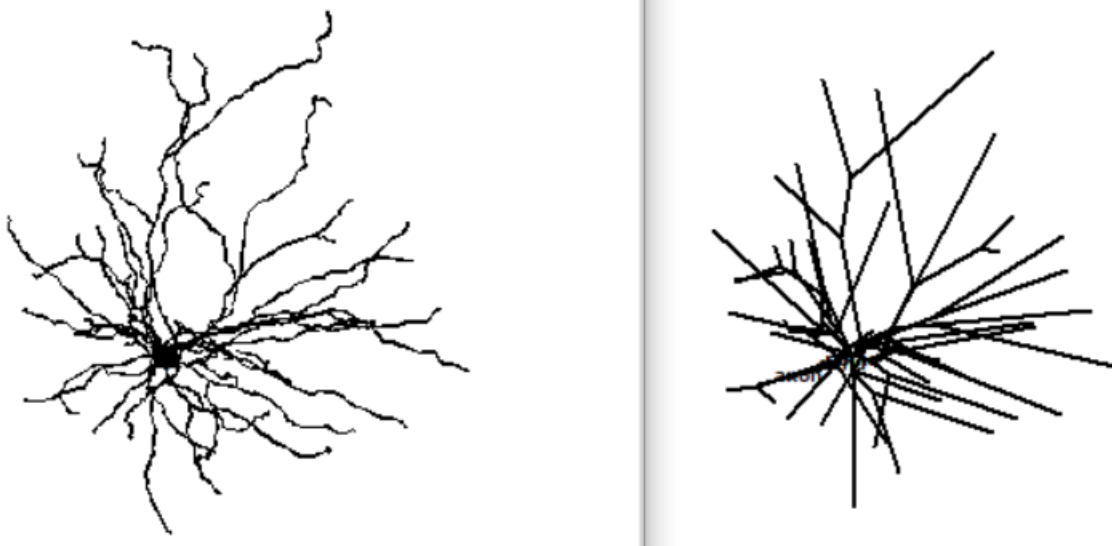


Step 3 – Make a model of the cell

Now that we've imported our cell from the reconstruction, we're ready to make a model. Luckily, CellBuilder makes the geometry part easy:



What happened to our beautiful geometry?! It's still there. Just click "Continuous Create" and go to Graph > Shape Plot.



The CellBuilder takes the shortest route between the endpoints of each section when it shows it on the screen but all of the complex geometry is still available.

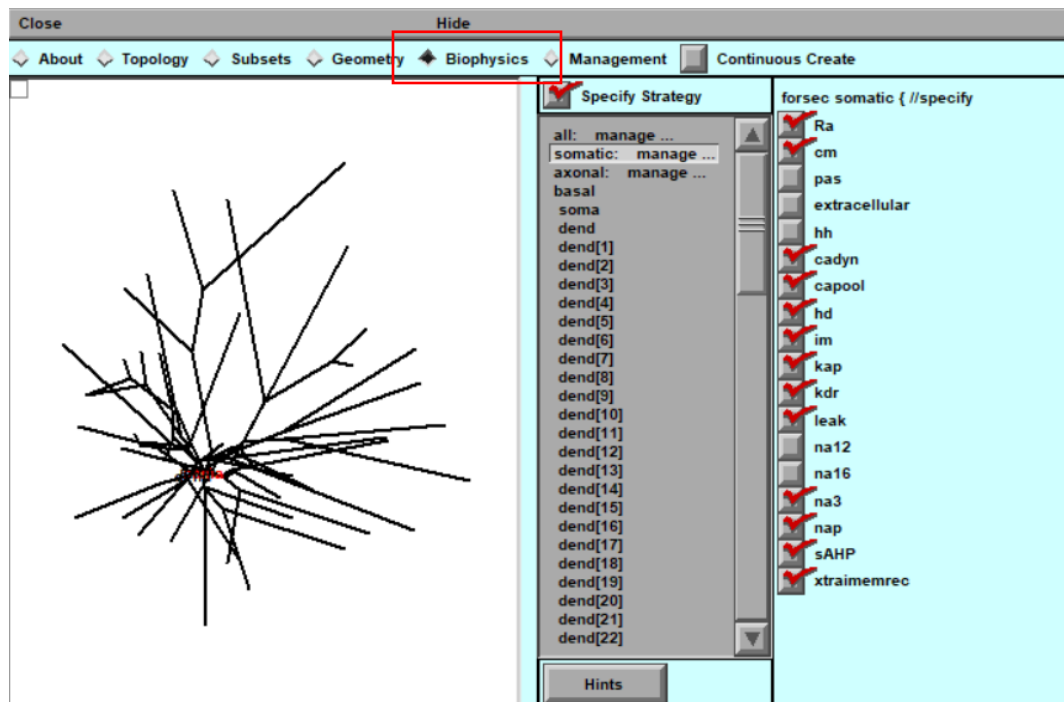
It'll be up to us to put in the channels. This is a good time to mention that at any time if you want to save your "session" so you can come back to it later, you have that option. Just click File > Save Session. It's a best practice to go ahead and save the "bare bones" session (before you embark on the biophysics) so that if you mess up later, you can come back to it.

Step 4 – Add some biophysics

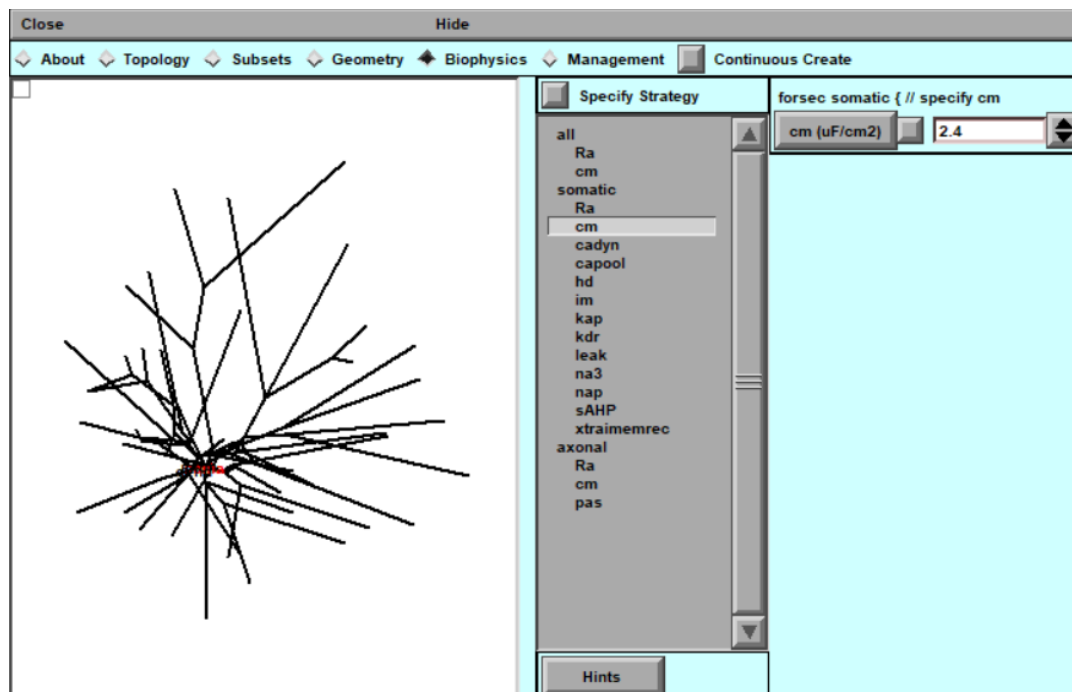
At this point, all we have is the skeleton of a cell. We need to specify what channels are involved and the size of the sections. If you have custom channels, you'll need to place those in the same directory where you opened NEURON. If you're just using the regular Hodgkin-Huxley sodium and potassium channels, they'll already be loaded.

Throughout the process, you'll use the "Specify Strategy" button to toggle between the list of sections and the values for those sections.

We're finally ready to add some channels. My example below has a lot of custom channels but if you are just going through this for the first time, feel free to just select "hh" which will give you access to an Na⁺ and K⁺ channel.

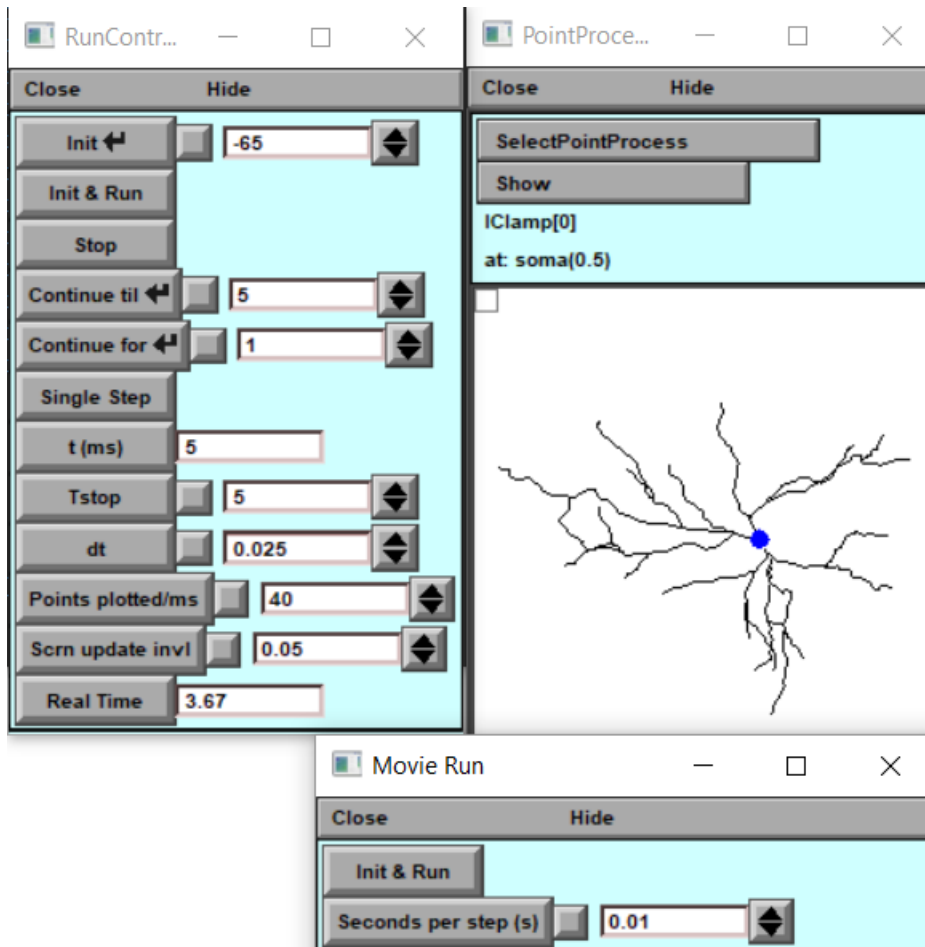


Now you can go through and specify the various conductances, capacitances, resistances, etc.



Step 5 – Put your new cell in a current clamp

You've added all the biophysics you think will be necessary to make your cell behave like you want. Now it's time to see if it really does. Toggle the "continuous create" button so that your neuron is the current accessed cell. Then go to File > Load session and find IClamprig.ses. You'll see some boxes like this:



To visualize what's going on, click Graph > Voltage axis. Then "Init & Run". You should see some baseline activity. You will want to change the parameters of the current clamp by clicking SelectPointProcess > IClamp. To make this more like an actual current clamp experiment, change the duration to 100 ms and the delay to 100 ms. Then change tstop (the length of the simulation) to 300 ms. Click "Init & Run" again.

At this point, you will need to "tune" the cell to match experimental data. Many of the parameters are unknown or may be in a range so they can be changed within reason to match the behavior seen in vitro.

To export the cell for use in a template, in CellBuilder click Management > Cell Type. Click Classname and give your cell type a name (i.e. PyramidaltypeA, axoaxoniccell, etc.). Then click "Save hoc code in file".