

# Where to learn more

## **The NEURON Book**

### **NEURON's web site**

[neuron.yale.edu](http://neuron.yale.edu)

Documentation

hints and tutorials

FAQ list

key papers about NEURON

Programmer's Reference

## **The NEURON Forum**

[neuron.yale.edu/phpBB](http://neuron.yale.edu/phpBB)

Getting started

Hot tips

Announcements (new releases, courses)

# Construction and Use of Models

## Cell models

Specify topology: create and connect sections

Specify geometry: stylized (L & diam)  
or 3D (x,y,z,diam)

Specify biophysics: insert density mechanisms,  
attach "biological" point processes (synapses)

## Network models

Define cell classes

Create cells (instances of cell classes)

Connect cells

# Step 0: Conceptualize the task

Shape

stick figure / anatomically detailed

Channel distribution

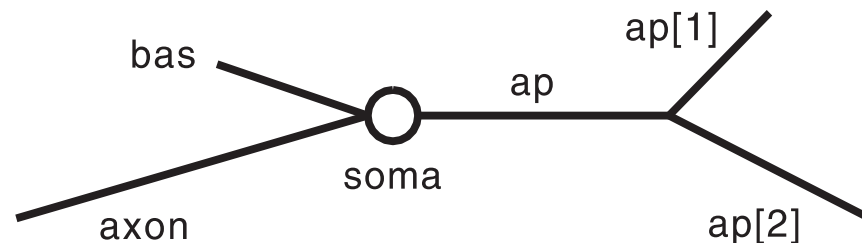
uniform / nonuniform

whole cell / region / individual  
neurite

Creation

single cell / use in a network

# Step 1: using the CellBuilder to make a stylized model



Section	L	diam	Biophysics
soma	20 $\mu\text{m}$	20 $\mu\text{m}$	hh
ap[0]	400	2	reduced hh *
ap[1]	300	1	reduced hh *
ap[2]	500	1	reduced hh *
bas	200	3	pas §
axon	800	1	hh

\*  $g_{\text{nabar\_hh}}$  and  $g_{\text{kbar\_hh}}$  reduced to 10%,  $e_{\text{hh}} = -64 \text{ mV}$

§  $e_{\text{pas}} = -65 \text{ mV}$

Throughout the cell  $R_{\text{a}} = 160 \text{ W cm}$ ,  $cm = 1 \mu\text{f} / \text{cm}^2$

# Launch NEURON with its GUI library

`nrngui`

*or*

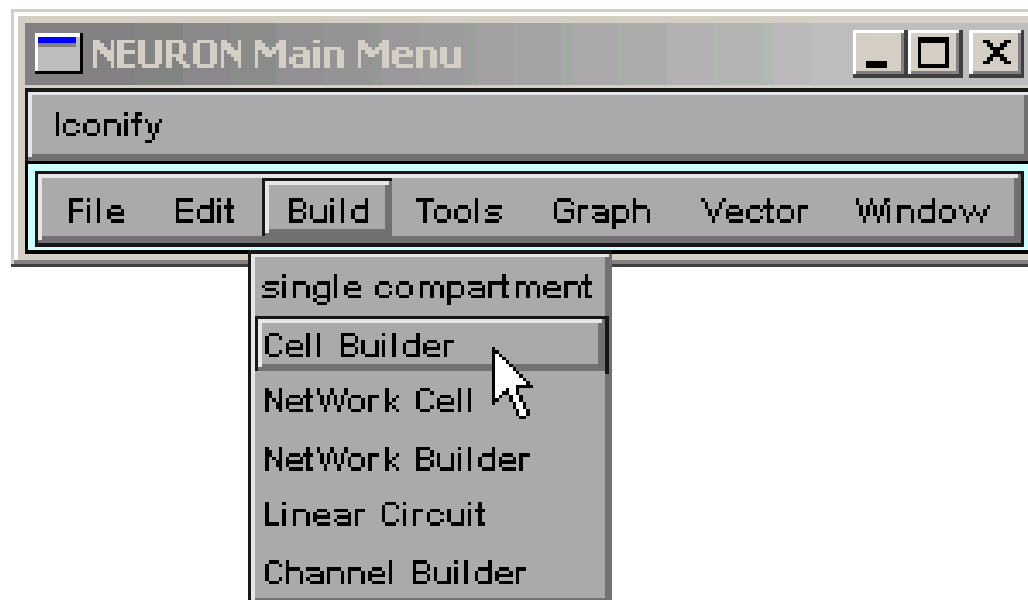
`python`

`from neuron import h, gui`

*or*

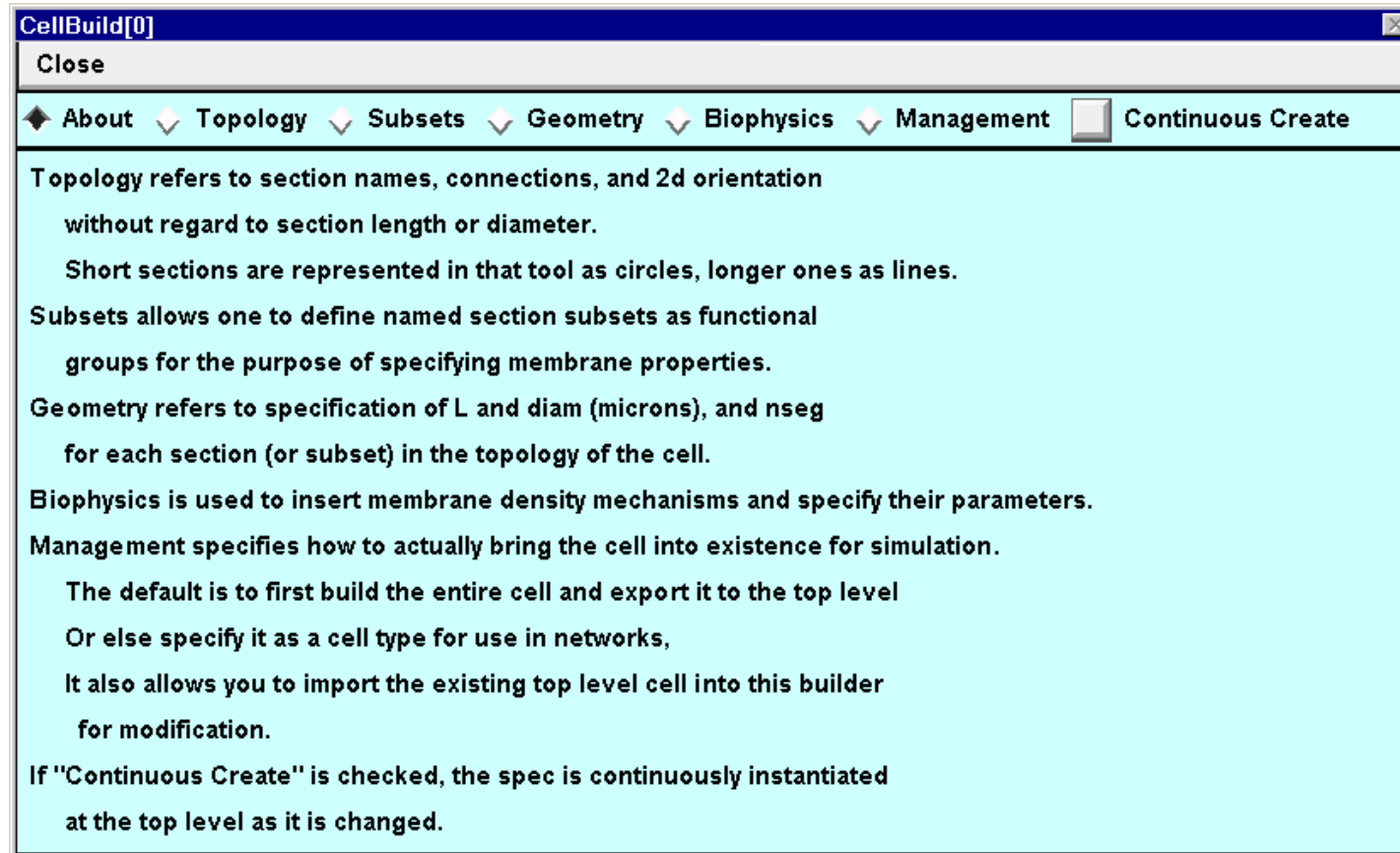
click on `nrngui` icon (MSWin, MacOS)

# Bring up a CellBuilder



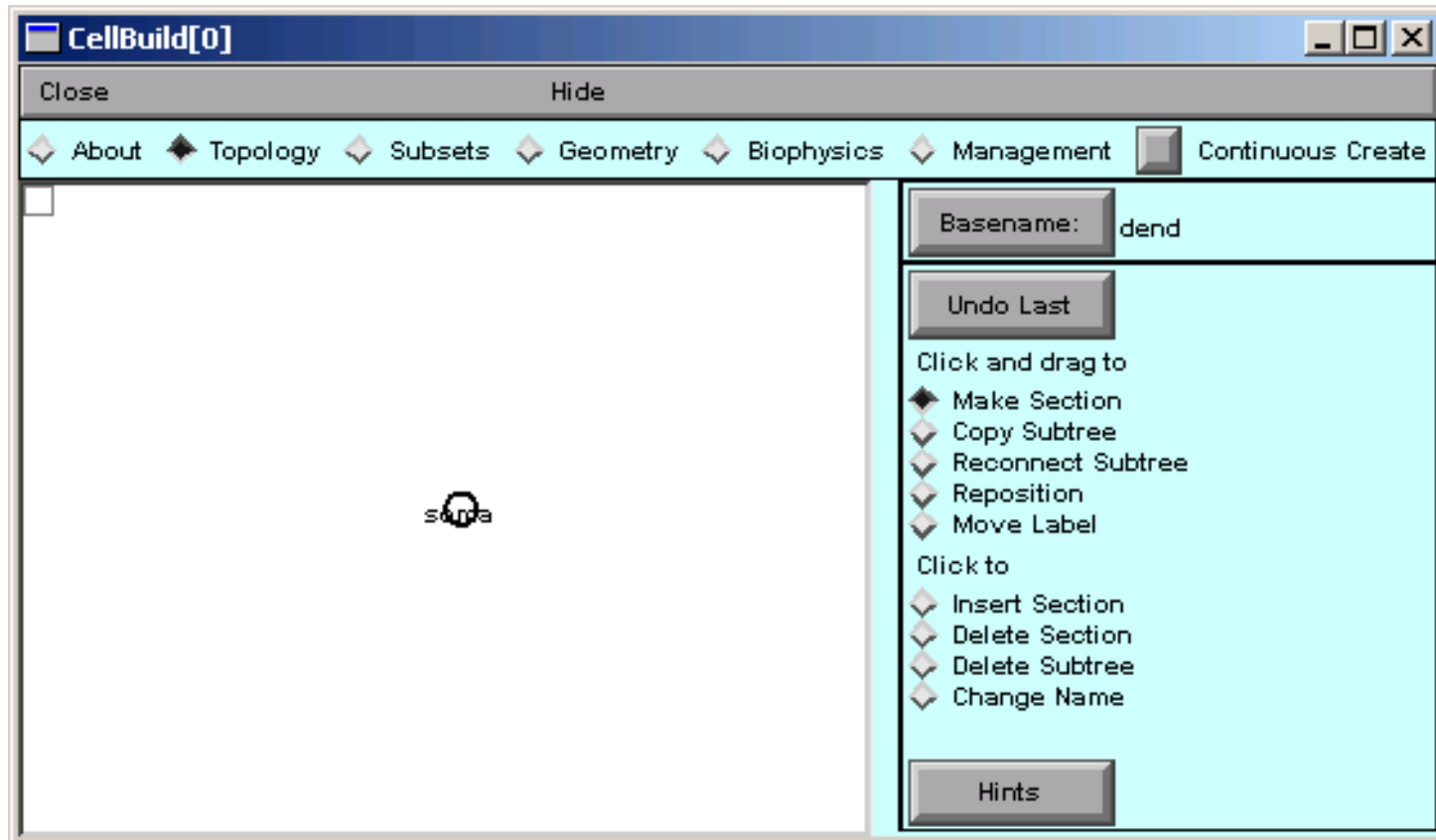
NEURON Main Menu / Build / Cell Builder

# The CellBuilder



Use buttons from left to right.

# Topology



CB starts with a "soma" section.  
We want to create new sections.



# Specifying the "Basename"

Basename: dend



# Making a new section

Place cursor near end  
of existing section



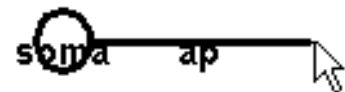
Click to start new section



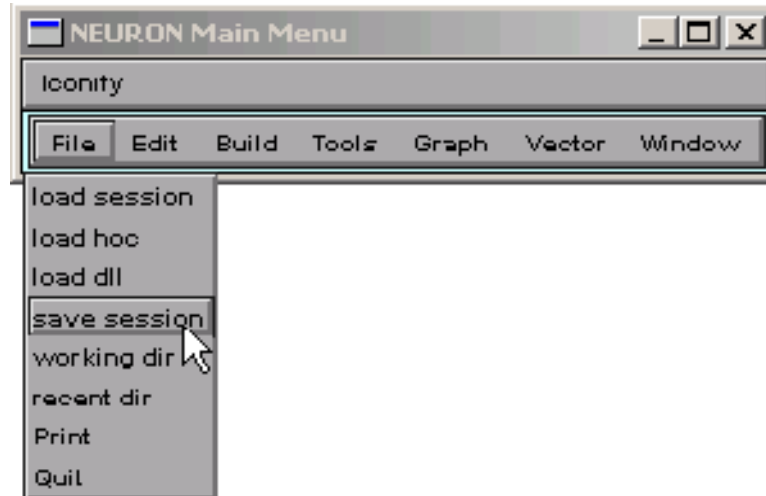
Drag to desired length



Release mouse button

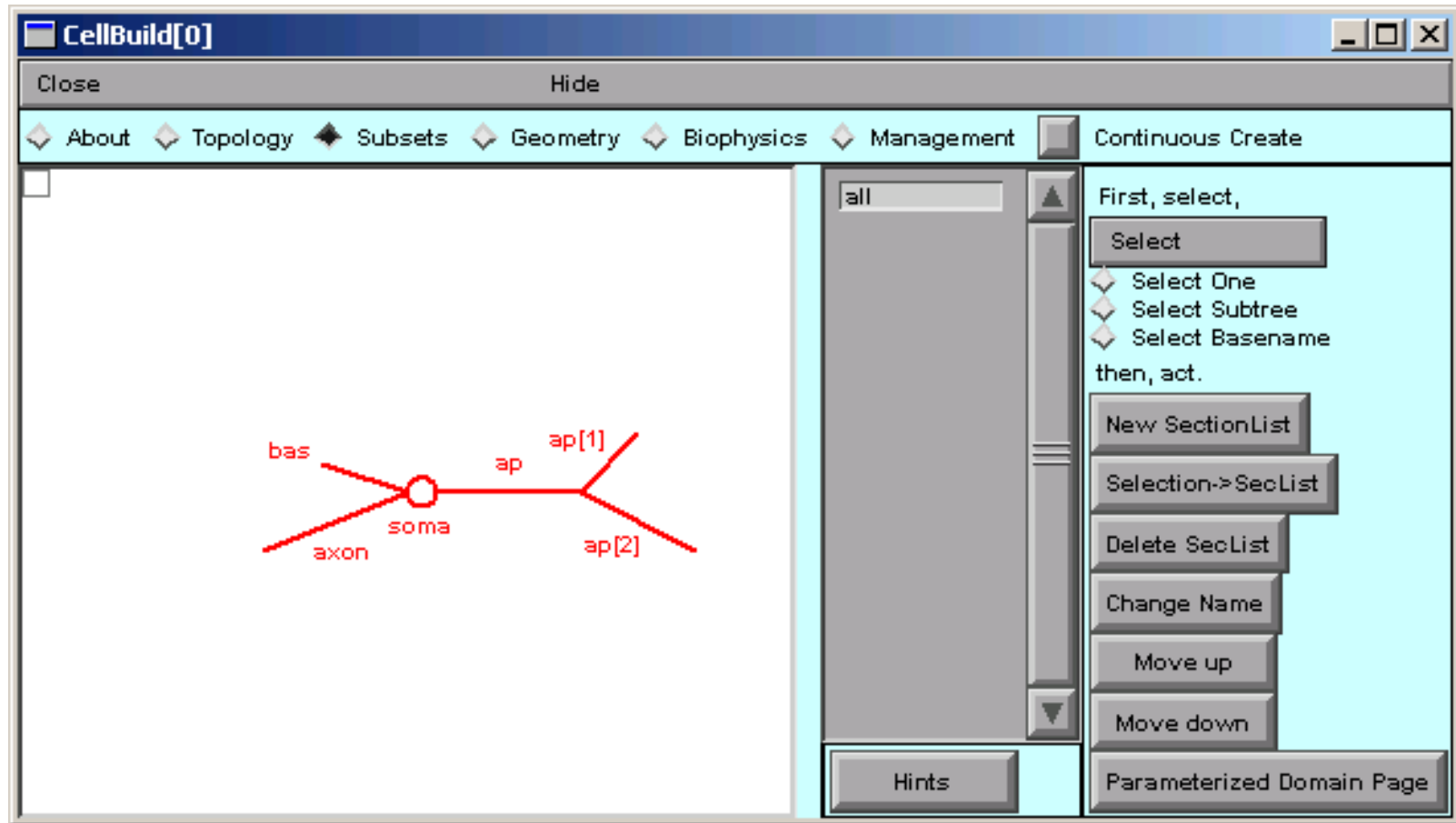


# Save your work as you make progress!



NEURON Main Menu / File / save session

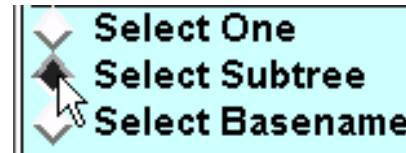
# Subsets



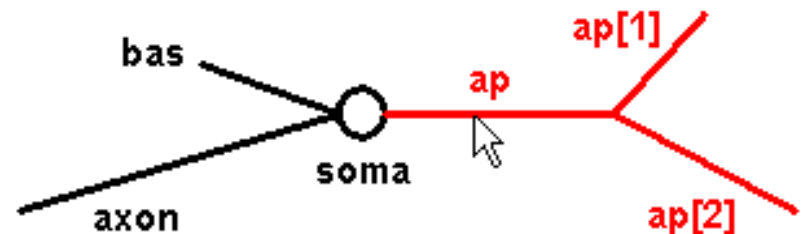
Group sections that have shared properties.  
We want to make an "apicals" subset.

# Making a new subset

Click "Select Subtree"



Click root of apical tree . . .



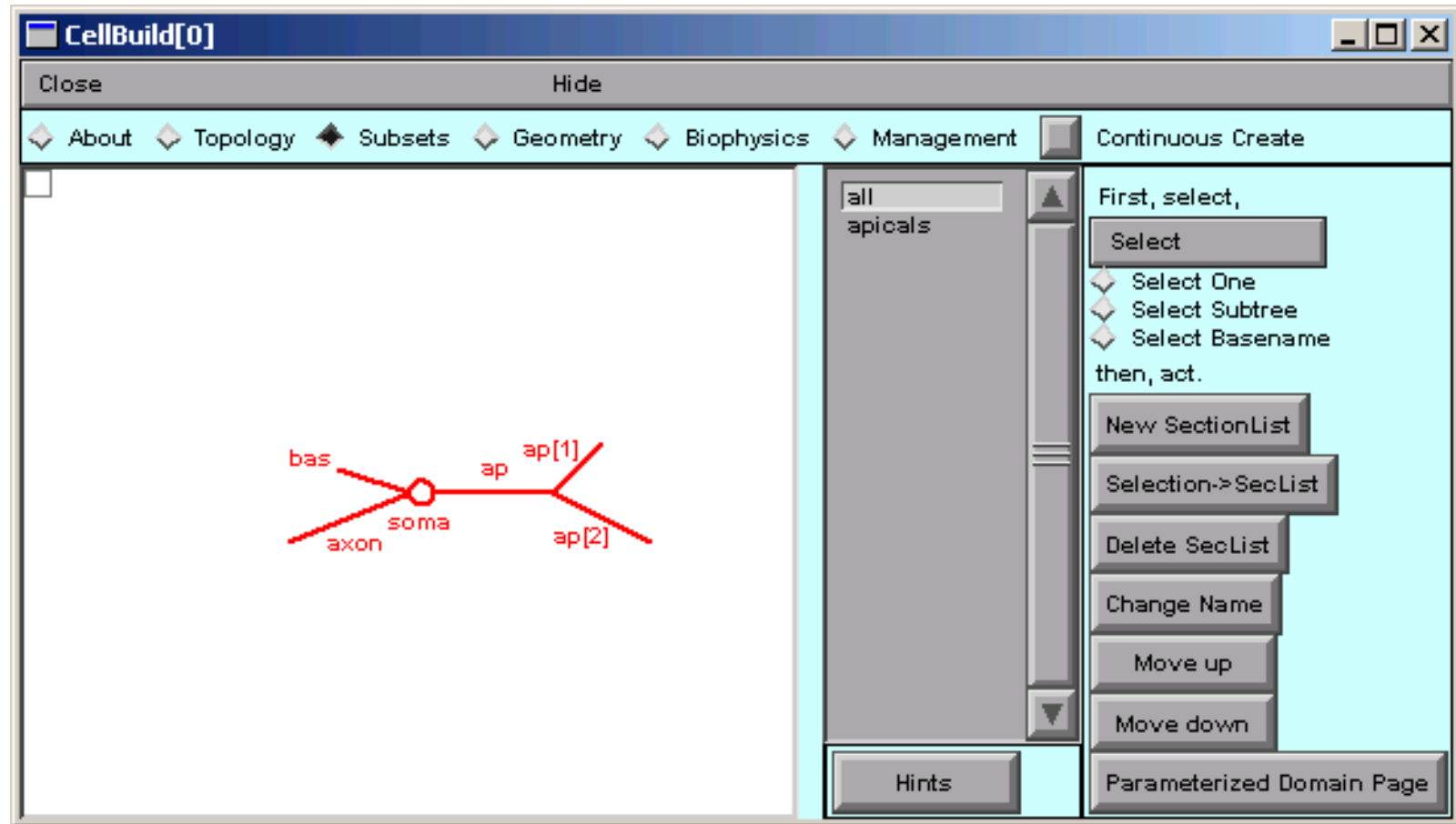
. . . then "New SectionList"



# Making a new subset *continued*



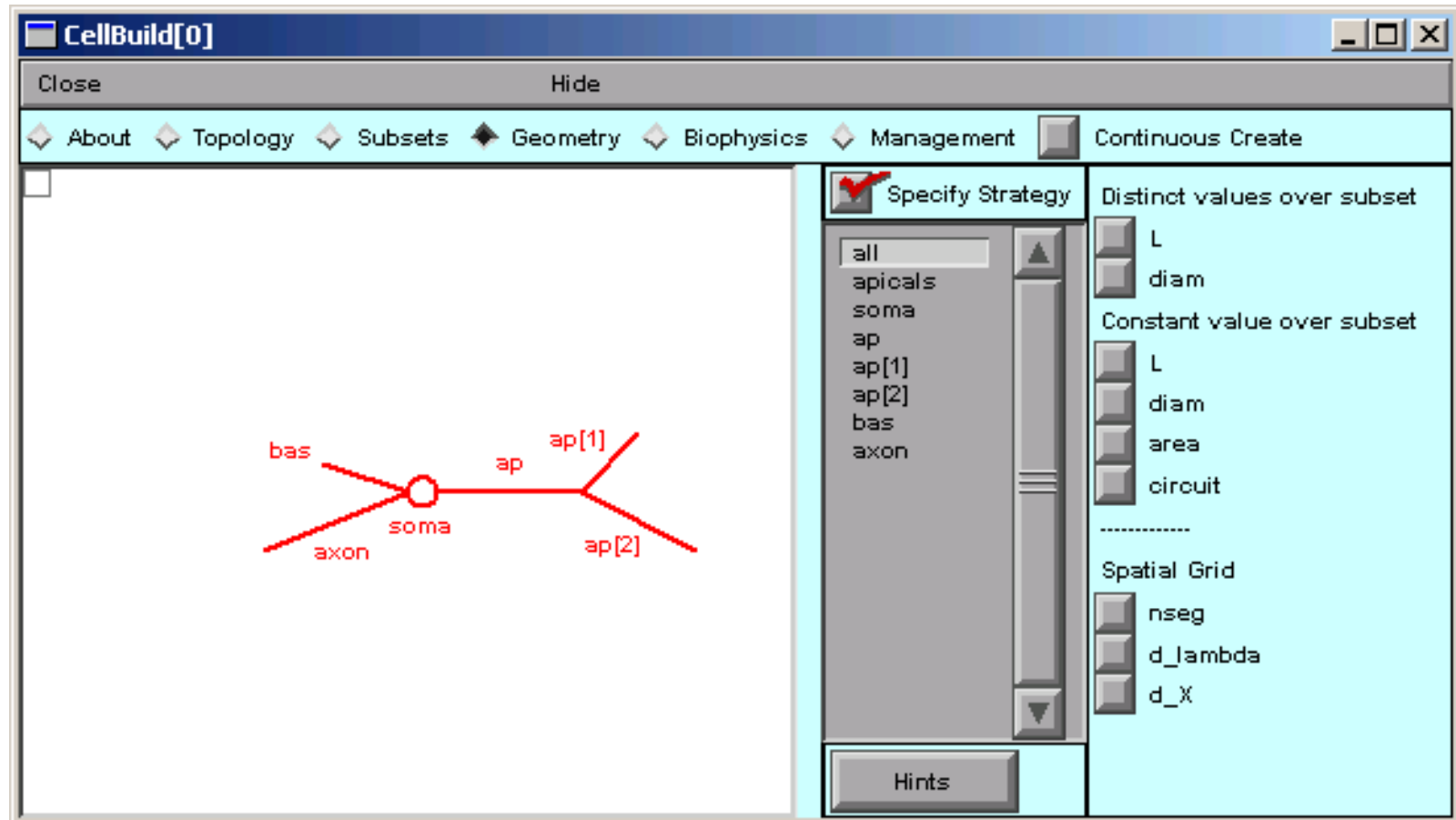
# Subsets finished



Note "apicals".

*Time to save a new session file.*

# Geometry

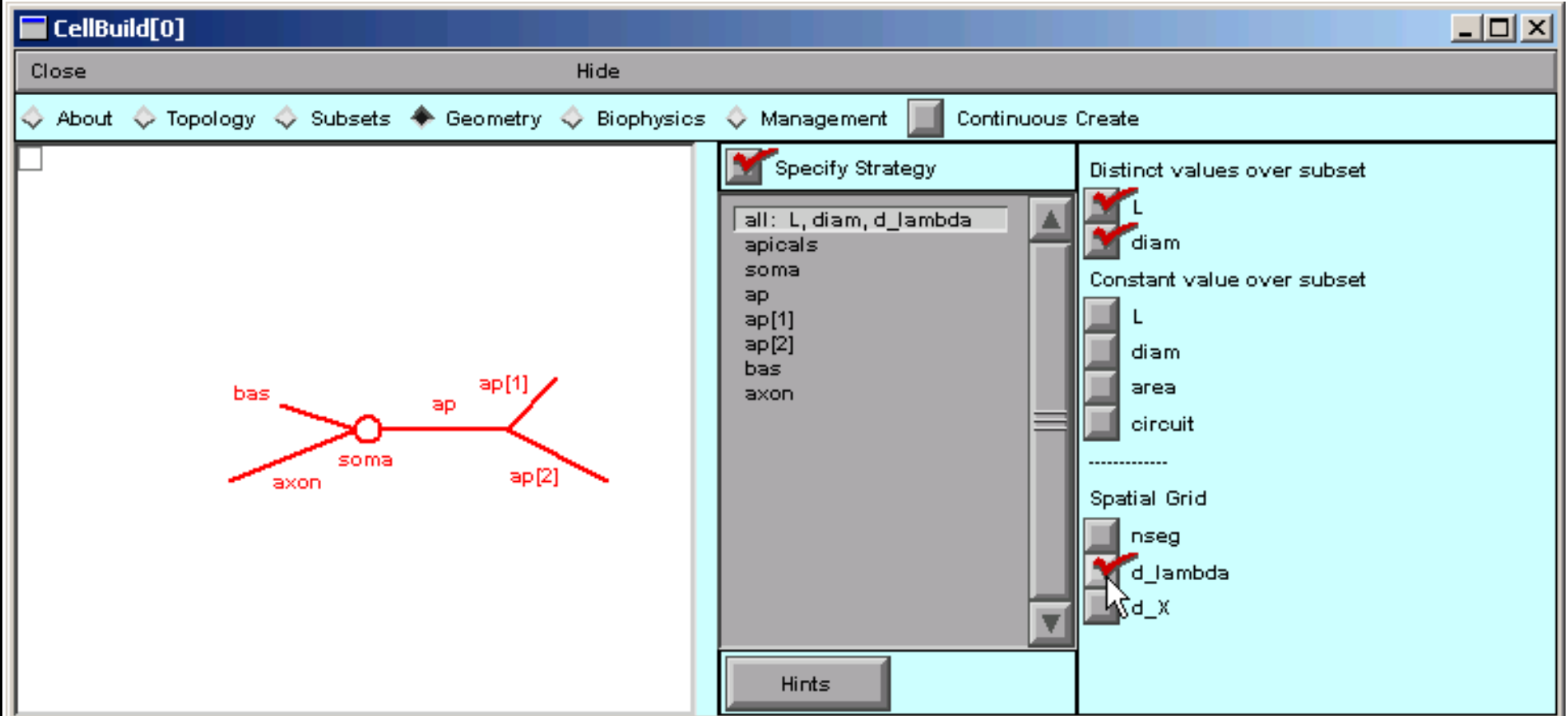


"Specify Strategy" is ON.

A good strategy is a concise strategy.



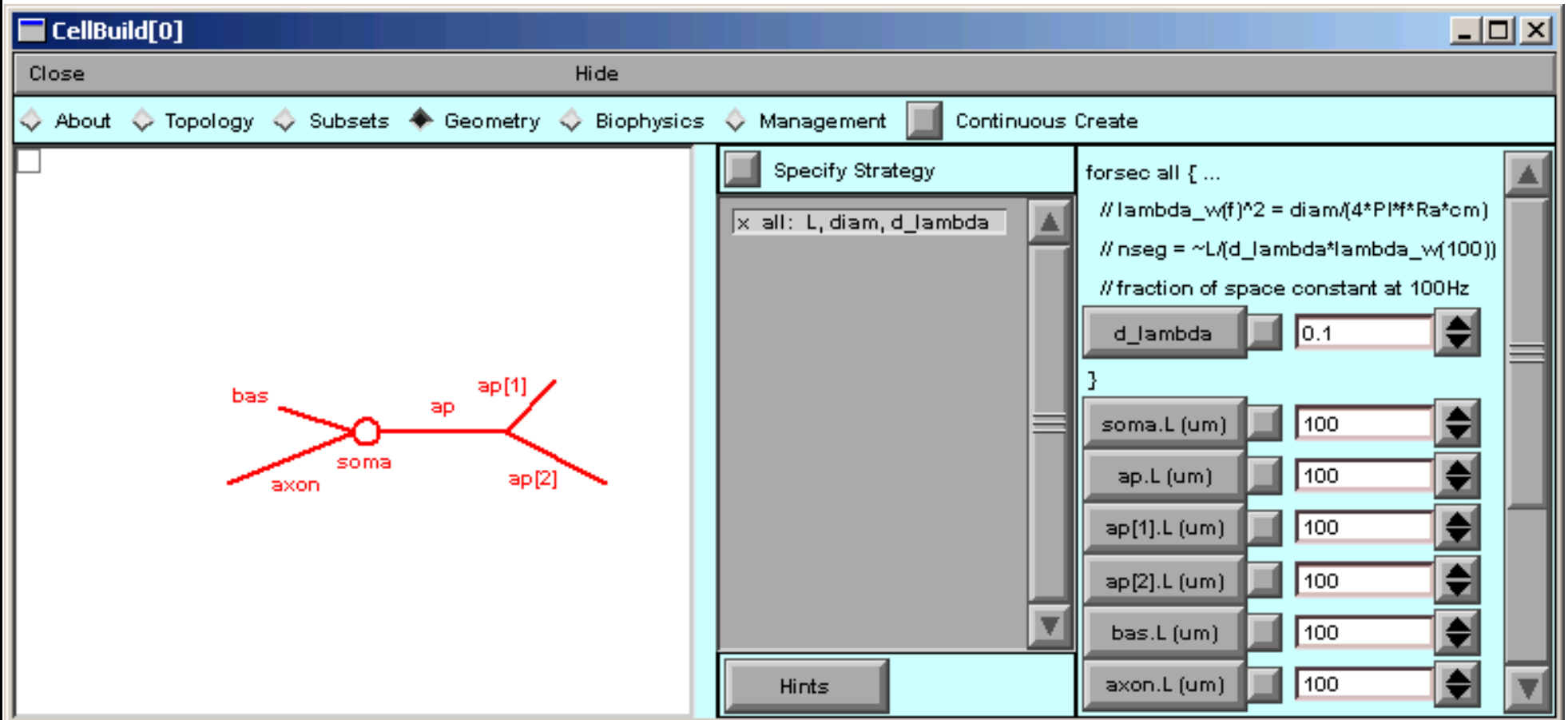
# Geometry strategy



Each section has a different L and diam.

Compartmentalize according to  $\lambda_{100 \text{ Hz}}$  (d\_lambda rule).

# Implementing geometry strategy



The screenshot shows the CellBuild software interface. On the left, a diagram of a neuron model is displayed with red lines and labels: 'bas' (basal dendrite), 'axon', 'soma', 'ap' (axon hillock), 'ap[1]', and 'ap[2]' (axon branches). The 'Specify Strategy' panel is active, showing a list of parameters to be defined: 'x all: L, diam, d\_lambda'. The 'd\_lambda' parameter is set to 0.1. Below the list, a code block shows the strategy definition:

```
forsec all { ...  
  // lambda_w(f)^2 = diam/(4*PI*f*Ra*cm)  
  // nseg = ~L/(d_lambda*lambda_w(100))  
  // fraction of space constant at 100Hz  
  d_lambda 0.1  
}
```

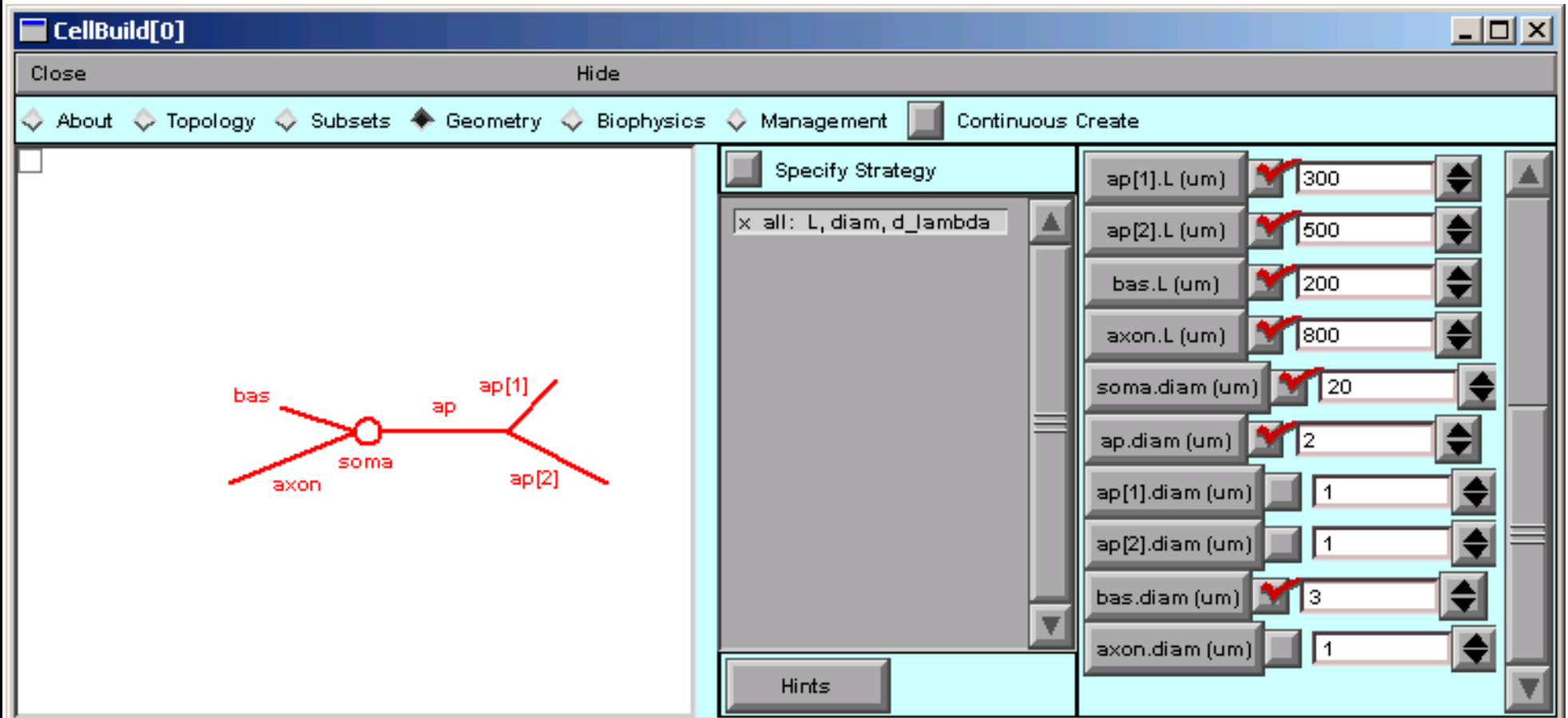
The 'Specify Strategy' panel also includes a 'Hints' button and a list of parameters with their values:

Parameter	Value
soma.L (um)	100
ap.L (um)	100
ap[1].L (um)	100
ap[2].L (um)	100
bas.L (um)	100
axon.L (um)	100

When strategy is complete, turn "Specify Strategy" OFF and start assigning values to parameters.

$d\_lambda = 0.1$  at 100 Hz usually gives good spatial accuracy.

# Implementing geometry *continued*

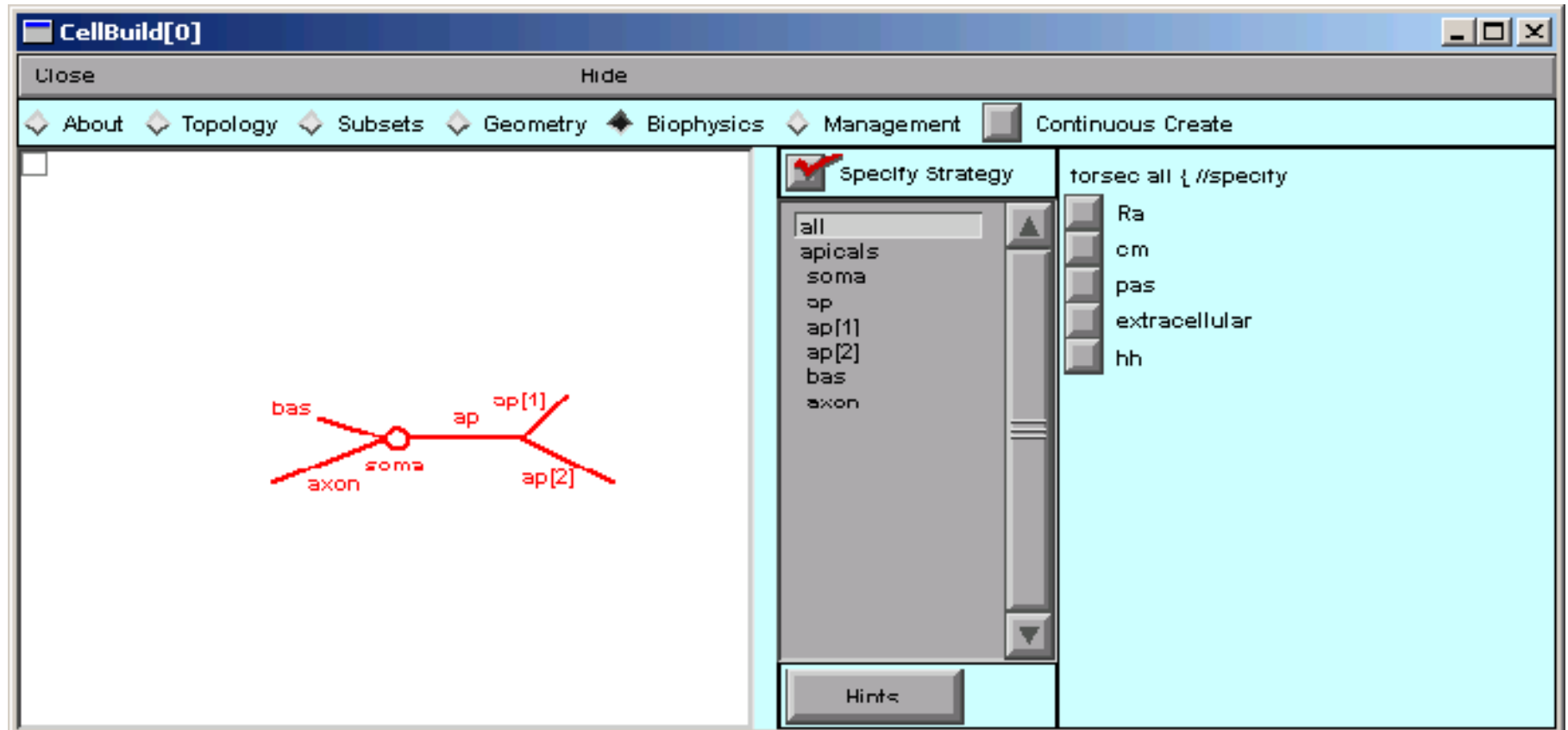


The screenshot shows the CellBuild software interface. On the left, a diagram of a neuron is displayed with red lines and labels: 'bas' (basal dendrite), 'axon', 'soma' (cell body), 'ap' (axon hillock), 'ap[1]' (axon branch 1), and 'ap[2]' (axon branch 2). The 'Geometry' menu is selected in the top navigation bar. The 'Specify Strategy' panel is open, showing a list of parameters: 'x all: L, diam, d\_lambda'. Below this, a 'Hints' button is visible. On the right, a list of parameters is shown with their values and status (checked or unchecked):

Parameter	Status	Value
ap[1].L (um)	Checked	300
ap[2].L (um)	Checked	500
bas.L (um)	Checked	200
axon.L (um)	Checked	800
soma.diam (um)	Checked	20
ap.diam (um)	Checked	2
ap[1].diam (um)	Unchecked	1
ap[2].diam (um)	Unchecked	1
bas.diam (um)	Checked	3
axon.diam (um)	Unchecked	1

Set L and diam for all sections.  
*Time to save to a session file!*

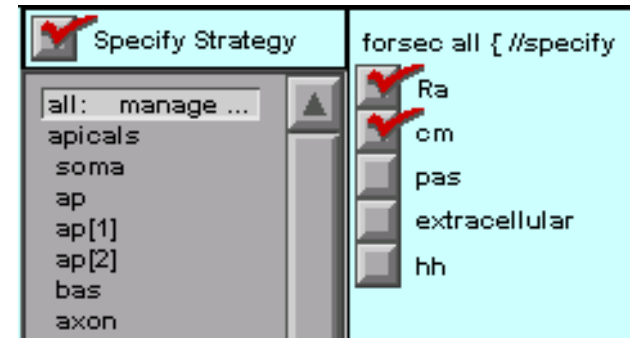
# Biophysics



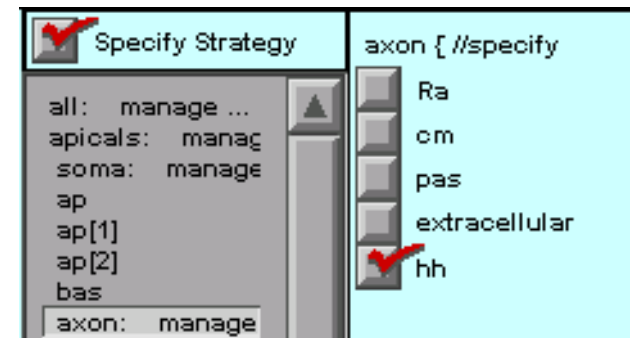
"Specify Strategy" is ON.  
Base the plan on shared properties.

# Biophysics strategy

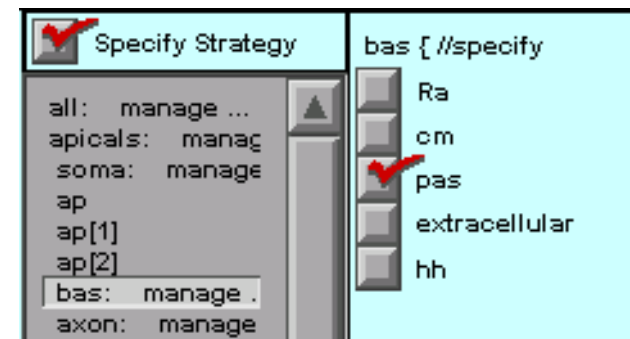
Ra and cm are homogeneous



apicals, soma and axon have hh

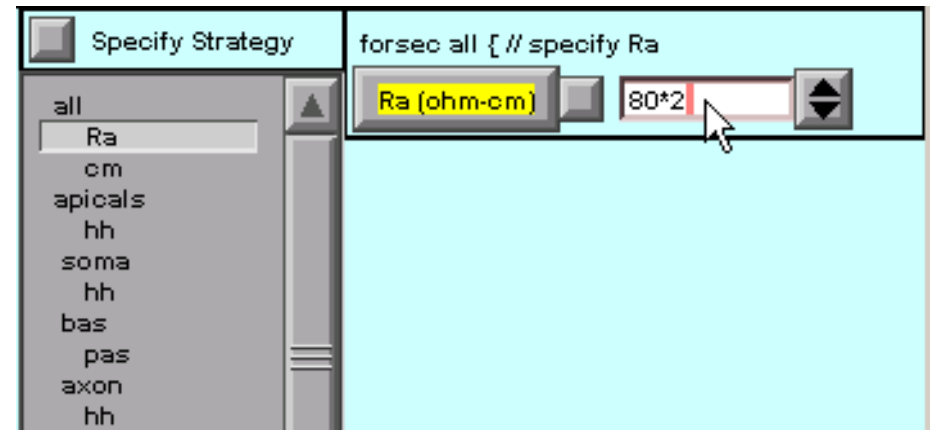


bas has pas

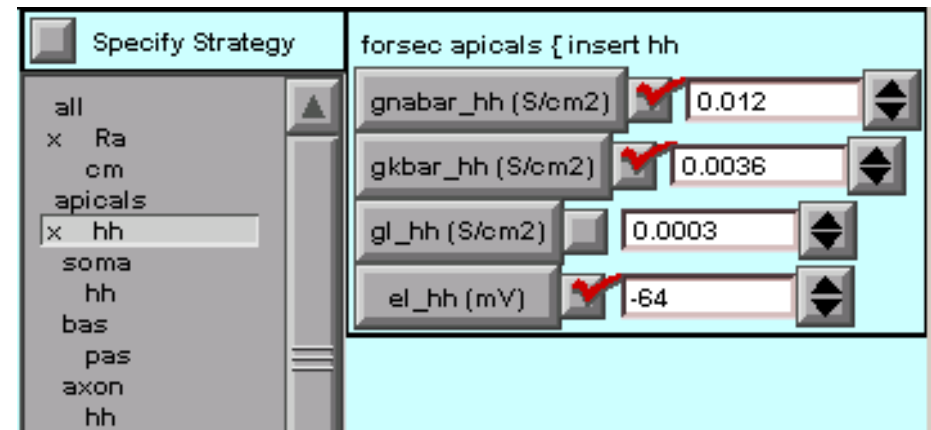


# Implementing biophysics strategy

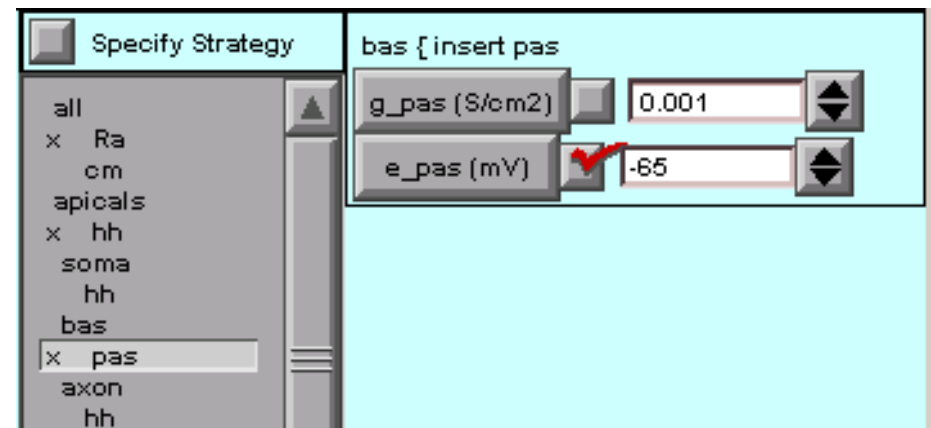
Double Ra



Fix apicals hh params



Shift e\_pas in bas



**Save another session file!!**

# Management

Option 1: save as a Cell Type  
for use in a network

The screenshot shows a software interface with a light blue background. At the top, there is a navigation bar with a diamond icon and the text "Management", followed by a checkbox labeled "Continuous Create". Below this is a secondary bar with a mouse cursor pointing to a diamond icon and the text "Cell Type", followed by "Export" and "Import" options, each with a downward-pointing triangle, and a "Hints" button. The main area contains the following text: "This is necessary only if the cell is used in a network", "This creates a file that declares a cell type with the current specification", and "Such a cell class is usable in networks and can be employed by the network builder tool." Below this text is a "Classname" input field containing the text "Cell". Further down is a "Select Output" section with a downward-pointing triangle and the text "soma.v (1)". At the bottom of the interface is a "Save hoc code in file" button.

◆ Management  Continuous Create

◆ Cell Type ▼ Export ▼ Import Hints

This is necessary only if the cell is used in a network

This creates a file that declares a cell type  
with the current specification

Such a cell class is usable in networks and  
can be employed by the network builder tool.

Classname  
Cell

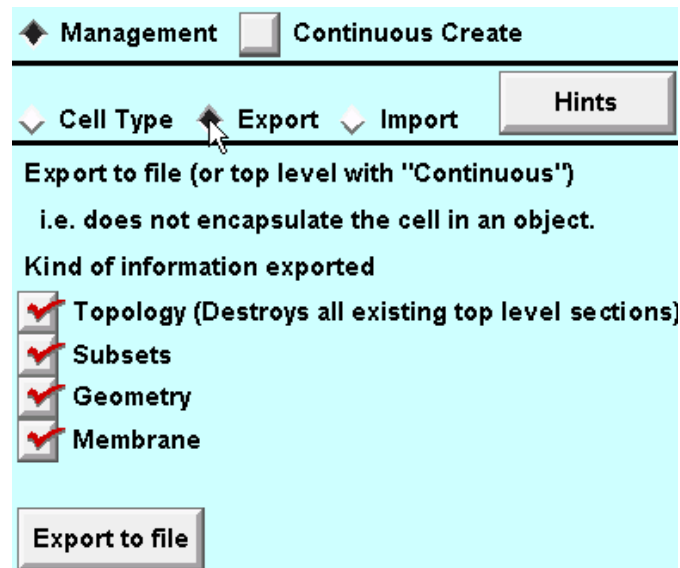
▼ Select Output  
soma.v (1)

Save hoc code in file



# Management *continued*

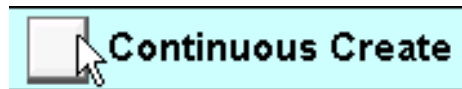
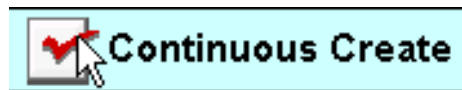
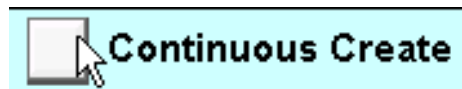
## Option 2: save as hoc file



# Management *continued*

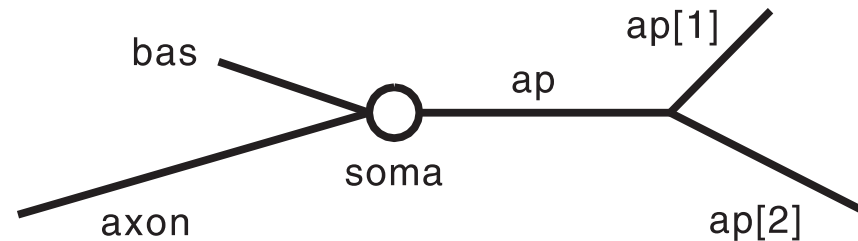
Option 3: export to interpreter

Toggle Continuous Create ON and OFF



or just leave it ON all the time.

## Step 2: creating and using an interface for running simulations



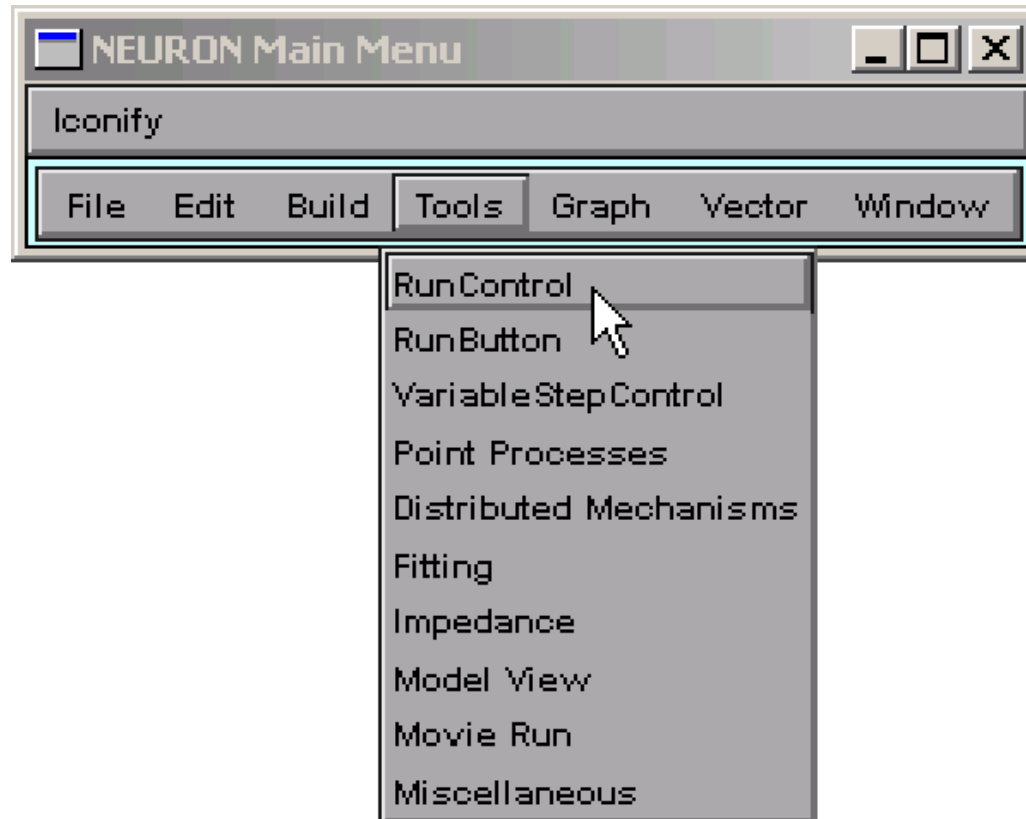
We want to

- attach a stimulating electrode
- evoke an action potential
- show time course of  $V_m$  at soma
- show  $V_m$  along a path from one end of the cell to the other

We need

- a "Run" button
- graphs to plot results
- a stimulator

# Get a "Run" button



NEURON Main Menu / Tools / RunControl

# RunControl panel

**Init** sets time to 0,  
Vm to displayed value, and  
conductances to steady-state

**Init & Run** does an Init,  
then starts a simulation

**Stop** interrupts the simulation

**Continue til** runs until displayed time

**Continue for** runs  
for displayed interval

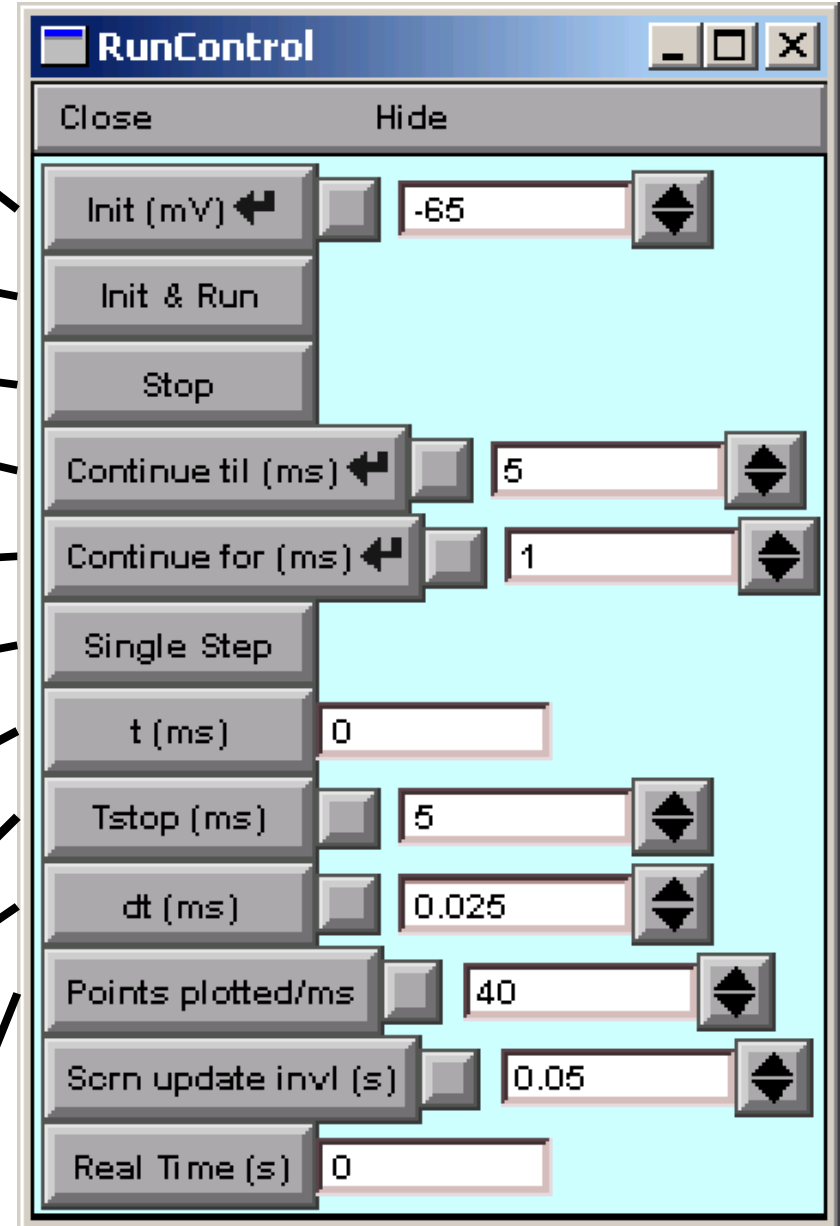
**Single step** advances by  
 $1/(\text{Points plotted/ms})$

**t** numeric field shows model time

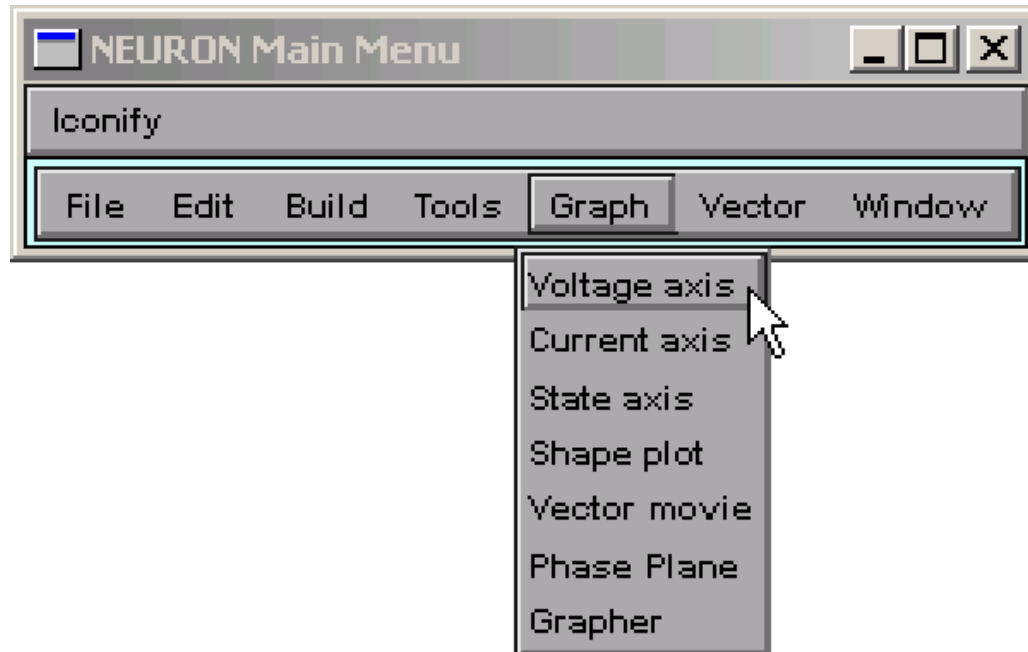
**Tstop** specifies when simulation ends

**dt** is integration time step;  
must be integer fraction of  
 $1/(\text{Points plotted/ms})$

**Points plotted/ms** is 1/plotting interval

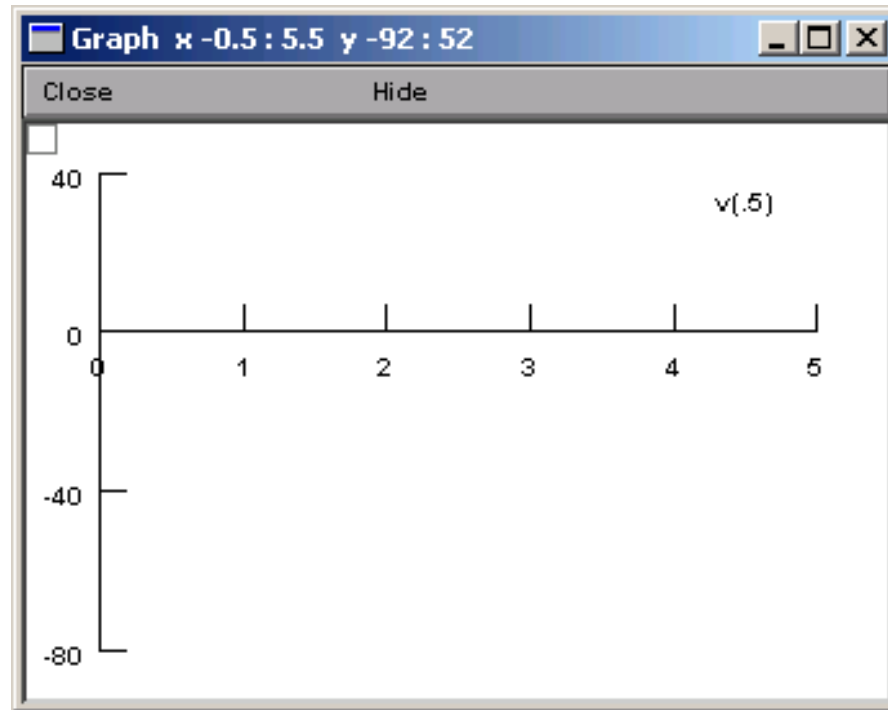


# We need to plot $V_m(t)$ at soma



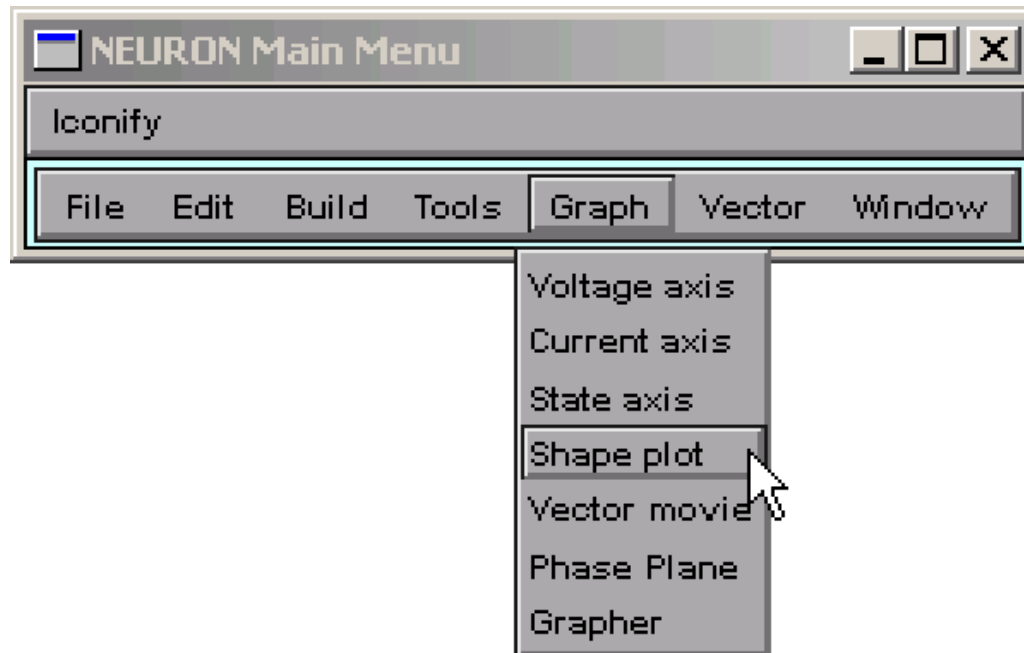
NEURON Main Menu / Graph / Voltage axis

# Graph window



$v(.5)$  is  $V_m$  at middle of default section  
(first section in the CellBuilder)

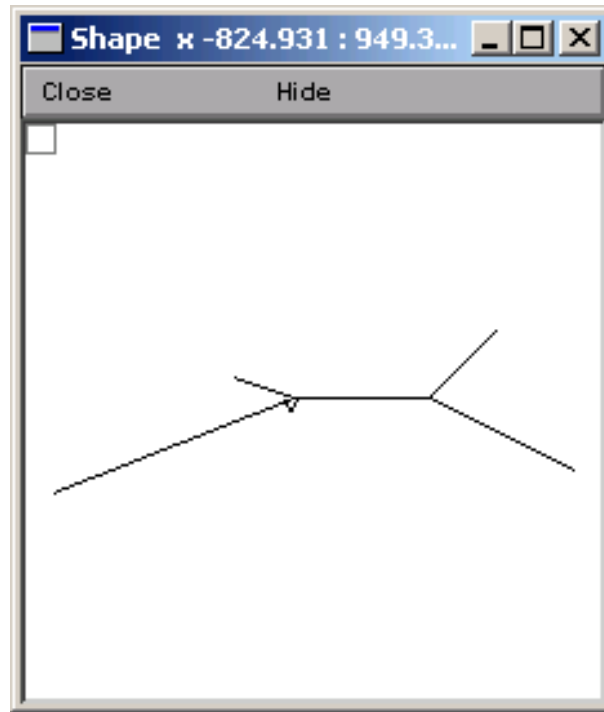
# We need to plot Vm along a path



NEURON Main Menu / Graph / Shape plot

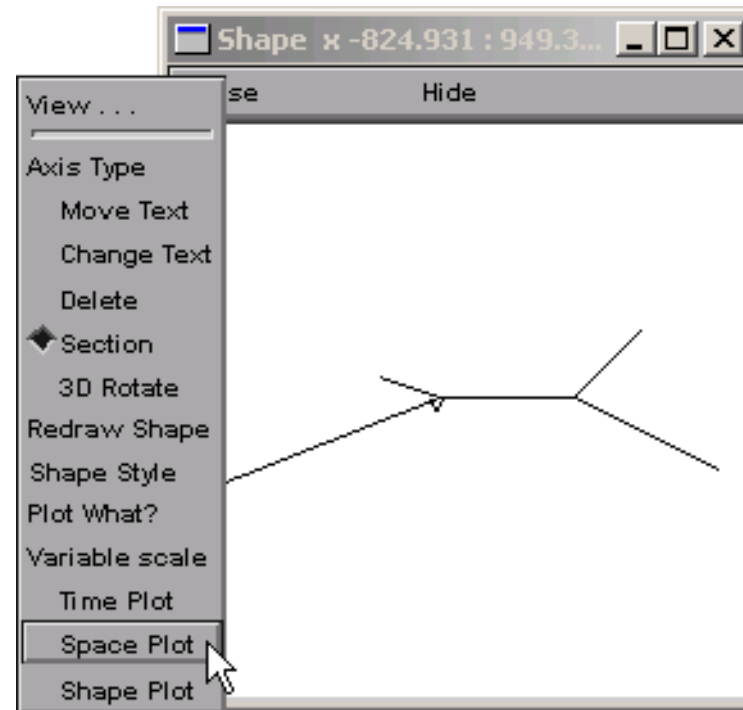


# Bringing up a space plot



Use this "shape plot" to create a "space plot".  
Click on its "menu box" . . .

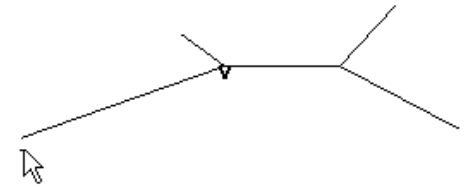
# Bringing up a space plot *continued*



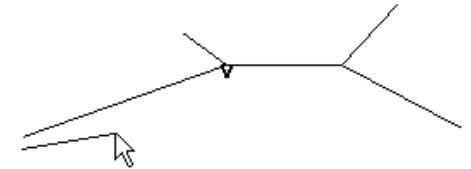
. . . and scroll down to "Space Plot".

# Bringing up a space plot *continued*

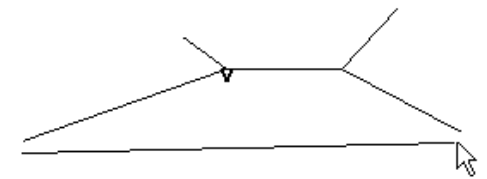
Click just left of the shape



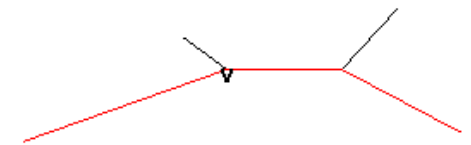
Hold button down while dragging  
from left . . .



. . . to right . . .

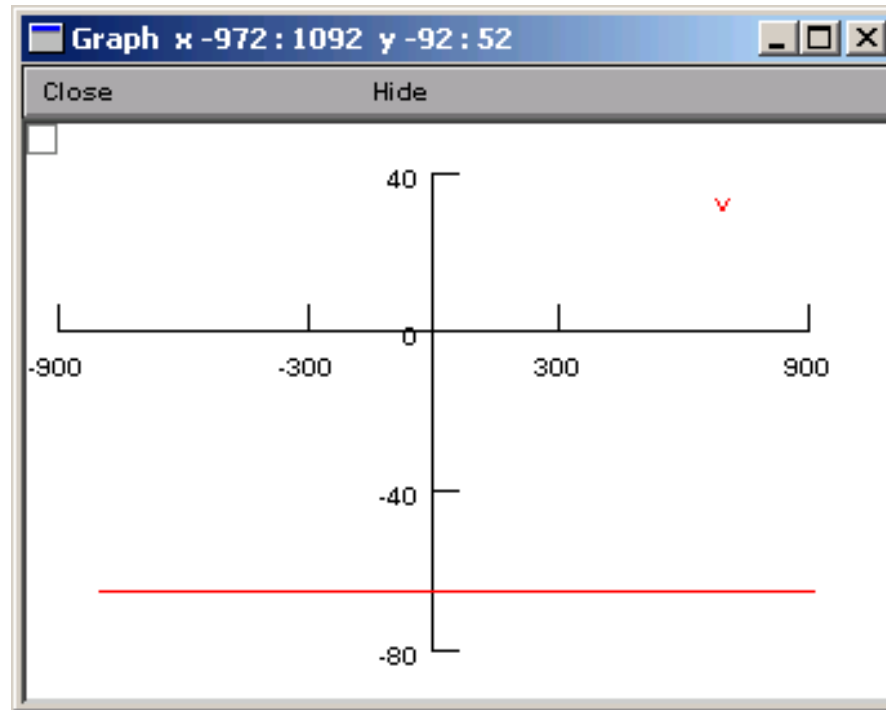


. . . then release button.



This pops up . . .

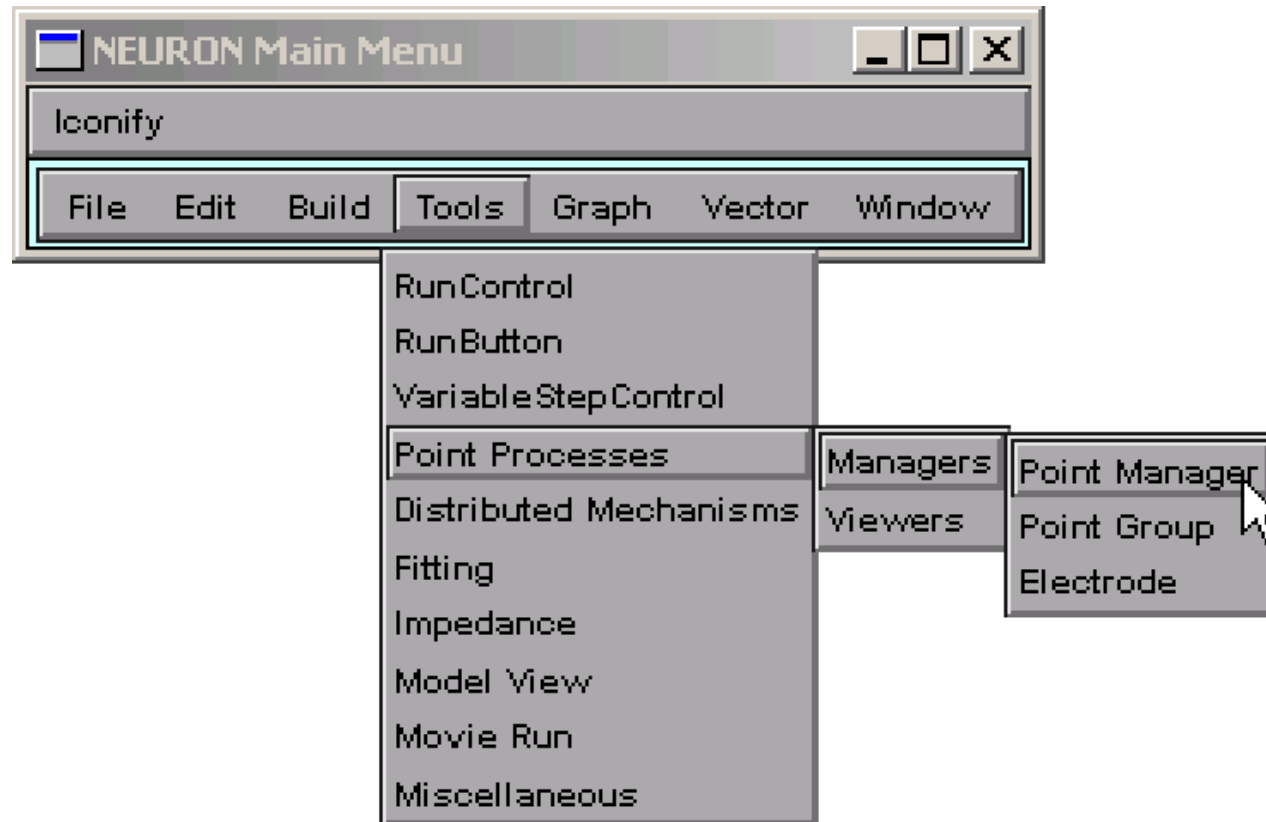
# Space plot



. . . a plot of  $V_m$  vs. distance along a path.

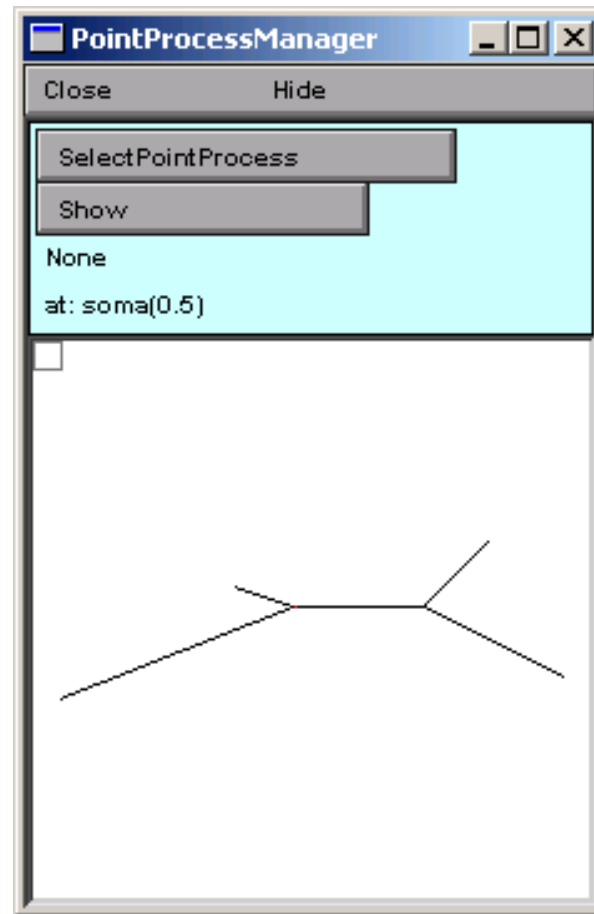
*Better save a session file.*

# We need a stimulator



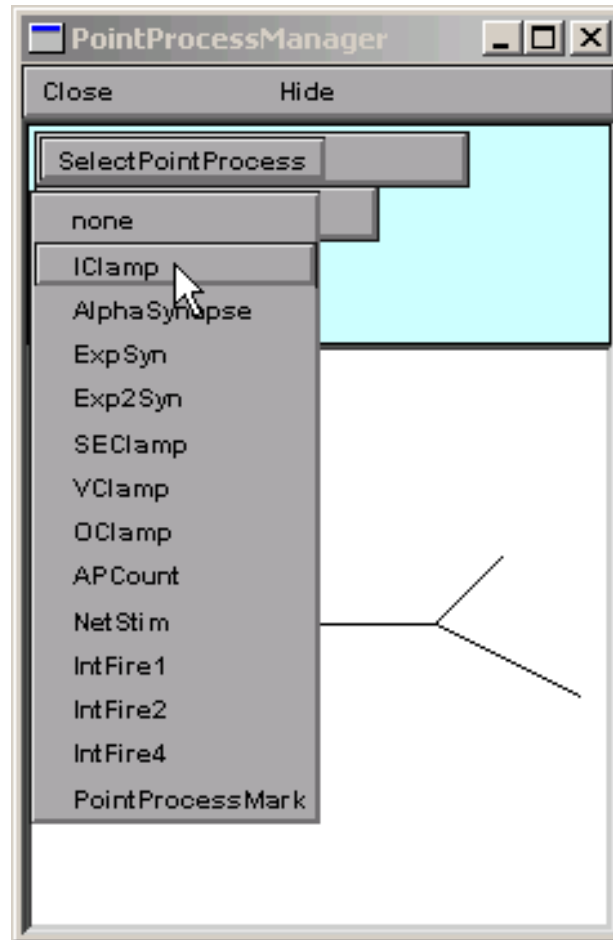
NEURON Main Menu / Tools / Point Processes  
/ Managers / Point Manager

# PointProcessManager window



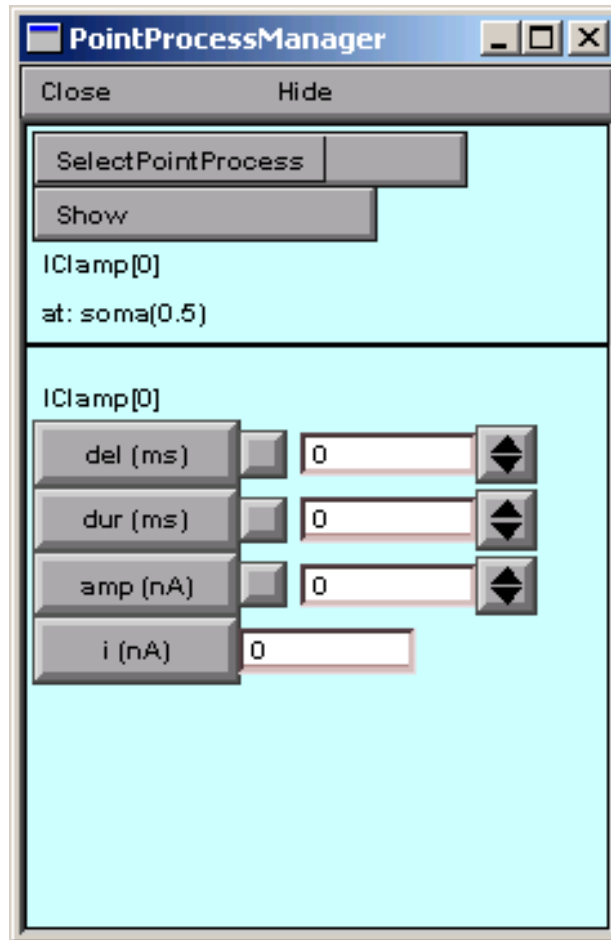
To make this an IClamp . . .

# Creating an IClamp



... click on SelectPointProcess  
and scroll down to IClamp.

# I Clamp parameter panel



Next: set parameter values.



# Entering values into numeric fields

Direct entry



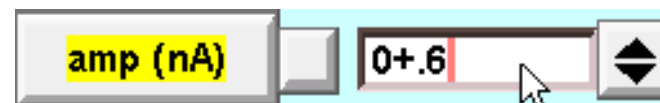
Note yellow highlight on button

Spinner

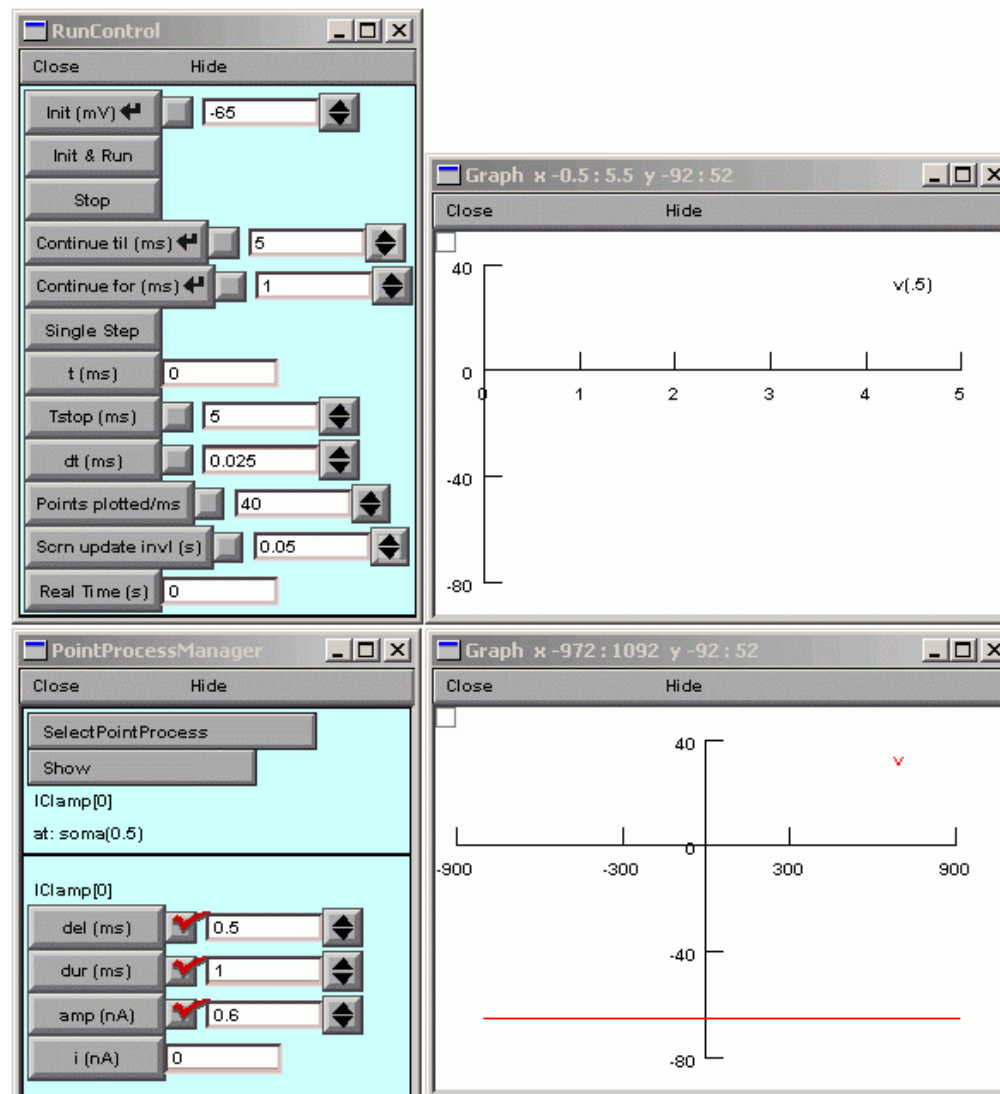


Red check means value has been changed from default

Mathematical expression

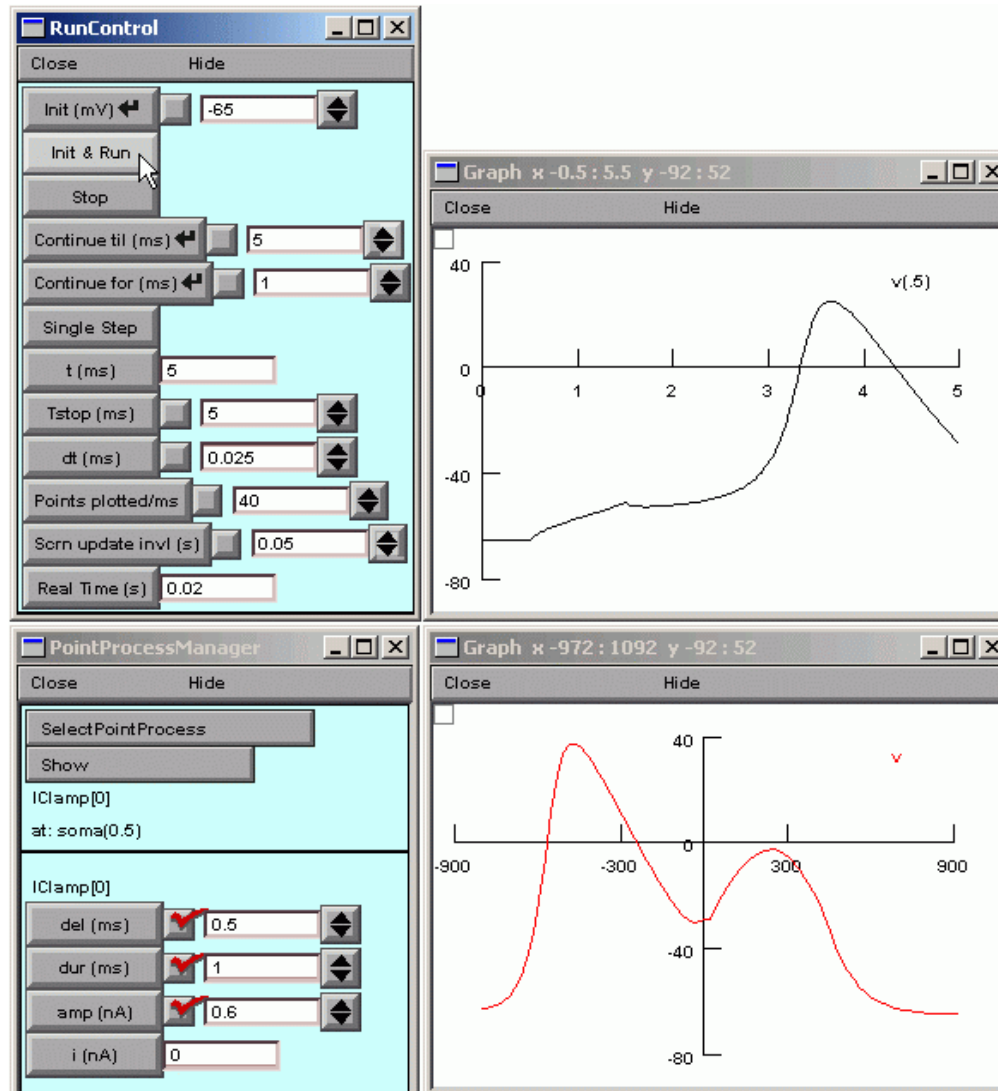


# Our user interface

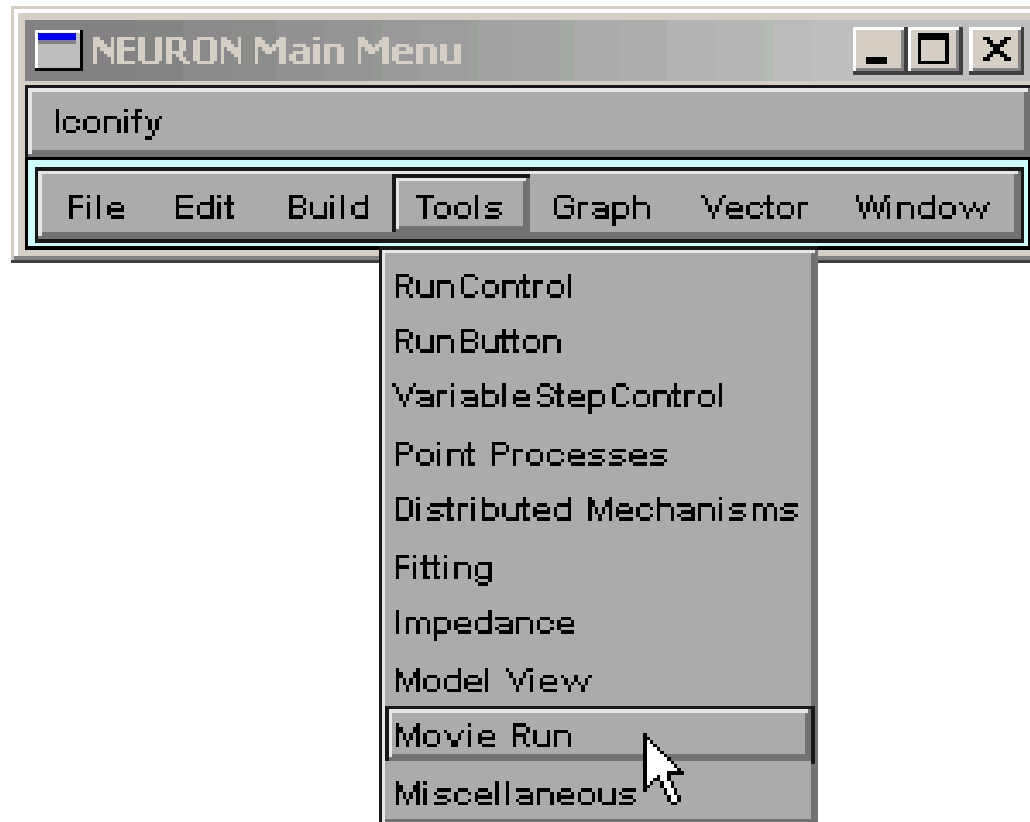


*Time to save to a new session file!*

# It works!



# How to get nice space plot "movies"



NEURON Main Menu / Tools / Movie Run

# Space plot "movies" *continued*



Movie Run / Init & Run

# CellBuilder advanced usage

Management of complex morphologies

Specifying subsets, e.g.

neurondemo's "ugly cell"  
cells from Import3d

"Cell surgery"

example: removing/substituting axon

Using exported (hoc) code in Python

# Specifying subsets

neurondemo's "ugly cell"

just an example of a subset-free morphology

Subsets page

- \* zoom in to identify and "tag" somatic, axonal, and apical dendrites
- \* Management / Import / "Don't draw short sections as circles" may be helpful
- \* refer to Shape plot as necessary
- \* helpful: Select One, Select Subtree, Select / Xor, Select / Subtract etc.

When done, save to new session file!

Export new cell class as necessary

# Cell surgery

Example: removing axon

With Continuous Create off

Identify axon sections on Topology  
or Subsets page (latter is usually best)

Topology page

zoom in and verify section/tree to be deleted

Select "Delete Section" or "Delete Subtree"

click to delete

Save CellBuilder to a new ses file

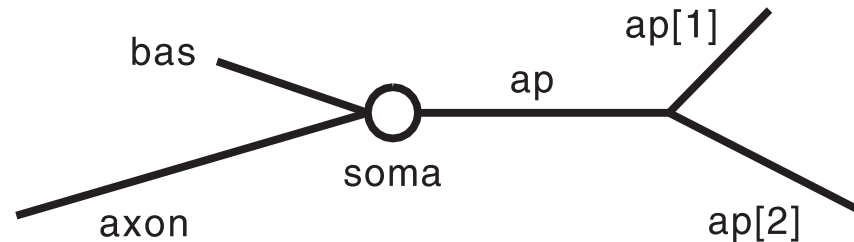
Export new cell class as necessary



# Using exported (hoc) code in Python

```
# NPyr.hoc, exported from CellBuilder
# defines the NPyr class
h.load_file("NPyr.hoc")
npcell = h.Npyr()
# verify
h.topology()
```

# Homework



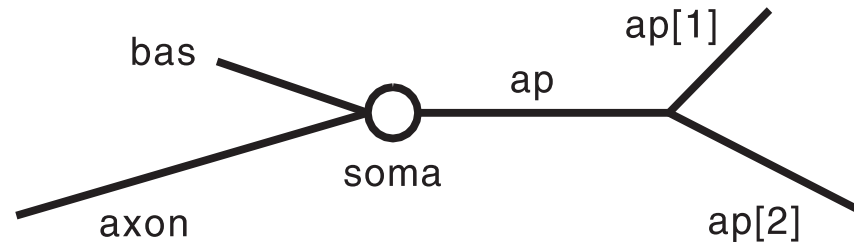
Using this model cell with "reduced hh" in the apical dendrites:

For a 0.1 ms depolarizing current pulse applied to soma(0.5) starting at  $t = 1$  ms, what is the smallest amplitude that will elicit a spike? (2 significant figures)

Replace the IClamp with an AlphaSynapse with  $\tau = 1$  ms, onset = 1 ms, and  $e = 0$  mV. What is the smallest  $g_{\max}$  (peak conductance) that will elicit a spike? (2 significant figures)

What  $g_{\max}$  elicits a 1 mV epsp at the soma? How much of the epsp spreads to ap(0.5)? ap[2](0.5)? bas(1)? (2 significant figs).

# Homework



Move the AlphaSynapse to `ap(0.5)` but don't change its `tau`, `onset`, `e`, or `gmax`. How big is the `epsp` at `ap(0.5)`, and how big is it after it spreads to the `soma`? (2 significant figures)

Repeat with the synapse at `ap[2](0.5)`.

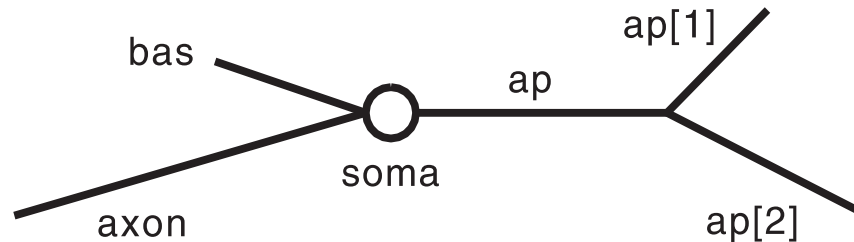
Finally, repeat with the synapse at `bas(1)`.

Organize your results in a table like this:

<b>Synaptic location</b>	<b>EPSP at synapse</b>	<b>"Downstream" location</b>	<b>EPSP downstream</b>
<code>soma(0.5)</code>	1 mV	<code>ap(0.5)</code>	<i>value observed</i>
<i>. . . etc. . . .</i>			

("Downstream" means away from the point of synaptic attachment)

# Homework



The properties of the AlphaSynapse are very similar to those of an AMPAergic excitatory synapse. Based on your observations,

1. Does an excitatory synapse act more like a voltage source or a current source?
2. What is the range of epsps amplitudes observed at the soma, and what is the range seen at the synaptic locations?
3. Is there approximate reciprocity between a given pair of locations? (i.e. is the downstream epsp relatively unaffected by swapping the synaptic and downstream locations)  
Does this surprise you?