

The NEURON Simulator

neuron.yale.edu

School of Brain Cells and Circuits; Erice 2015

Supported by NINDS

General

Slides available at:

<http://neuron.yale.edu/ftp/neuron/neuron-erice2015.pdf>

NEURON + Python

<http://neuron.yale.edu/ftp/neuron/neuron-python-erice2015.pdf>

NEURON + Python tutorial

<http://neuron.yale.edu/neuron/static/docs/neuronpython/index.html>

Documentation | NEURON - Mozilla Firefox

Hines, Michael - Outl... x Documentation | NEURON x +

neuron.yale.edu/neuron/docs valgrind gdb

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NEURON

for empirically-based simulations of neurons and networks of neurons

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Documentation

[FAQ](#)
[Programmer's Reference](#)
Get a pkzip archive of the Programmer's Reference
The mercurial repository change log and sources

Guides and Tutorials

[Help for the total beginner](#)
What to read first.
[Suggestions for how to develop models](#)
Important practical hints about model development for anyone who is starting to work with NEURON.
[Construction and Use of Models: Part 1. Elementary Tools](#)
A good beginner's tutorial. Introduces some of NEURON's basic GUI tools.
[Import3D tutorials](#)

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Hands-on exercises: table of contents - Mozilla Firefox

Hines, Michael - Outl... x Hands-on exercises: ta... x +

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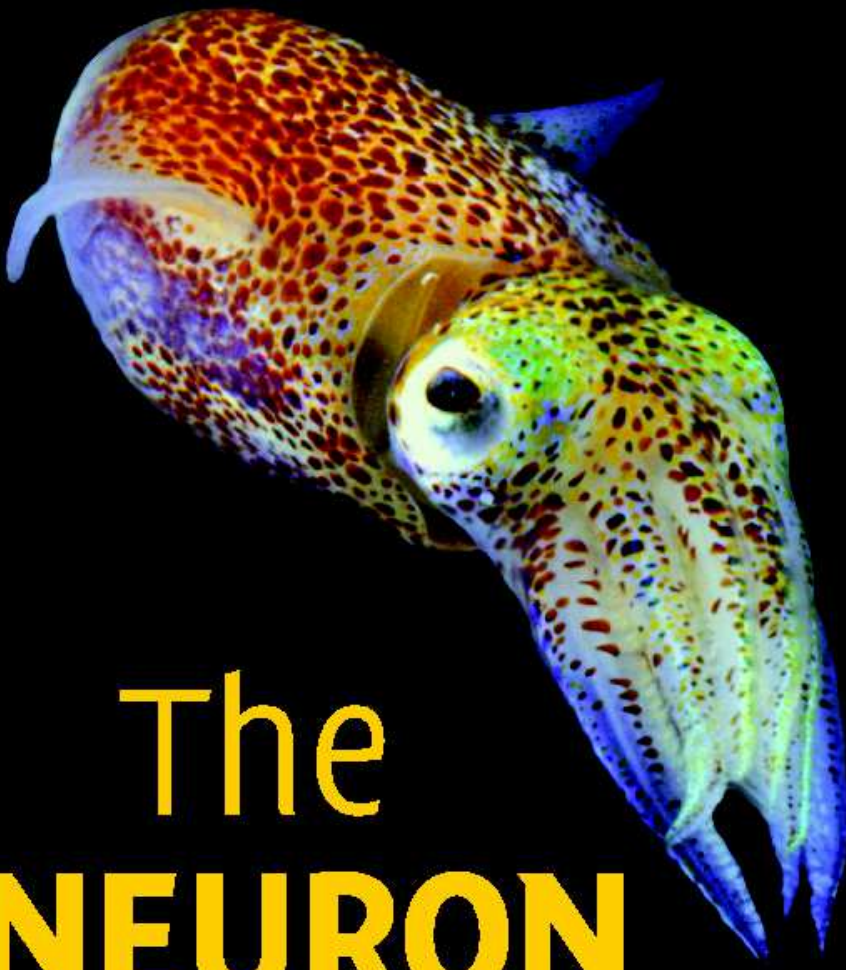
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NEURON Hands-on Course

EXERCISES

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The **NEURON** Book

**Nicholas T. Carnevale
and Michael L. Hines**

CAMBRIDGE

Where does it fit in the overall modeling process?

What kind of models?

How is the program organized?

Methods.

Using:

Building

Running

Analysing

Networks (Inhibitory Synchronization).

Published models: ModelDB.

Where does it fit in the overall modeling process?

Physical System



Model



Representation in NEURON

Create Representation

**Investigate/Explore/Control/Use
Representation**

Physical System



Model



Simulation

Squid axon



Hodgkin-Huxley cable equations

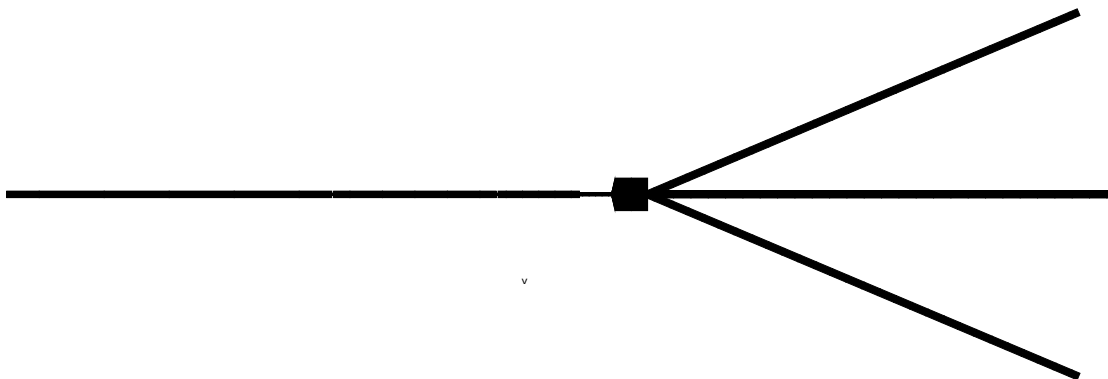
$$\frac{D}{4R_a} \cdot \frac{\partial^2 V}{\partial x^2} = C_m \frac{\partial V}{\partial t} + \bar{g}_{na} m^3 h \cdot (V - E_{na}) + \bar{g}_k n^4 \cdot (V - E_k) + g_l \cdot (V - E_l)$$

$$\begin{aligned} \frac{dm}{dt} &= -\alpha_m m + \beta_m \cdot (1 - m) & \alpha_m &= \frac{.1(V+40)}{1 - e^{-.1(V+40)}} & \beta_m &= 4e^{-(V+65)/18} \\ \frac{dh}{dt} &= -\alpha_h h + \beta_h \cdot (1 - h) & \alpha_h &= .07e^{-.05(V+65)} & \beta_h &= \frac{1}{1 + e^{-.1(V+35)}} \\ \frac{dn}{dt} &= -\alpha_n n + \beta_n \cdot (1 - n) & \alpha_n &= \frac{.01(V+55)}{1 - e^{-.1(V+55)}} & \beta_n &= .125e^{-(V+65)/80} \end{aligned}$$

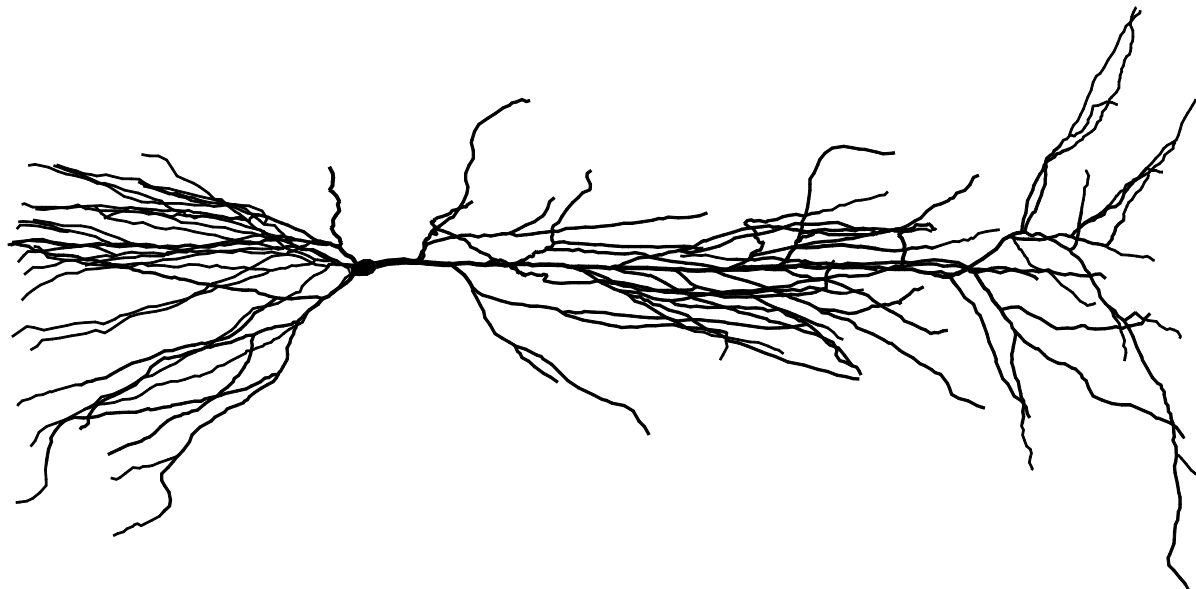
NEURON representation

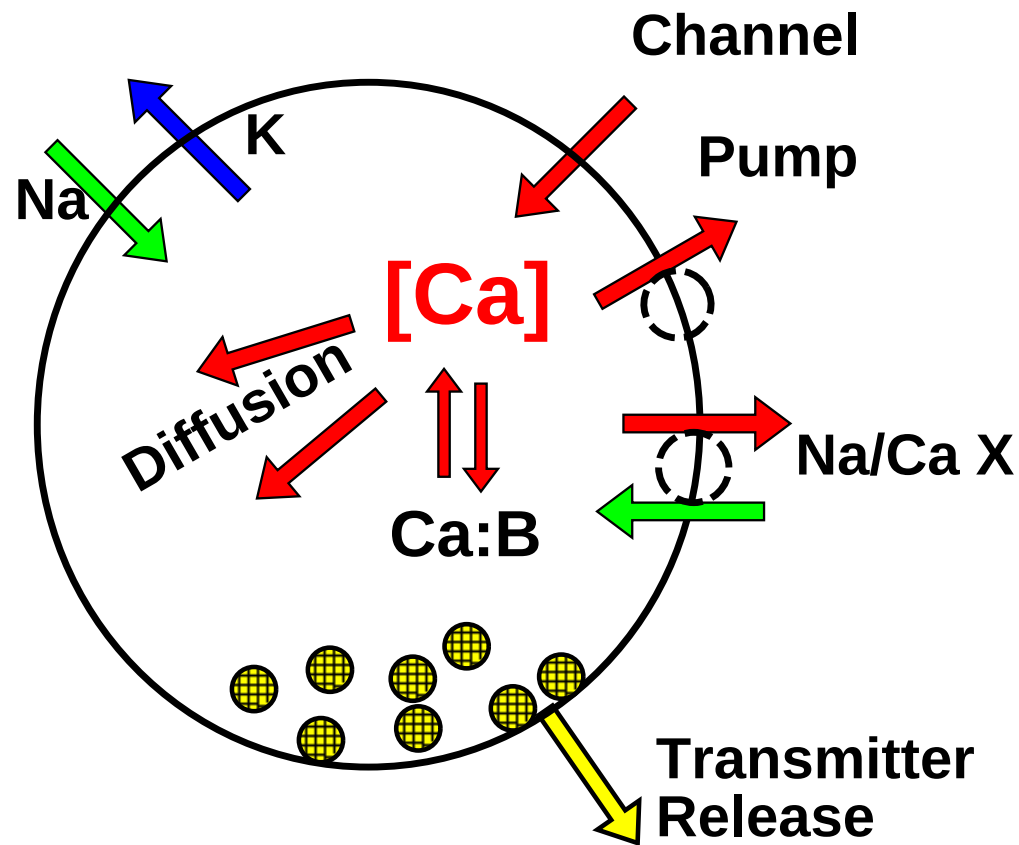
```
create axon
axon {
    nseg = 75
    diam = 100
    L = 20000
    insert hh
}
```

What kind of models?



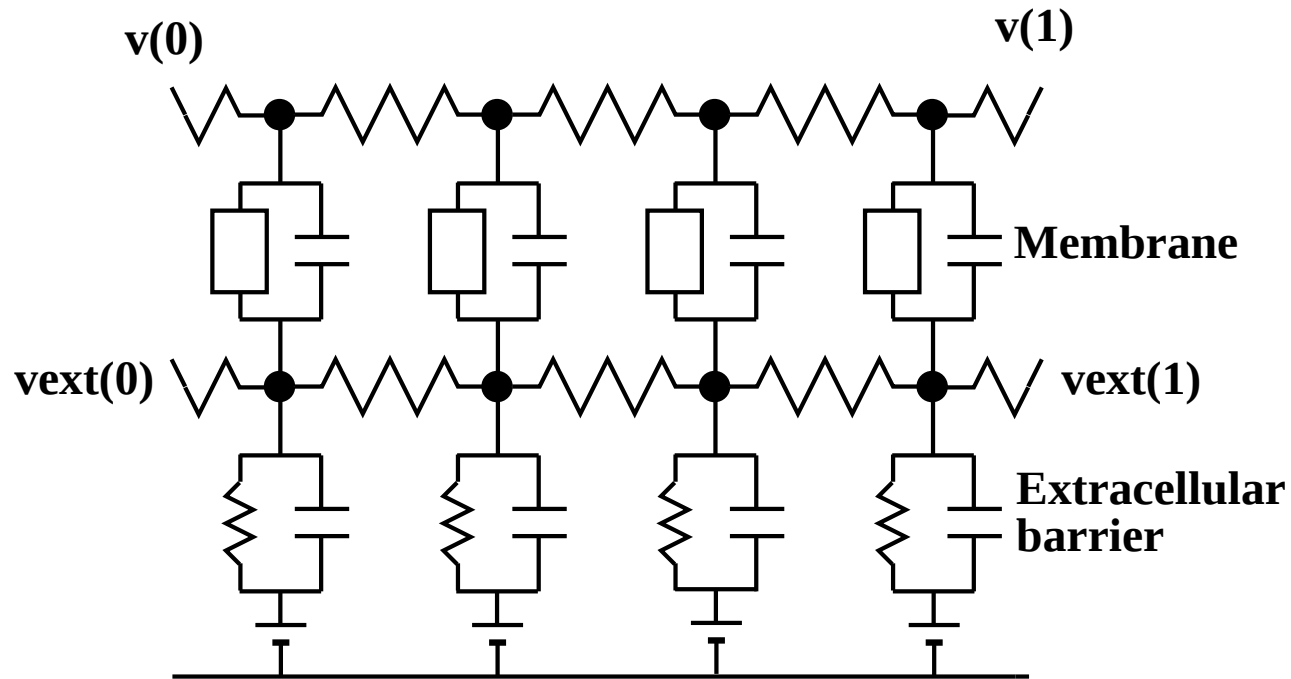
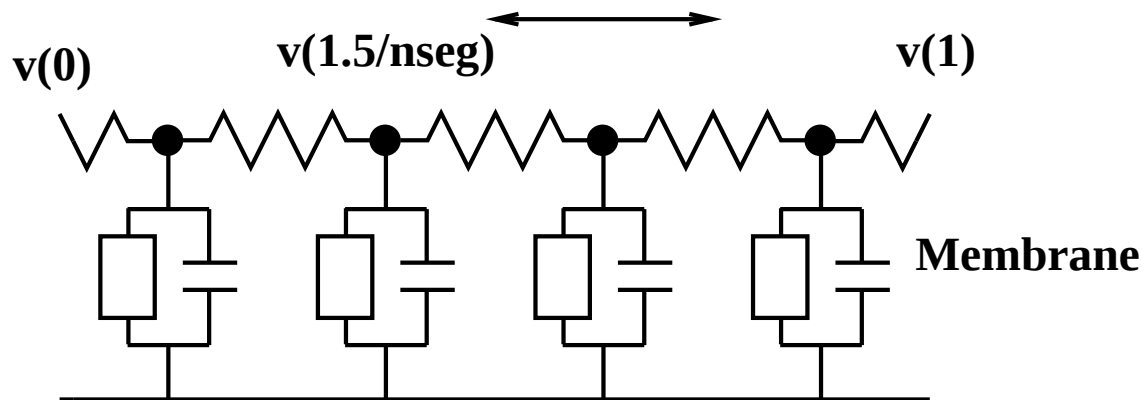
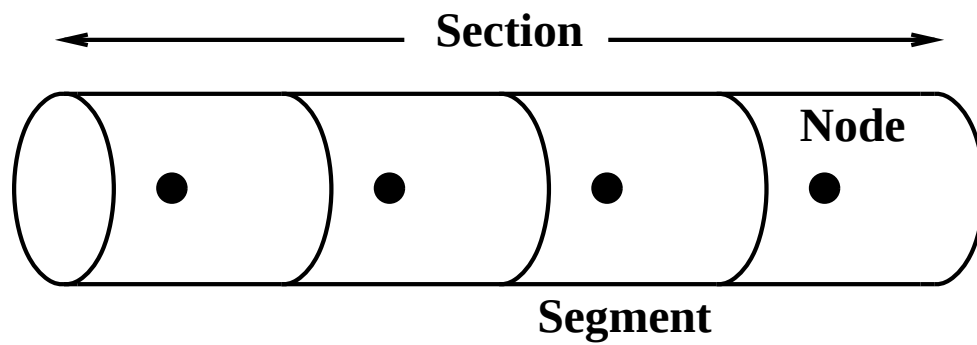
v

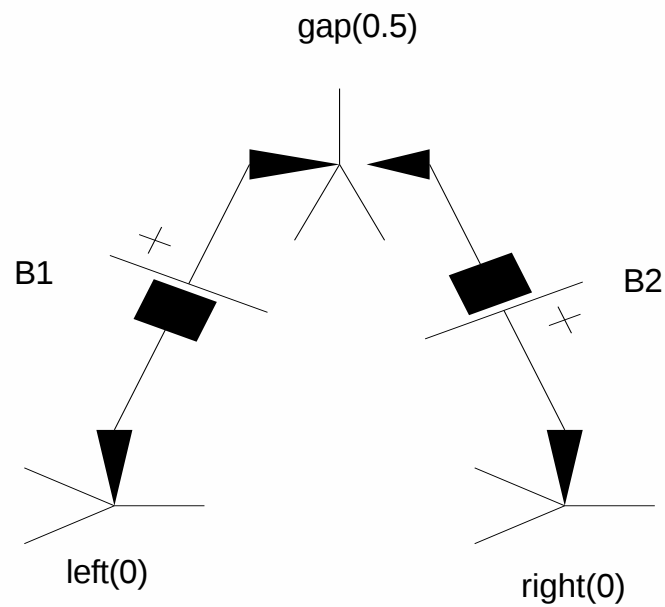
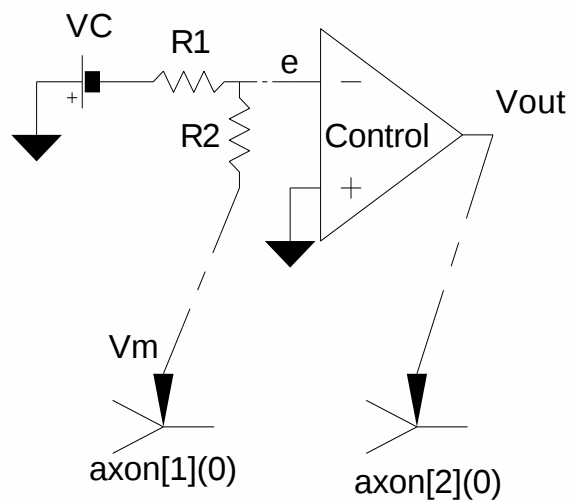
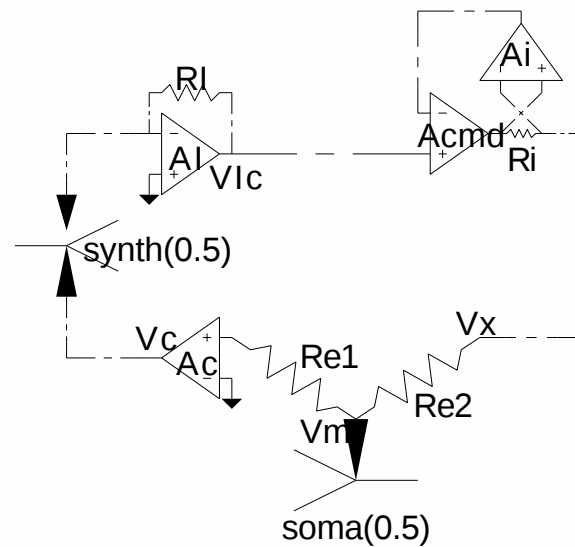
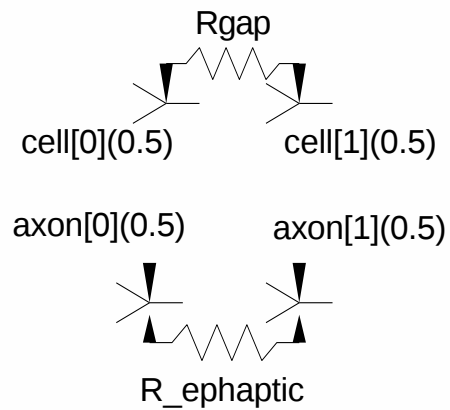
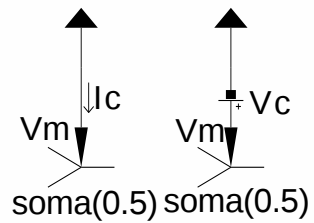


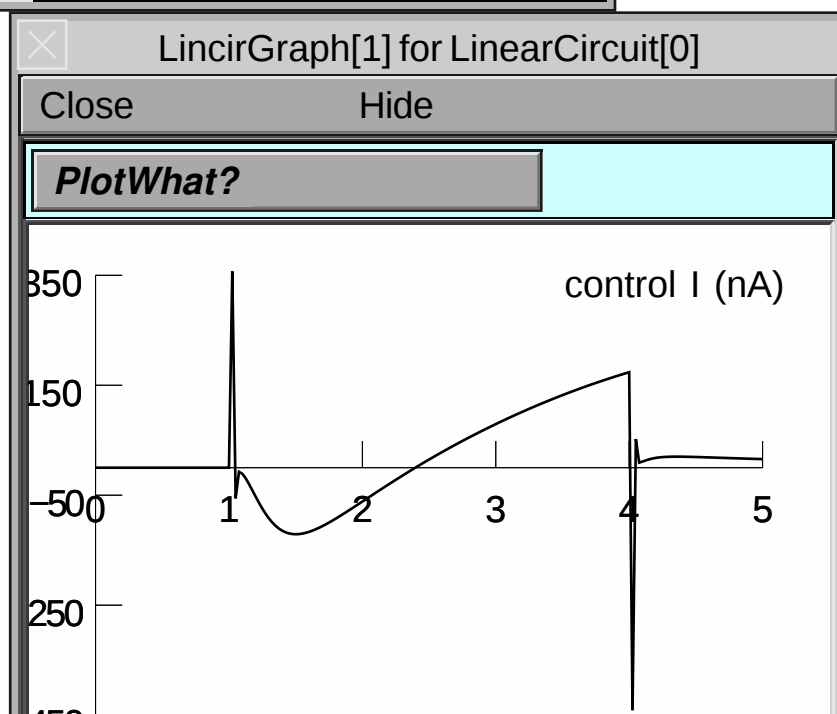
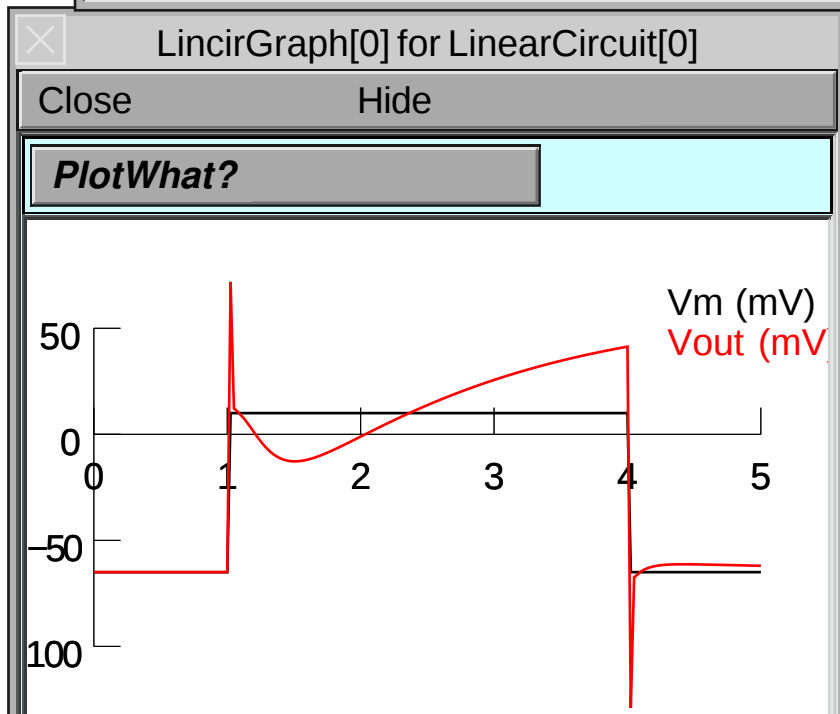
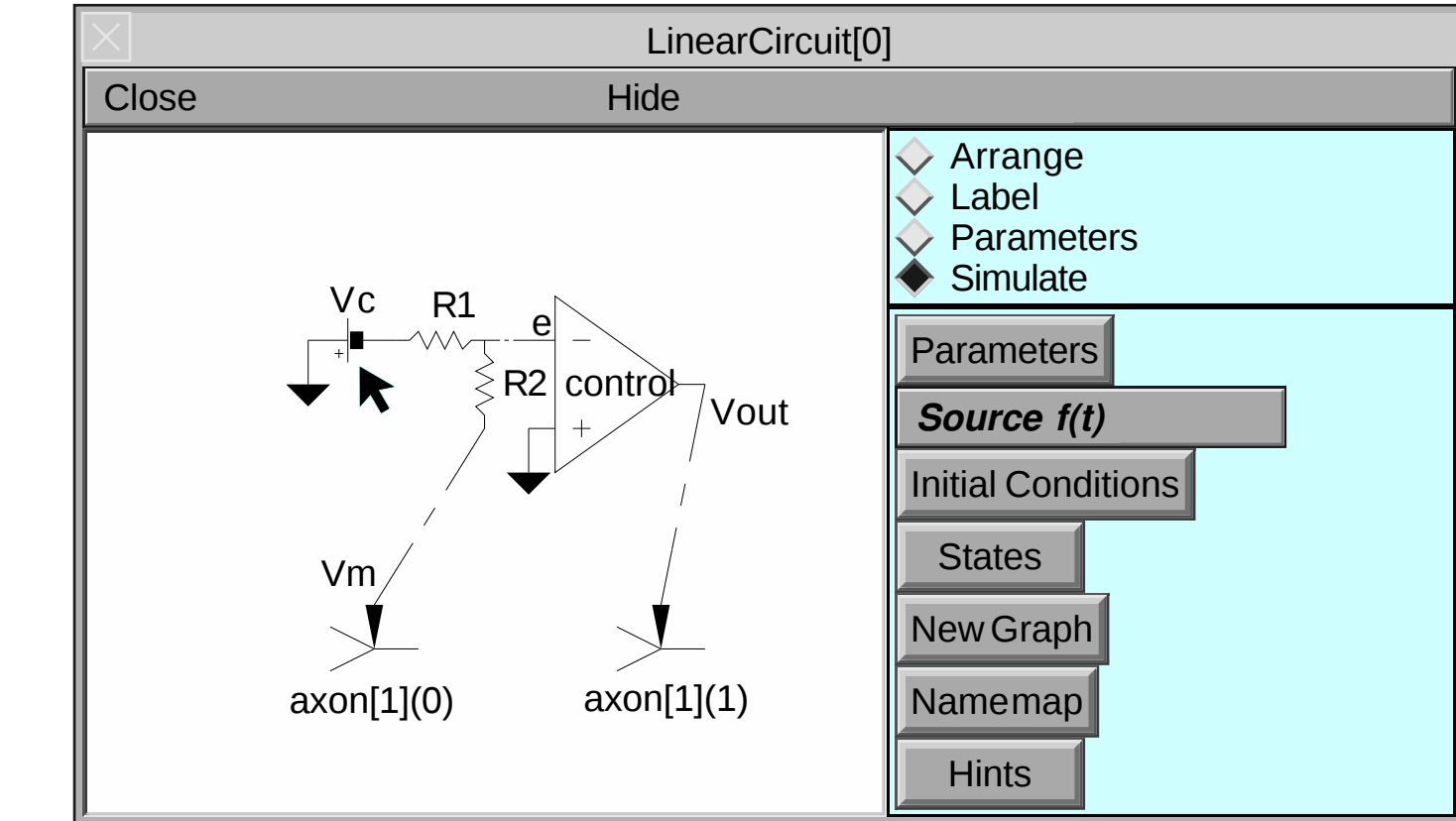


Single Channels
Extracellular fields
Linear circuits
Synapses
Networks

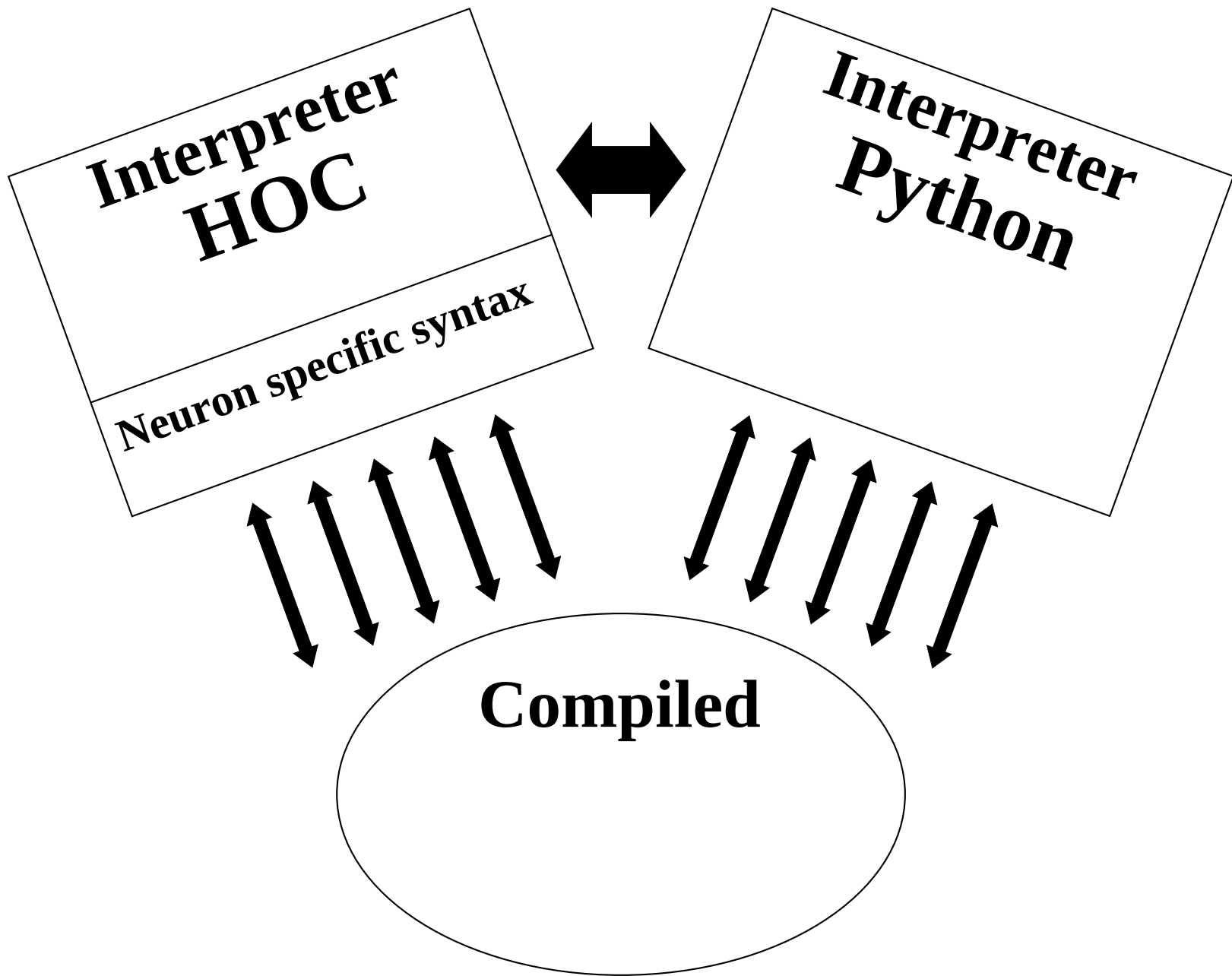
Discrete Event Simulation
Artificial Spiking Cells

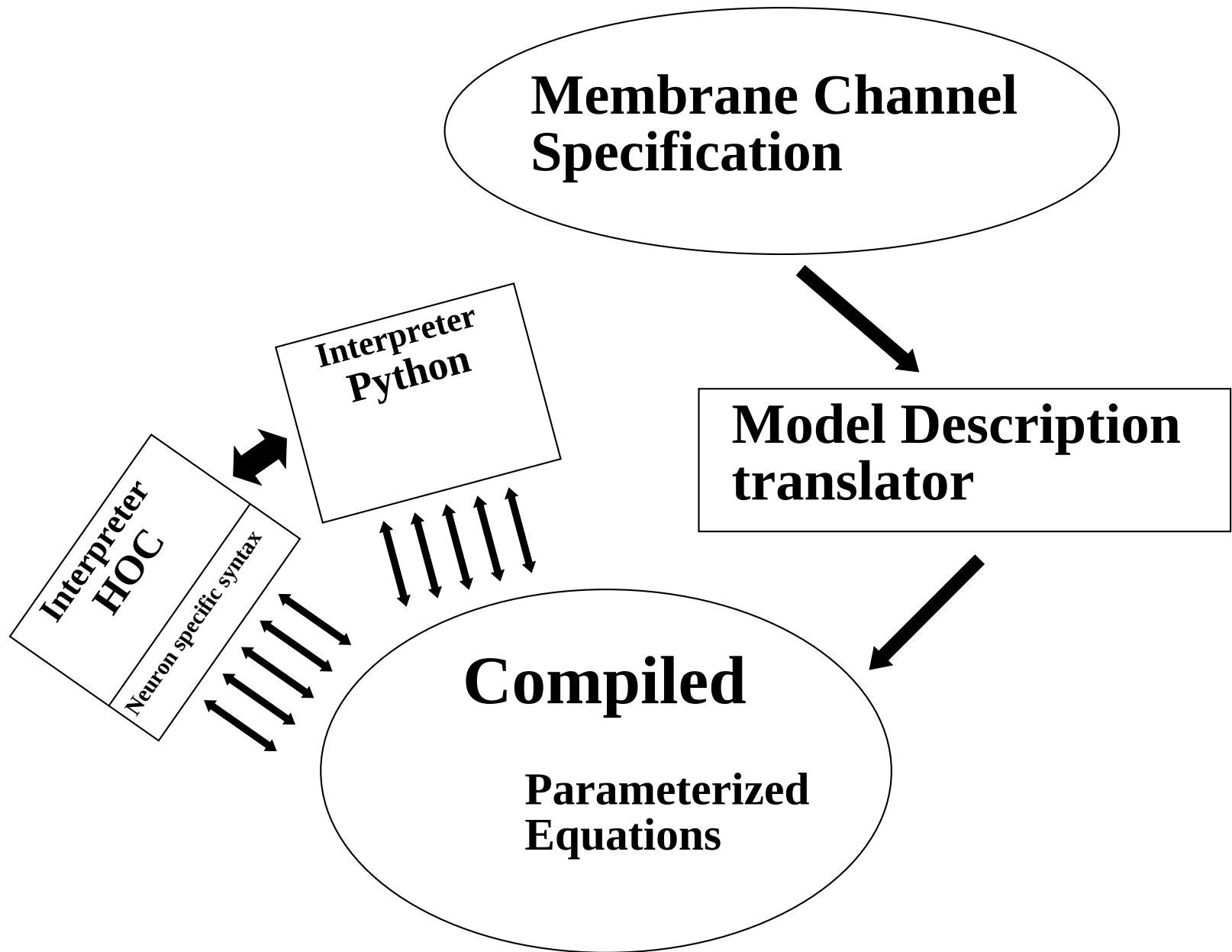






How is the program organized?



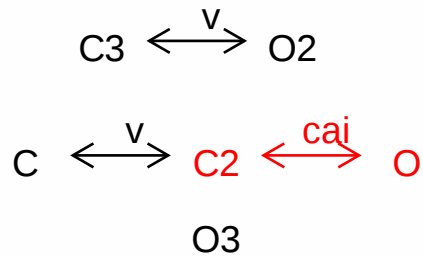


Close

Hide

◆ States ◆ Transitions ◆ Properties

Select hh state or ks transition to change properties



(0.25*C2 + O)

(0.25*C2 + O): 3 state, 2 transitions

Power

1

Fractional Conductance

C2 fraction

0.25

O fraction

1

◆ Adjust

Run

ChannelBuild[0]managedKSChan[

Close

Hide

Properties

kca Density Mechanism

k ohmic ion current

$$i_k (\text{mA/cm}^2) = g_{\text{kca}} * (v - e_k)$$

$$g = g_{\text{max}} * (0.25 * \text{C2} + \text{O}) * \text{O2} * \text{O3}$$

Default gmax = 0 (S/cm2)

(0.25*C2 + O): 3 state, 2 transiti

O2: 2 state, 1 transitions

$$\text{O3}' = a\text{O3} * (1 - \text{O3}) - b\text{O3} * \text{O3}$$

C2 + cai <=> O (a, b) (KSTrans[29])

Display inf, tau

aC2O = A

aC2O

bC2O

ChannelBuild[3]managedKSChan[3]

Close Hide

Properties

nahh0 Point Process (Allow Single Channels)

na ohmic ion current

$ina \text{ (mA/cm}^2\text{)} = nahh0.g * (v - ena)*(0.01/area)$

$g = gmax * m3h1$

Default gmax = 0.12 (uS)

m3h1: 8 state, 10 transitions

SingleComp

Close Hide

soma

☐

pas

☐

hh

☐

nahh

☒

khh

☒

leak

PointProcessManager

Close Hide

SelectPointProcess

Show

nahh0[0]

at:soma(0.5)

nahh0[0]

Nsingle

0

gmax (uS)

0.12

ChannelBuildGateGUI[0]forChannelBuild[3]

Close Hide

States

Transitions

Properties

Select hh state or ks transition to change properties

m3h1

m3h1: 8 state, 10 transitions

Power

1

Fractional Conductance

m0h0fraction

0

m1h0fraction

0

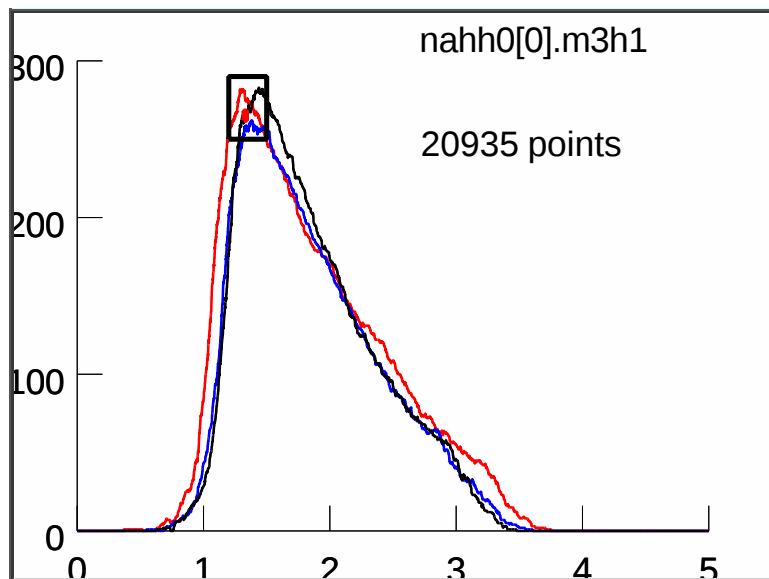
Adjust

Run

m0h0 <-> m1h0 (a, b) (KSTrans[14])

☒ Display inf, tau

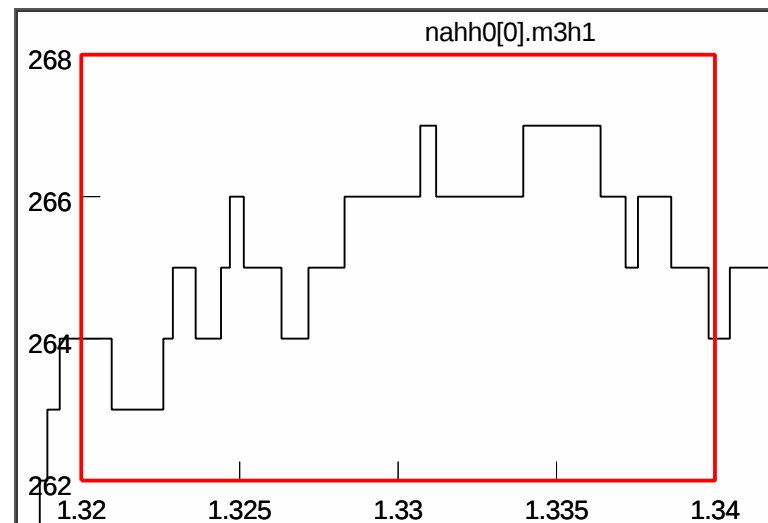
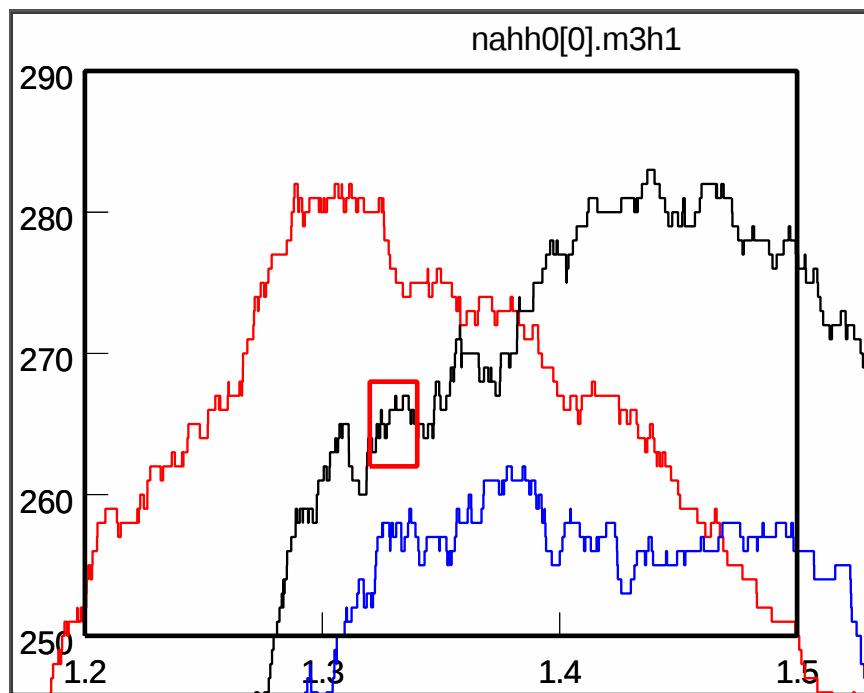
$am0h0m1h0 = A*x/(1 - \exp(-x))$ where $x = k*(v - d)$



☒ Use variable dt

Absolute Tolerance

Atol Scale Tool Details



Methods.

VariableTimeStep

☒ Use variable dt

Absolute Tolerance

0.001

Atol Scale Tool

Details

Absolute Tolerance Scale Factors

Analysis Run

Rescale

Original

*10

/10

Hints

v	1	65	0
ca_cadifpmp	1e-06	3e-06	0
pump_cadifpmp	1e-15	1e-13	0
pumpca_cadifpmp	1e-15	3.6e-15	0
oca_cachan	1	0.053	0
n_HHk	1	0.32	0
m_HHna	1	0.053	0
h_HHna	1	0.6	0
Ves_trel	1	0.0004	0
B_trel	1	0	0
Ach_trel	1	0	0
X_trel	1	0	0

Numerical Method Selection

Refresh

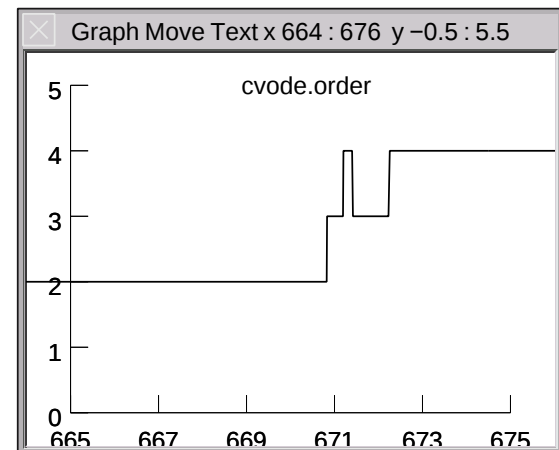
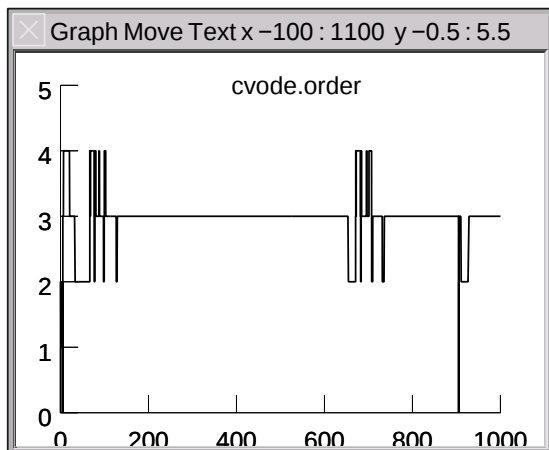
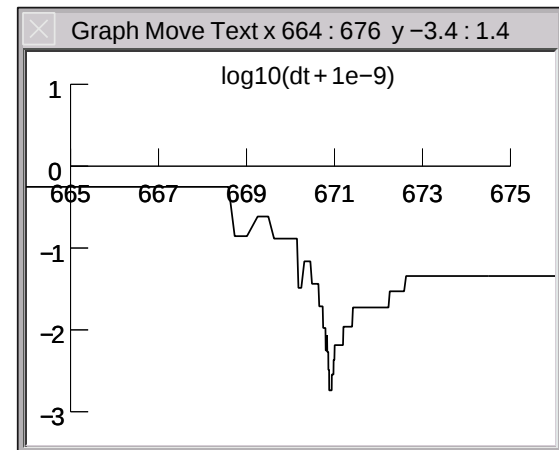
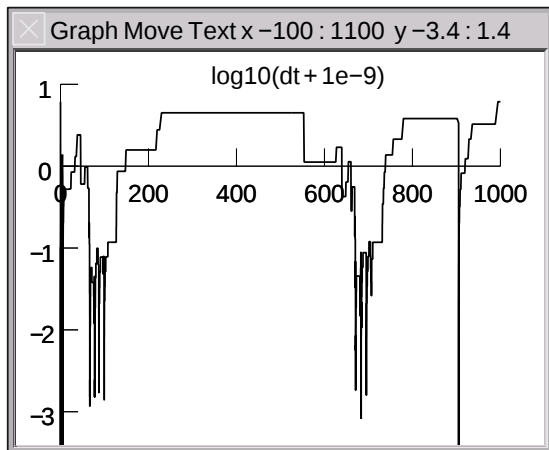
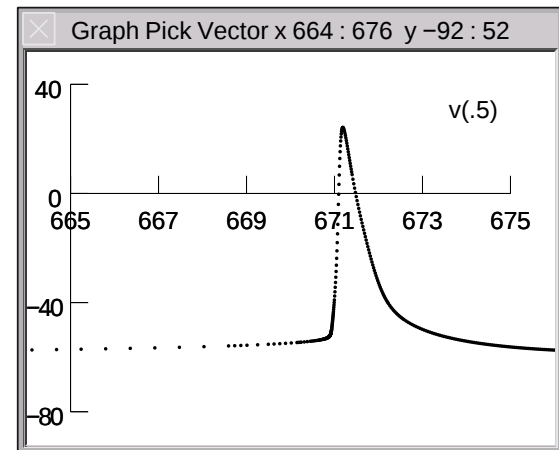
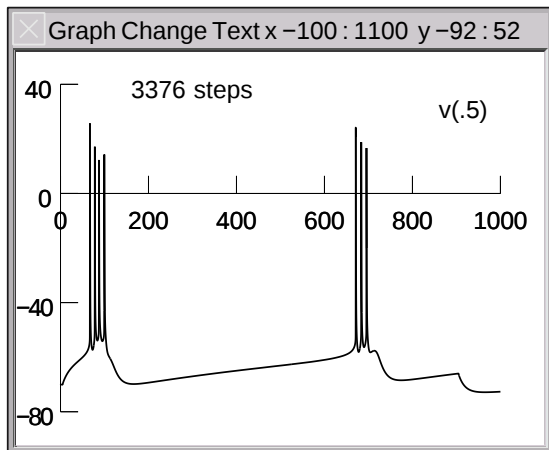
current model type: <*ODE*> DAE
 ODE model allows any method
 DAE model allows implicit fixed step or daspk

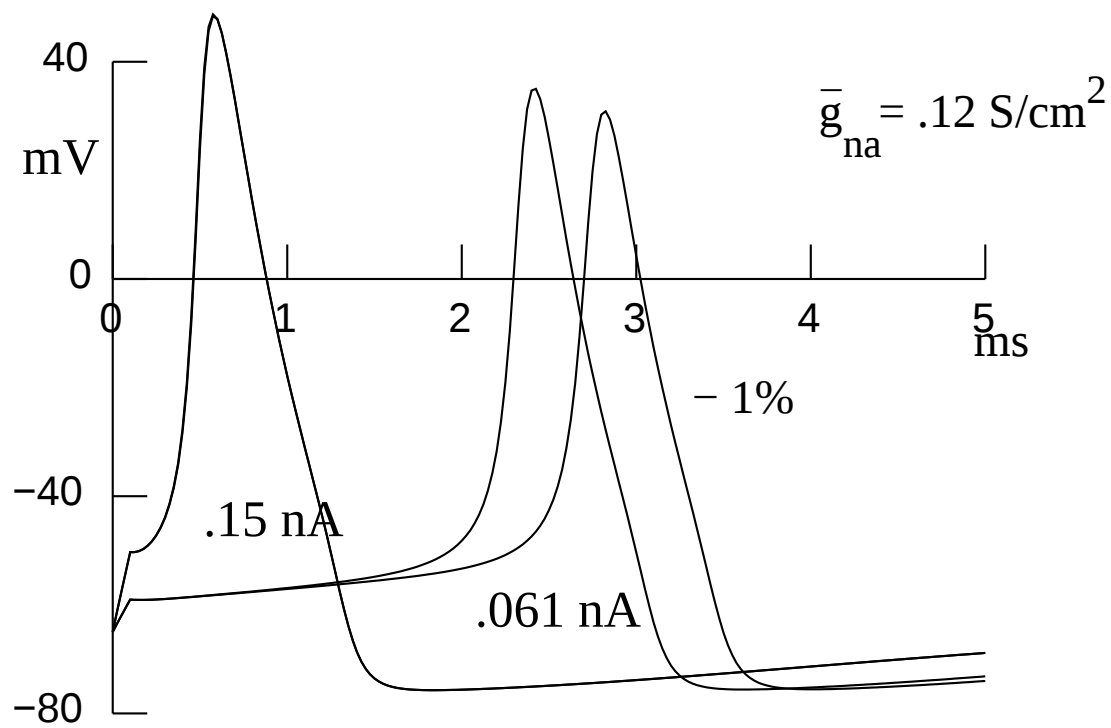
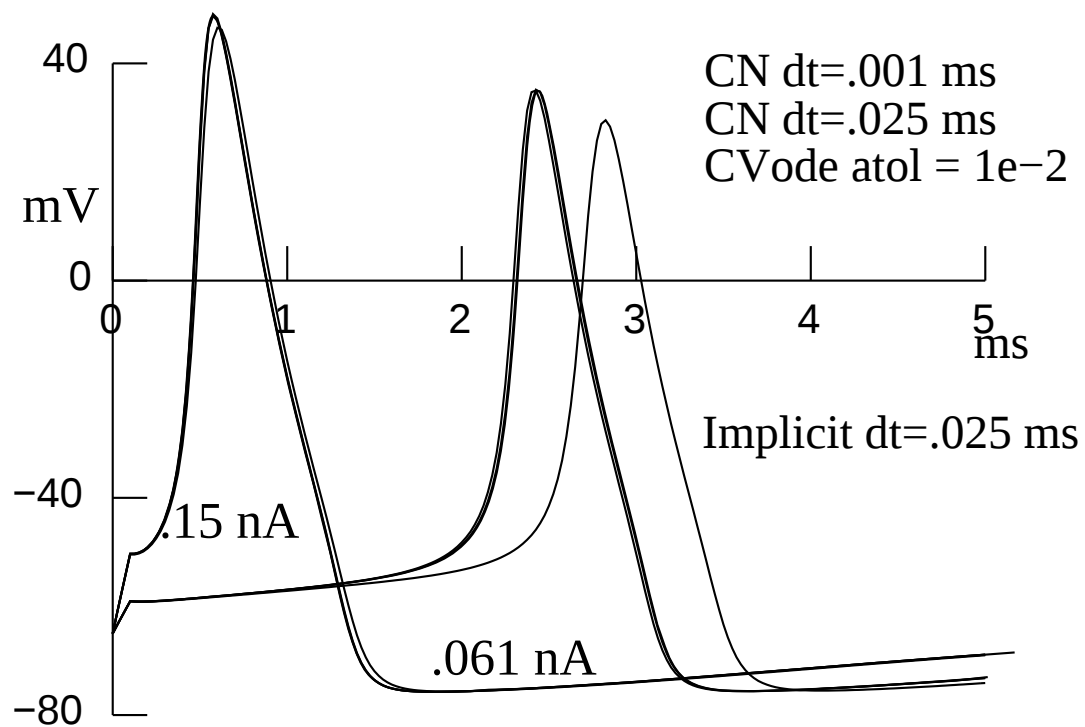
☐ Implicit Fixed Step
☐ C-NFixedStep
☒ Cvode
☐ Daspk
☐ Local step

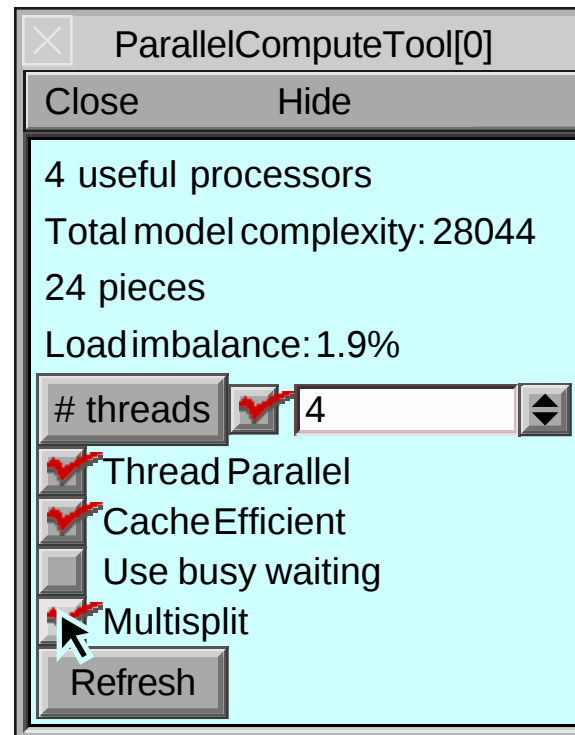
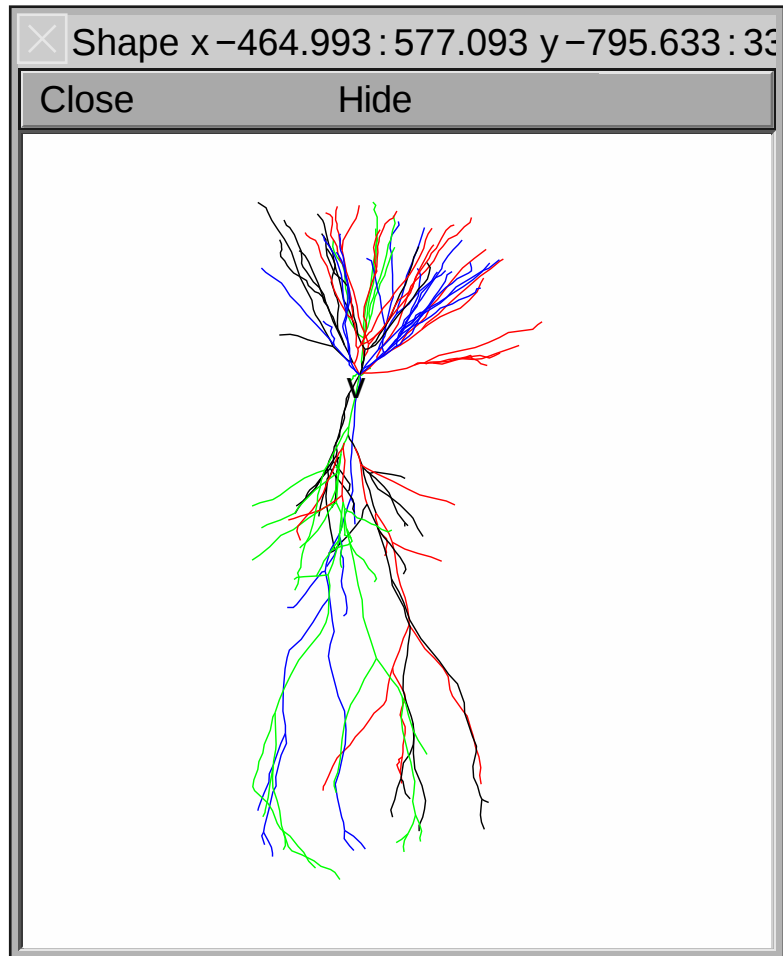
DAE and daspk require sparse solver, cvode requires tree solver

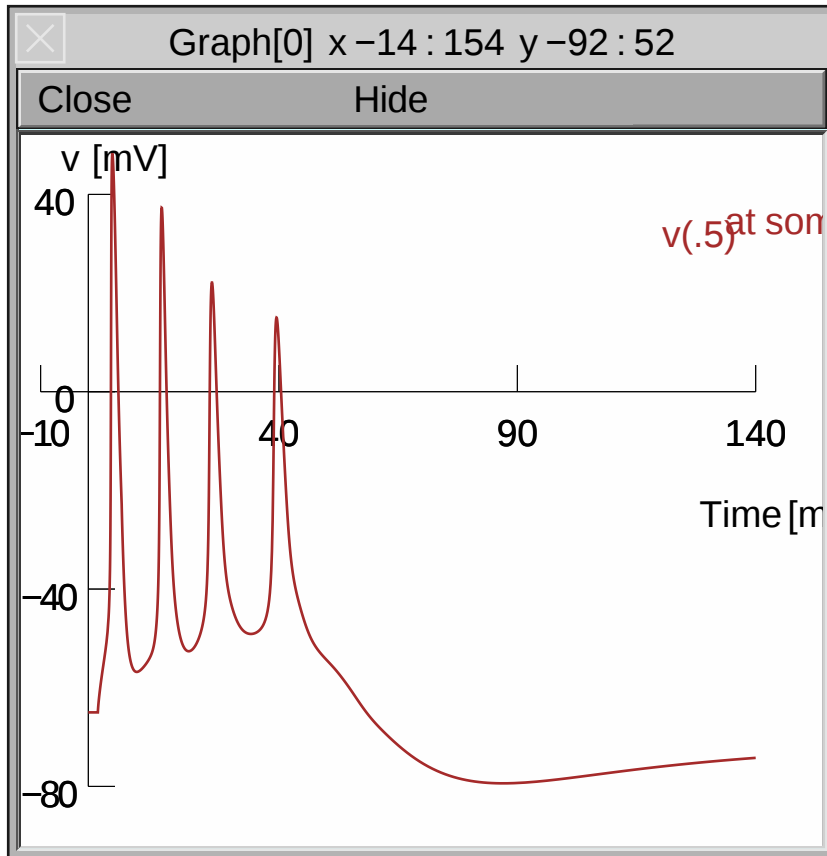
☒ Mx=b tree solver
☐ Mx=b sparse solver

☐ 2nd order threshold (for variable step)









RunControl

Close Hide

Init (mV) ← -65

Init & Run

Stop

Continue til (ms) ← 5

Continue for (ms) ← 1

Single Step

t (ms) 140

Tstop (ms) 140

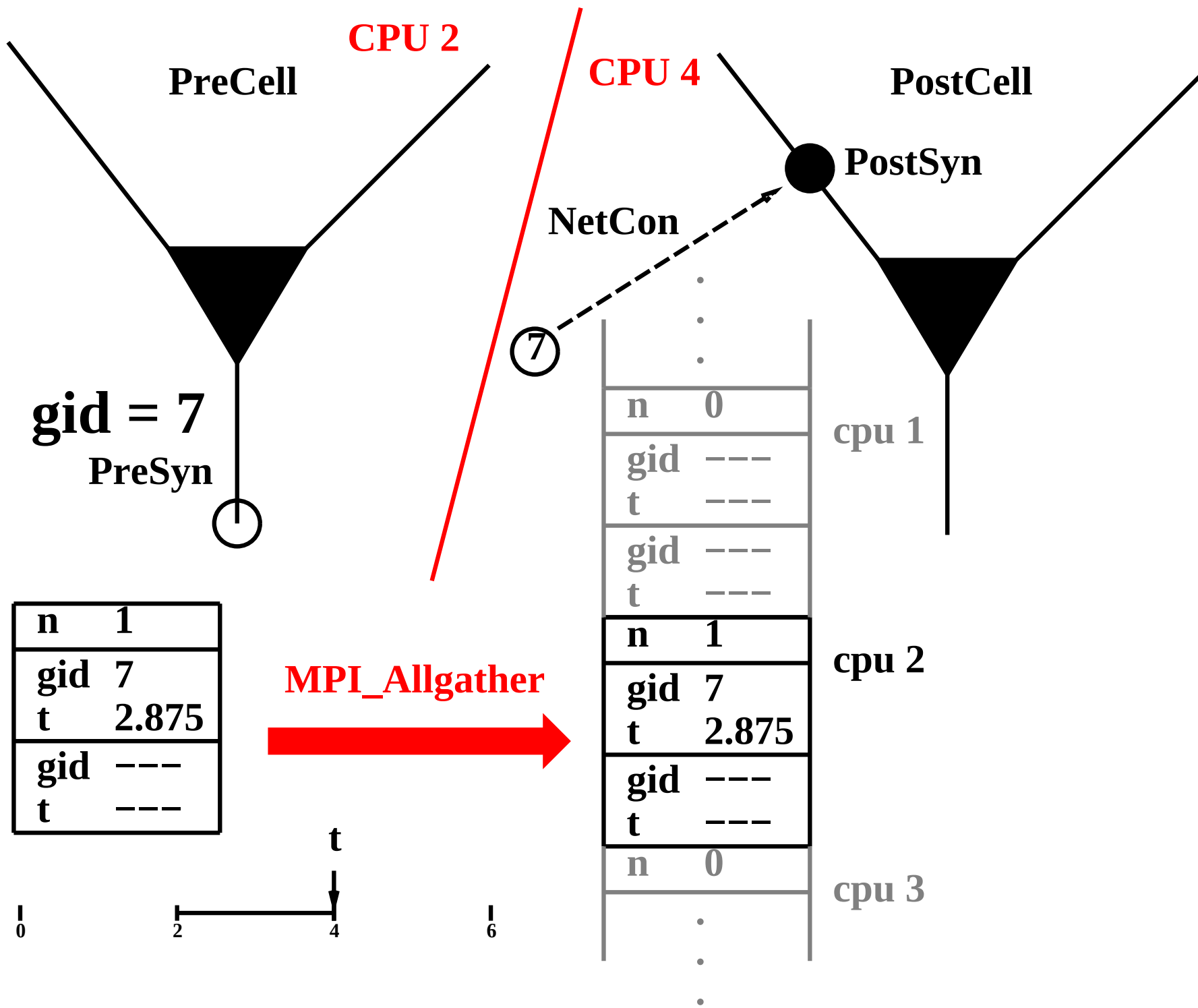
dt (ms) ✓ 2.3008

Points plotted/ms 40

Scrn update invl (s) 0.05

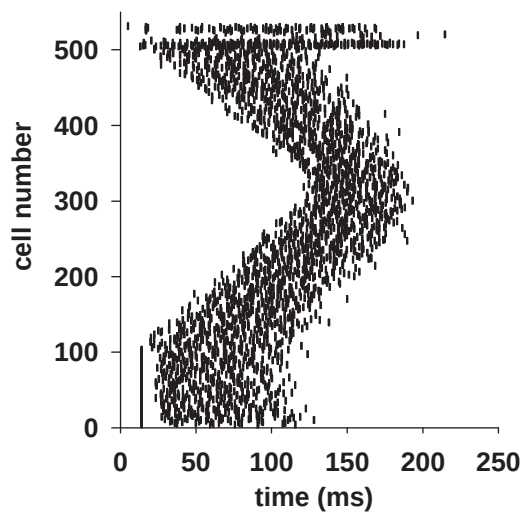
Real Time (s) 9.77

instead of 35.4s

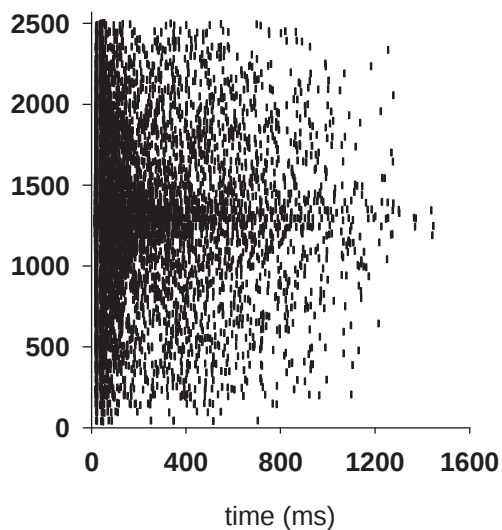


Migliore et al (2006) J. Comput. Neurosci. 21(2):119

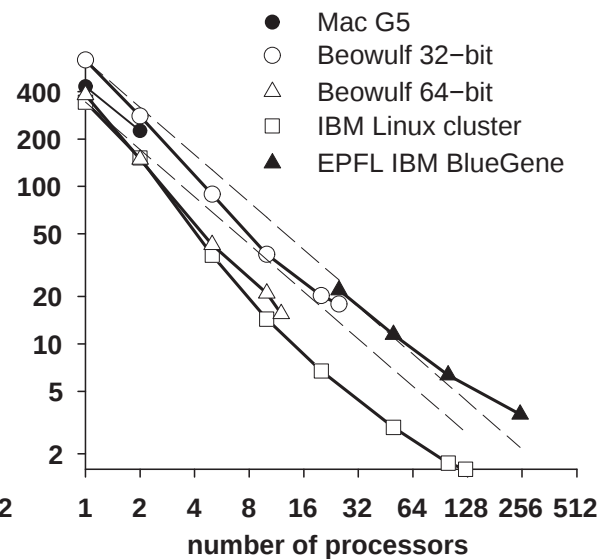
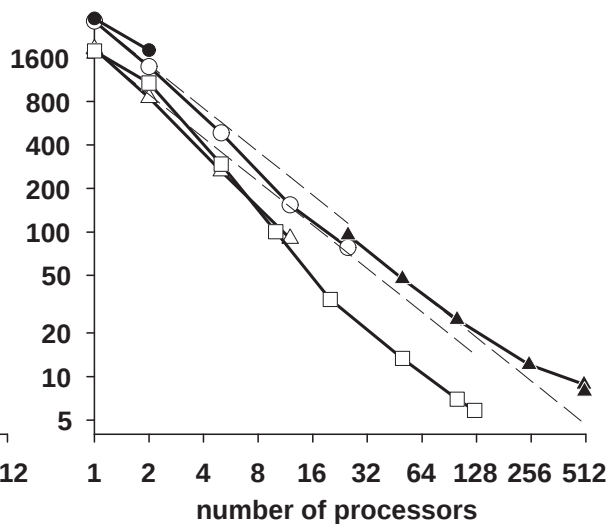
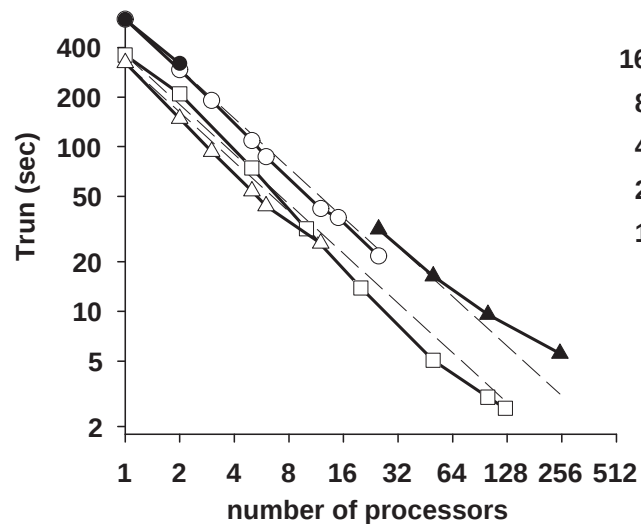
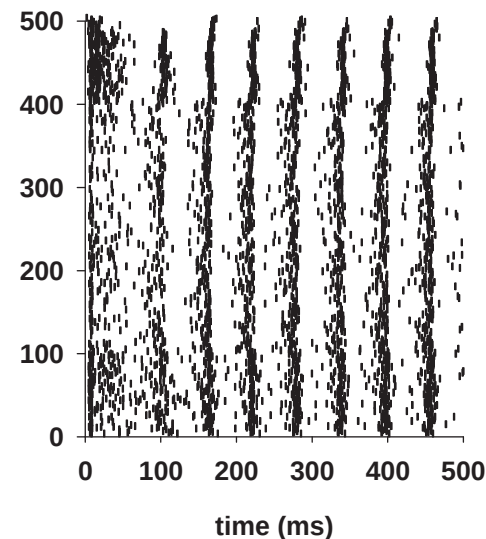
Santhakumar et al. (2005)



Davison et al., (2003)



Bush et al., (1999)



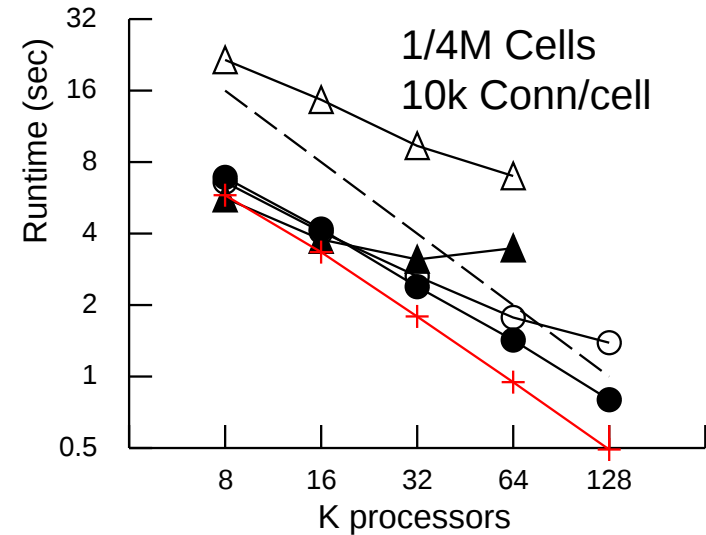
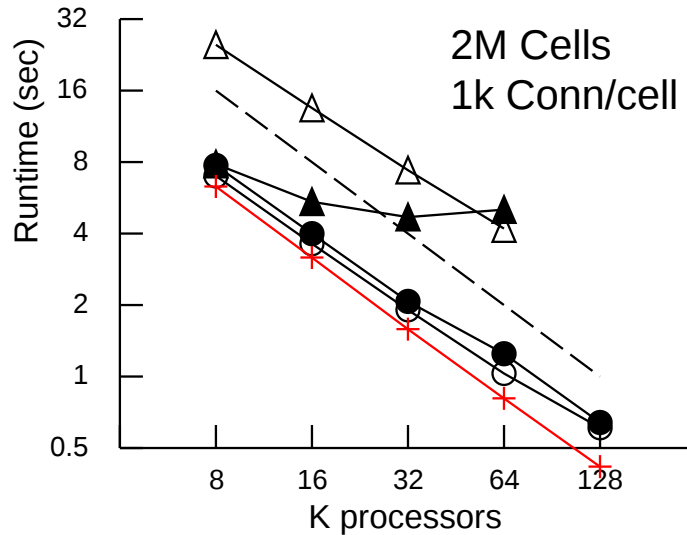
Artificial Spiking Net

Blue Gene/P

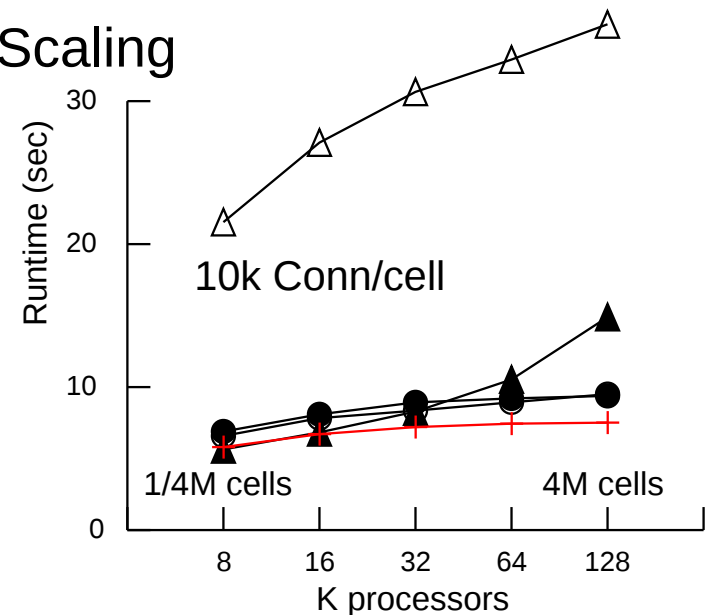
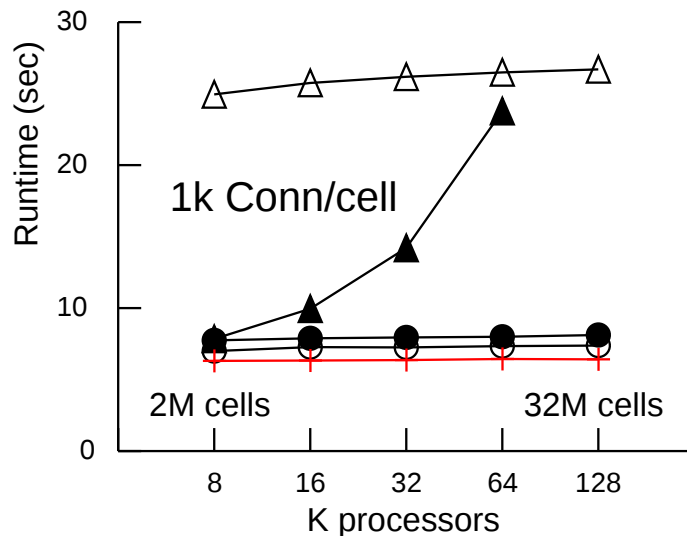
Argonne National Lab

- △ MPI_Send – Two Phase, Two Subinterval
- ▲ Allgather
- DCMF_Multicast – Two Phase, Two Subinterval
- Record-Replay – One Subinterval
- + Computation Time (includes queue)

Strong Scaling



Weak Scaling



Using:

Building

Running

Analysing

Building a Cell

Shape

- Draw stylized

- Import 3-d reconstructions

Channel Distribution

- Density

 - Homogeneous

 - Inhomogeneous

- ...over...

 - Whole cell

 - Regions

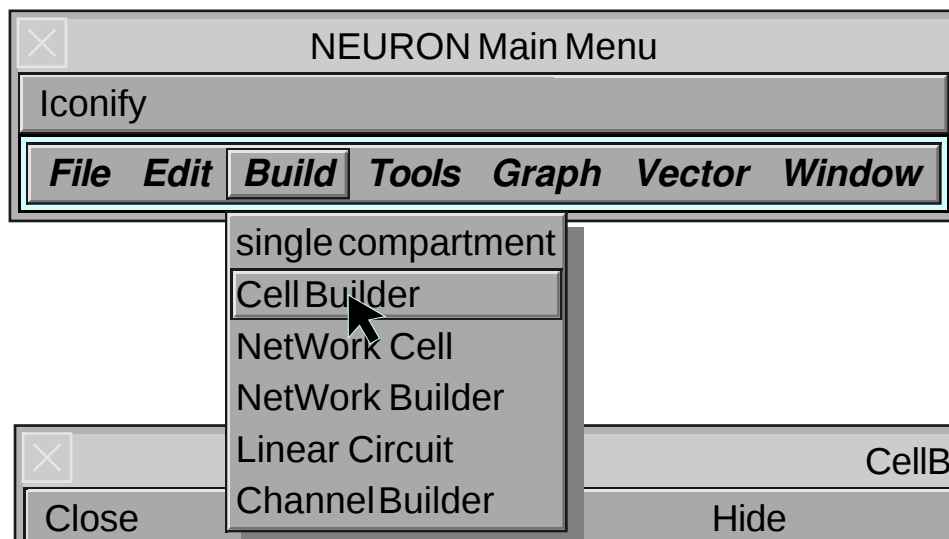
 - Individual sections

Creation

- Single cell

- Class for use in Network

Starting from scratch



Topology refers to section names, connections, and 2d orientation without regard to section length or diameter.

Short sections are represented in that tool as circles, longer ones as lines.

Subsets allows one to define named section subsets as functional groups for the purpose of specifying membrane properties.

Geometry refers to specification of L and diam (microns), and nseg for each section (or subset) in the topology of the cell.

Biophysics is used to insert membrane density mechanisms and specify their parameters.

Management specifies how to actually bring the cell into existence for simulation.

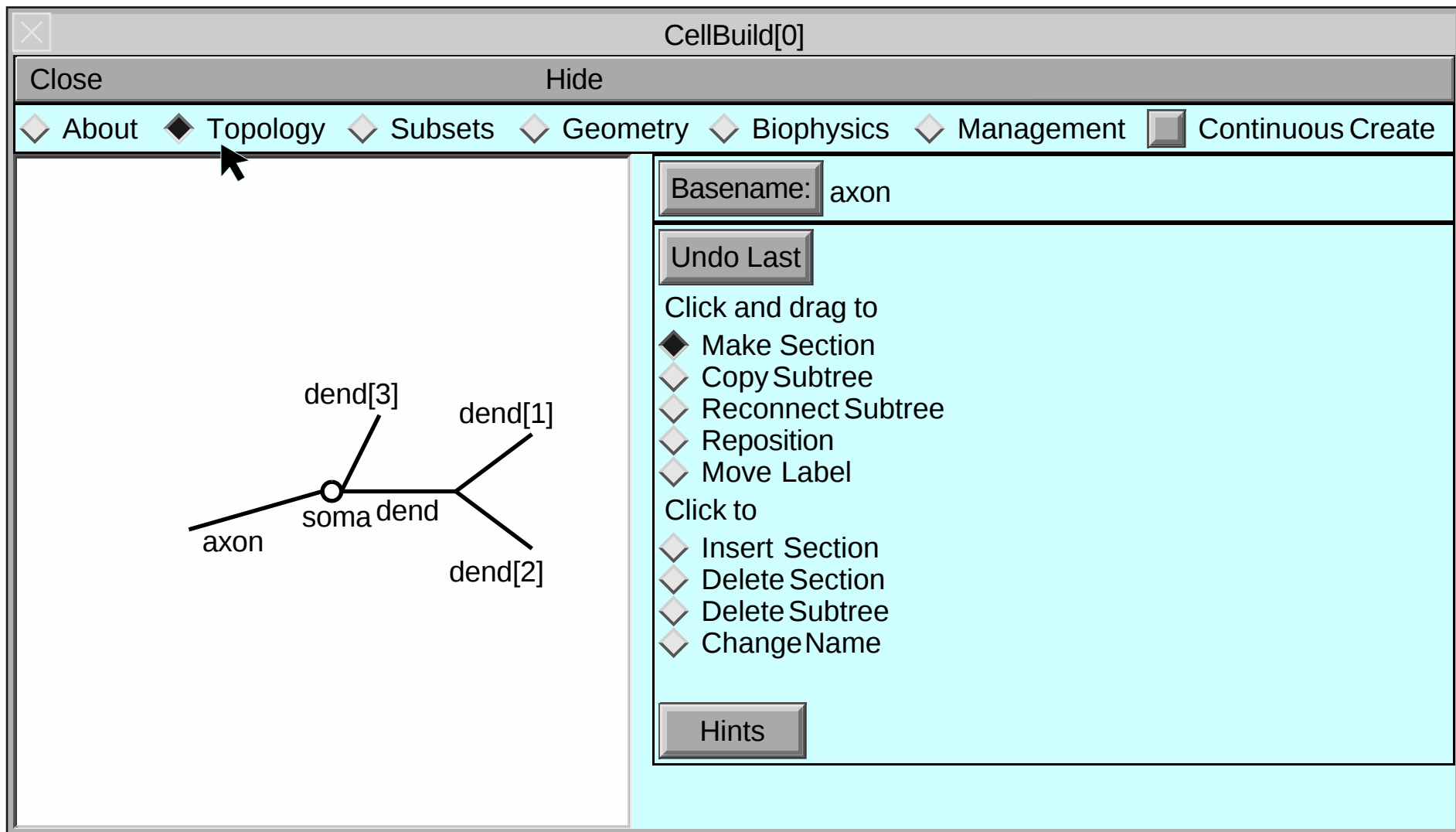
The default is to first build the entire cell and export it to the top level

Or else specify it as a cell type for use in networks,

It also allows you to import the existing top level cell into this builder for modification.

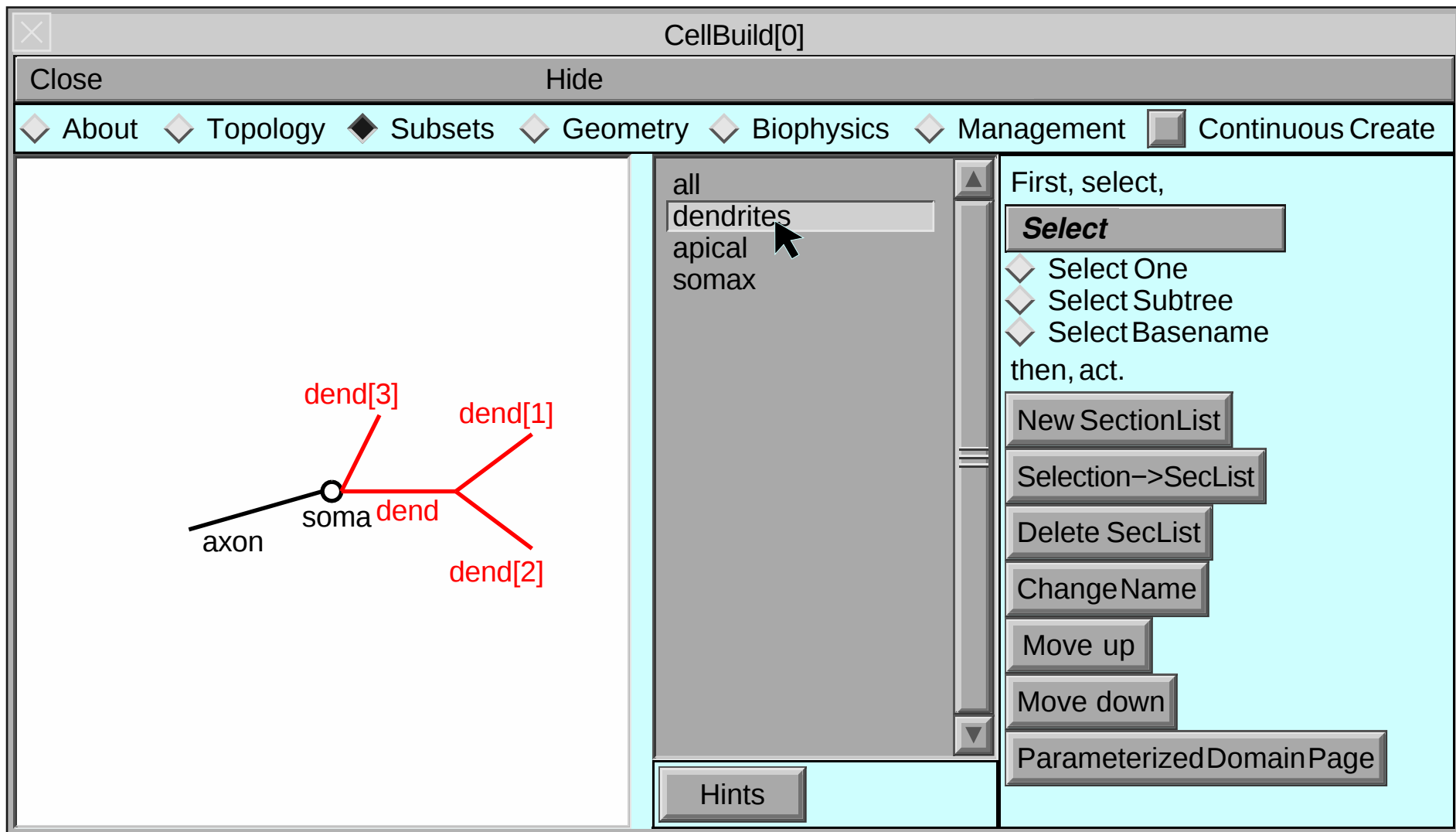
If "Continuous Create" is checked, the spec is continuously instantiated at the top level as it is changed.

Topology defines section names and connectivity.

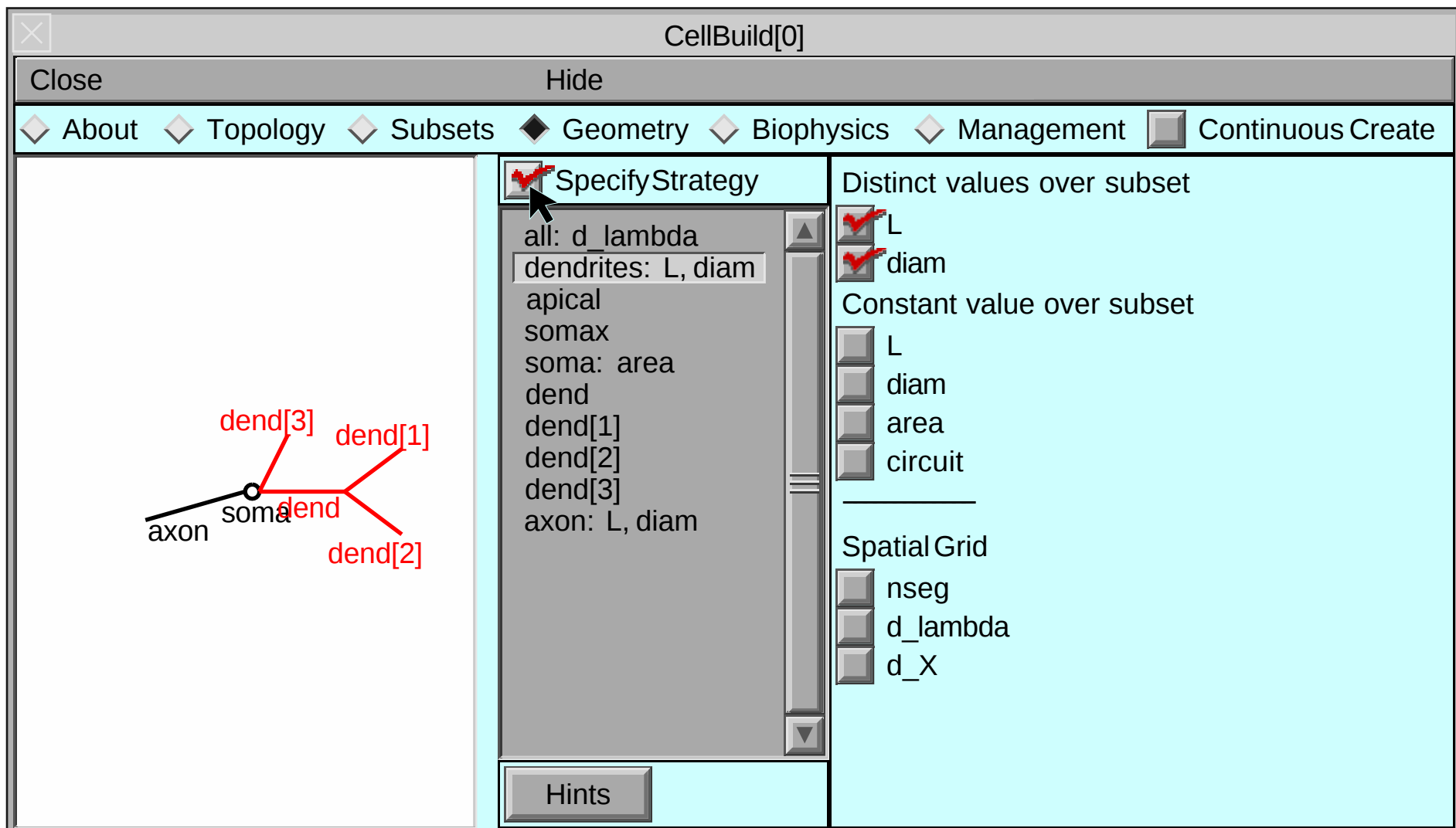


Cell subsets help to concisely specify membrane properties.

Constant and Inhomogenous distributions



Geometry is where Length, Diameter, and spatial discretization are specified.



Good strategy



Concise Spec

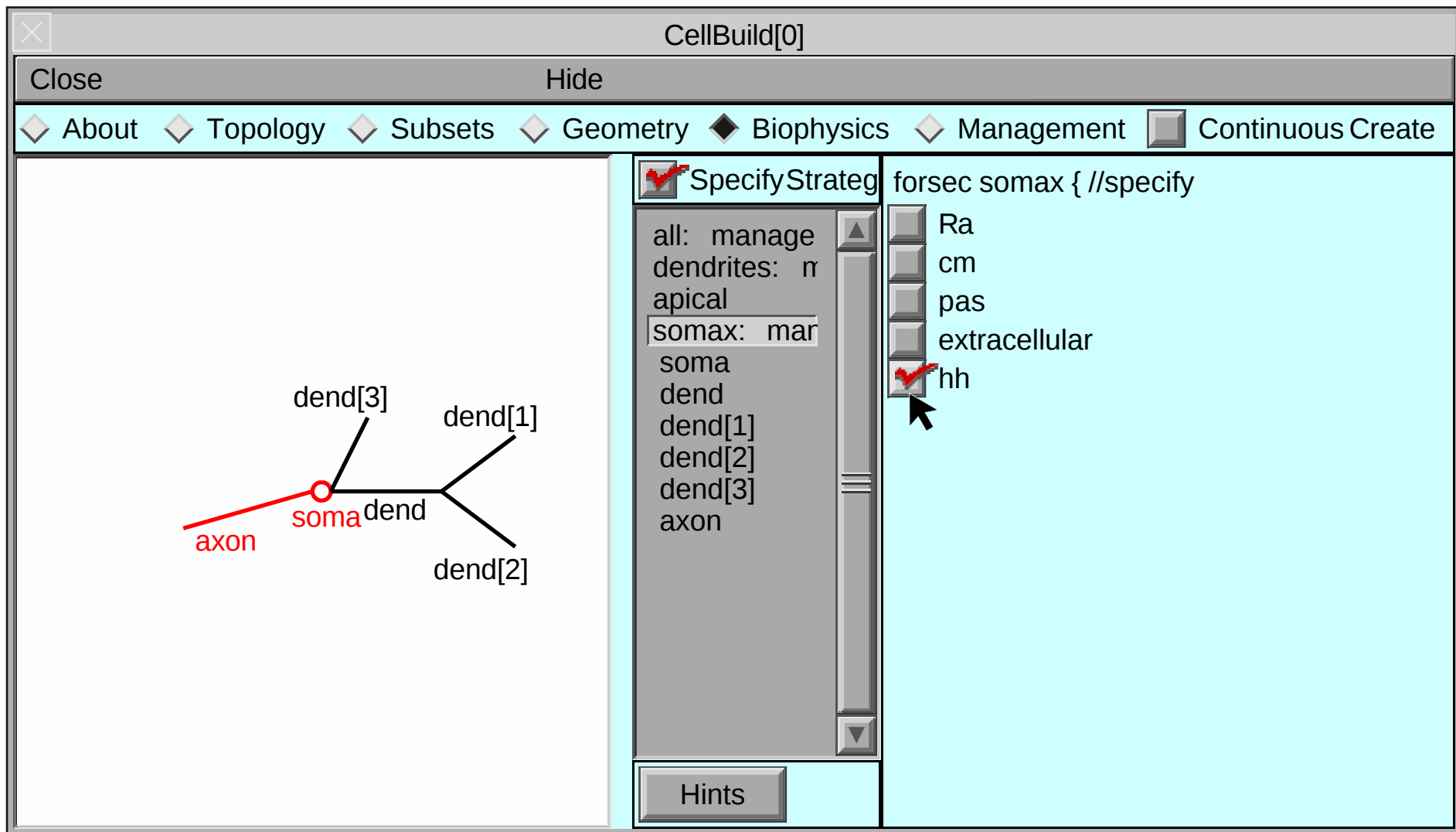
```
oc>topology()  
|-| soma(0-1)  
  '----| dend[0](0-1)  
        '----| dend[1](0-1)  
        '----| dend[2](0-1)  
          '---| dend[3](0-1)  
          '-----| axon(0-1)
```

Note: Compartmentalization based on medium frequency space constant is always a good idea.

The screenshot shows the CellBuild[0] software interface. The main window has a title bar "CellBuild[0]" and a menu bar with "Close" and "Hide". Below the menu bar is a toolbar with buttons for "About", "Topology", "Subsets", "Geometry", "Biophysics", "Management", and "Continuous Create". The "Geometry" button is selected. The main area is divided into two panes. The left pane shows a diagram of a compartmental model with a central node labeled "soma" and four branches labeled "axon", "dend[1]", "dend[2]", and "dend[3]". The right pane shows a "SpecifyStrategy" dialog box with a list of compartments: "all: d_lambda", "dendrites: L, diam", "soma: area", and "axon: L, diam". Below the list is a "Hints" button. The right pane also contains a code editor with the following text:

```
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  
}
```

Sprinkling channels onto the cell begins with a strategy.



... and ends by specifying a few parameters as constant over a few subsets.

(Inhomogeneities are a bit more complicated)

CellBuild[0]

Close Hide

◇ About ◇ Topology ◇ Subsets ◇ Geometry ◆ Biophysics ◇ Management □ Continuous Create

SpecifyStrategy

all
Ra
cm
dendrites
pas
soma
hh

forsec somax { insert hh

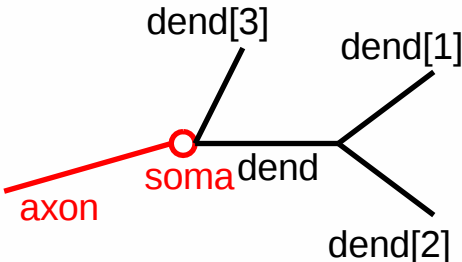
gnabar_hh (S/cm2) 0.12

gkbar_hh (S/cm2) 0.036

gl_hh (S/cm2) 0.0003

el_hh (mV) -54.3

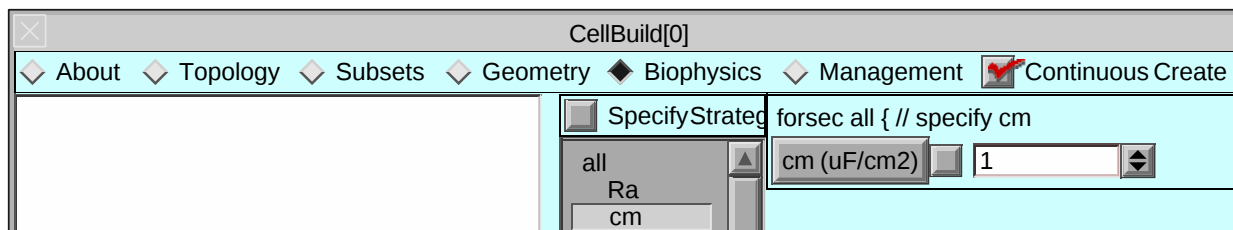
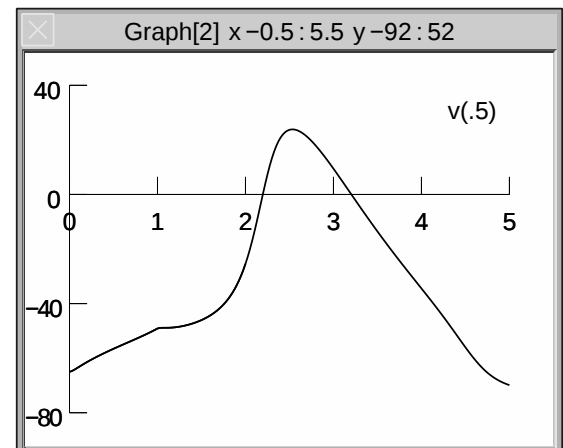
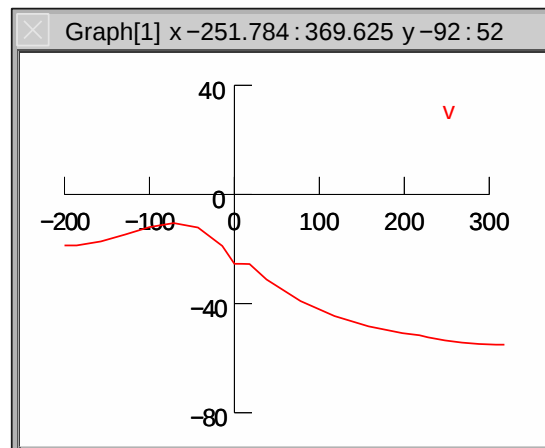
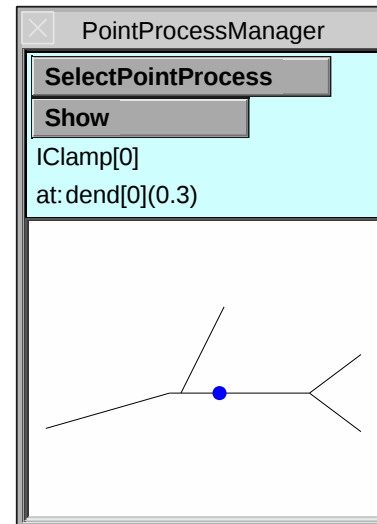
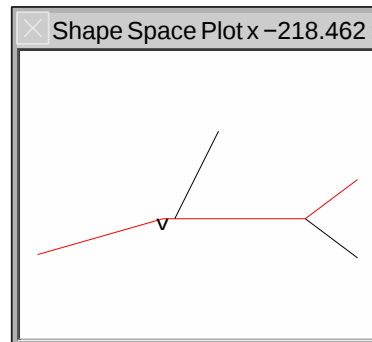
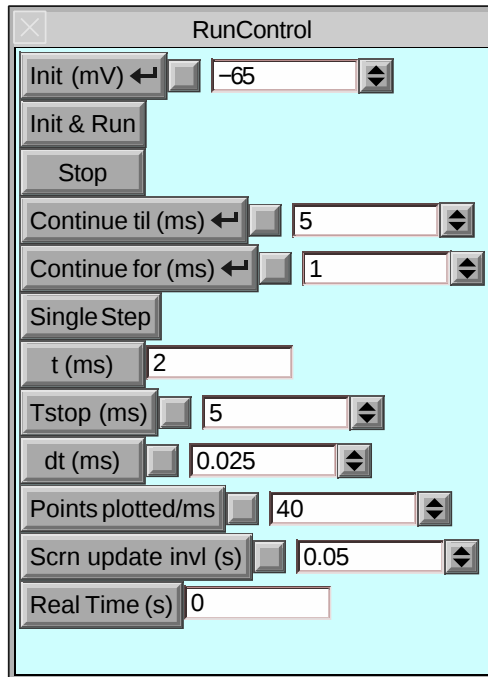
Hints



The diagram shows a neuron model structure. A central soma is connected to an axon (highlighted in red) and three dendrites labeled dend[1], dend[2], and dend[3]. The axon is labeled 'axon' and the soma is labeled 'soma'.

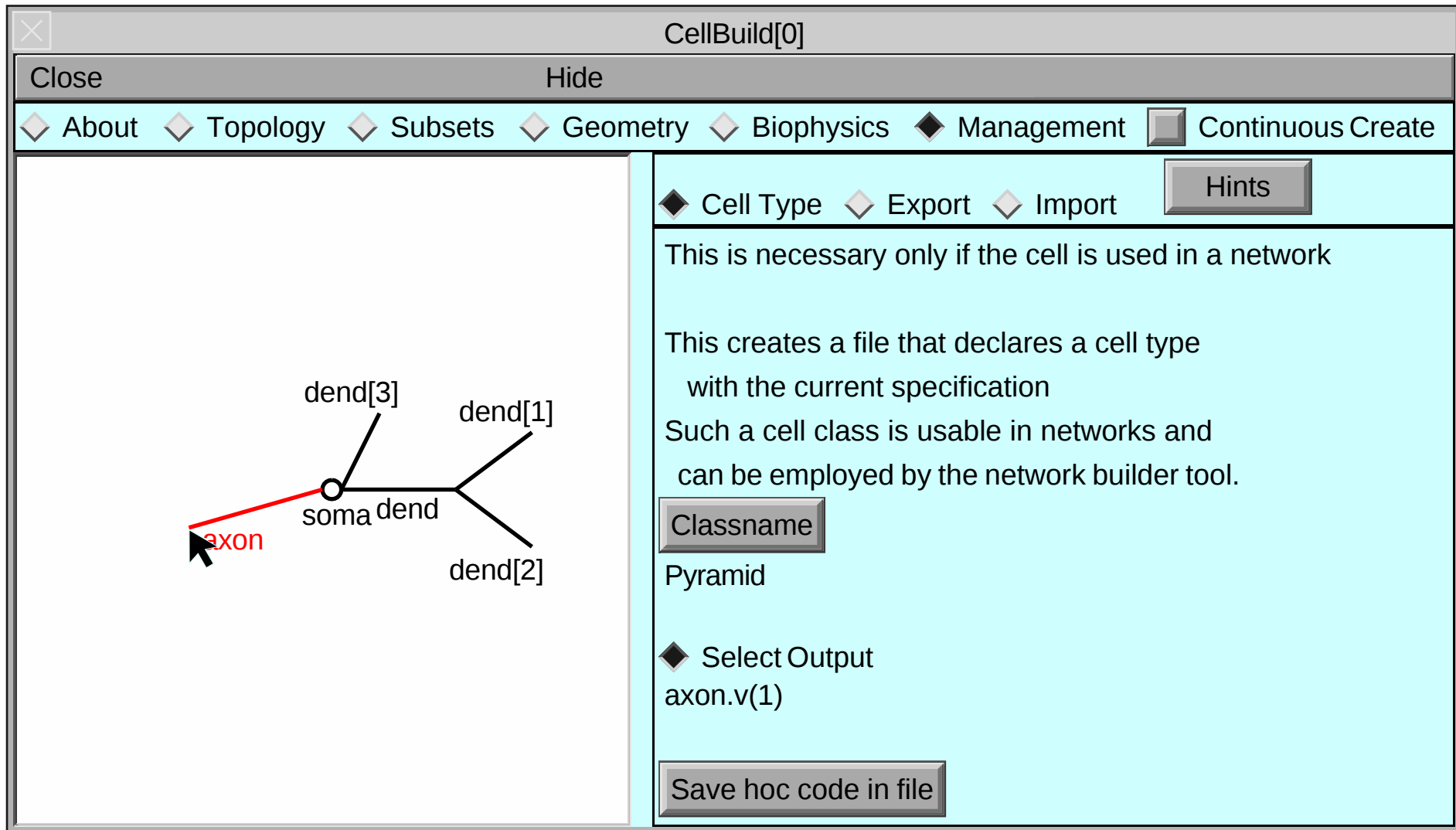
The cell comes into existence when "Continuous Create" is turned on.

(Windows derive from NEURONMainMenu "Tools" and "Graph".)



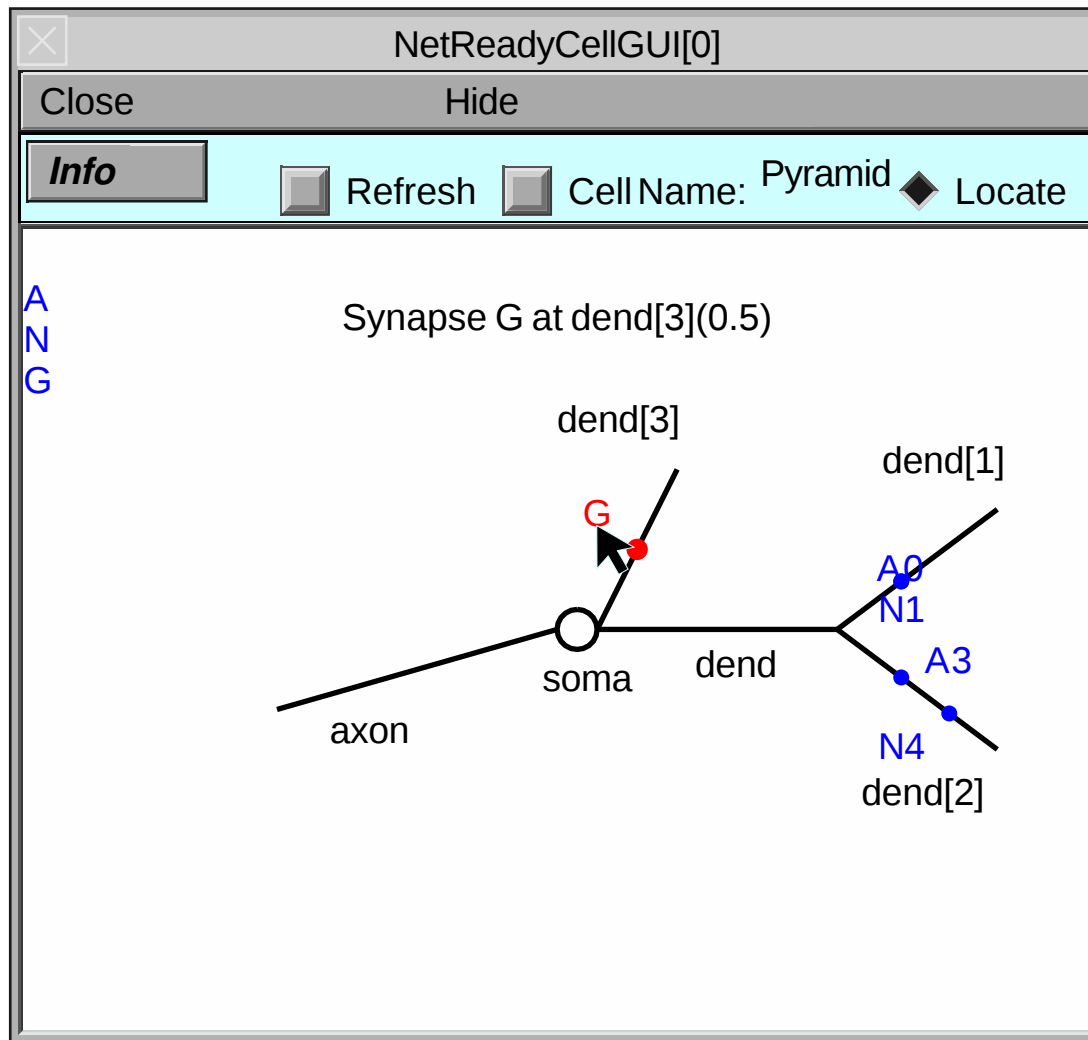
Using the cell in a network takes three steps.

- 1) Encapsulate in class so many cells can be created with the same type.
- 2) Specify the location of the output spike detector.



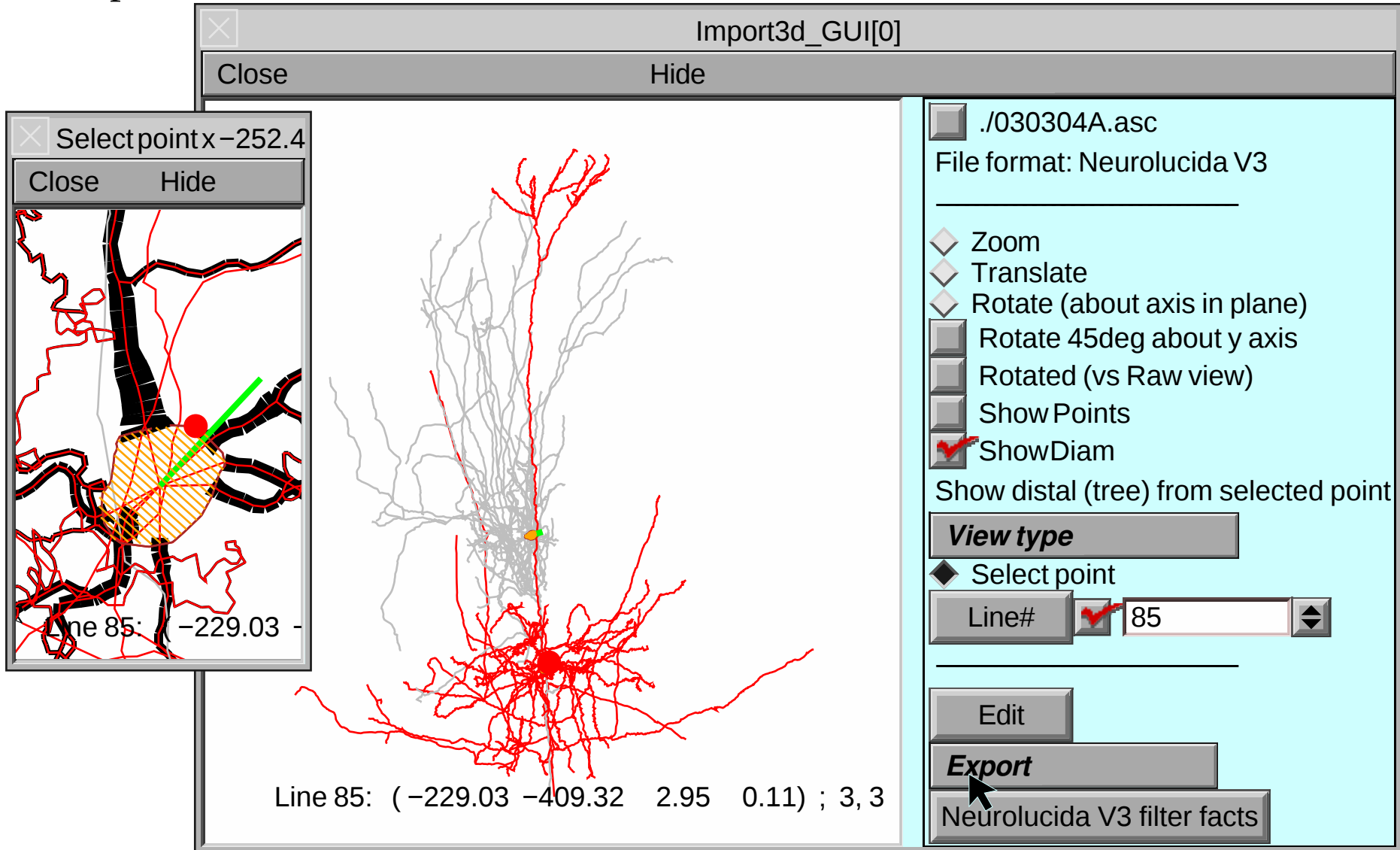
A NetworkReadyCell needs to be able to send and receive spikes.

3) Sprinkle synapses that can receive input spikes.



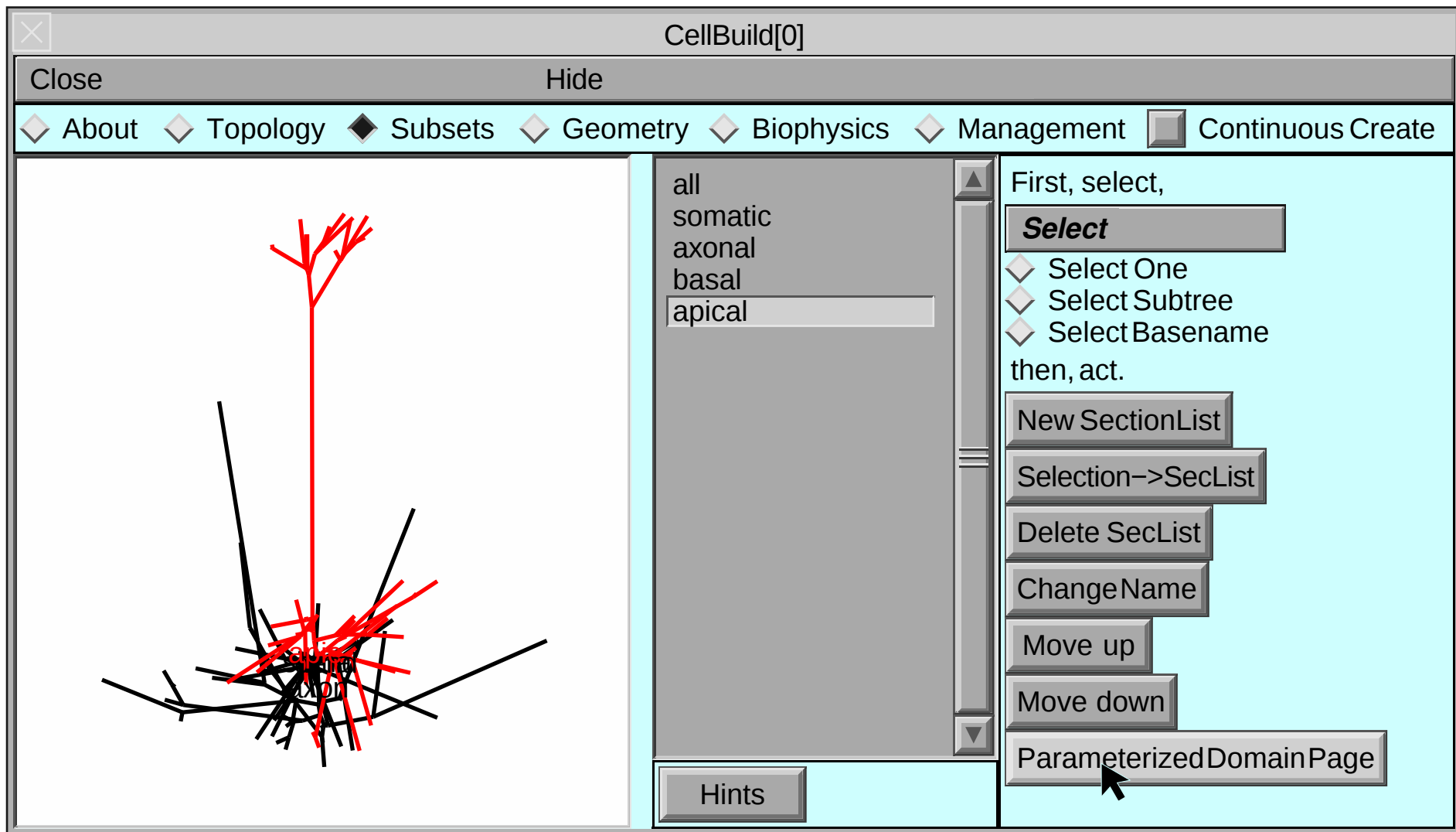
Starting from a 3-D Reconstruction.

Use NEURONMainMenu/Tools/Miscellaneous/Import3D.
Export to Cell Builder.



Import3D export to CellBuild—automatically gives Topology, Geometry, and some Subsets.

But don't forget to compartmentalize with dlambda.



Inhomogeneous parameters.

$$\text{gnabar_hh}(\text{location}) = f(p(\text{location}))$$

p: subset domain parameter

path distance from soma

physical distance along line

physical distance from point

normalized distance

closest point is 0

farthest point is 1

The subset domain parameter defines a value at every location on the subset.

CellBuild[0]

Close

Hide

About

Topology

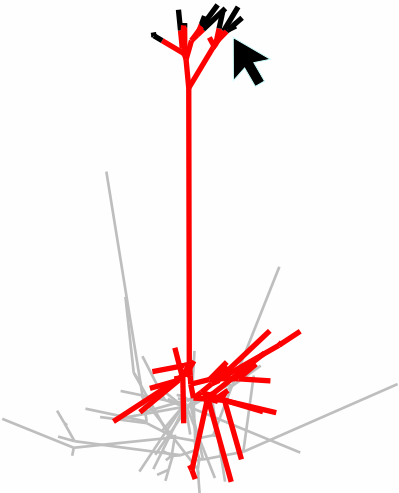
Subsets

Geometry

Biophysics

Management

Continuous Create



$p=0.902366$
apic[32] (0.880567)

all
somatic
axonal
basal
apical
apical_x

Hints

ParameterizedDomainSpecification

Return to Subset Selection Page

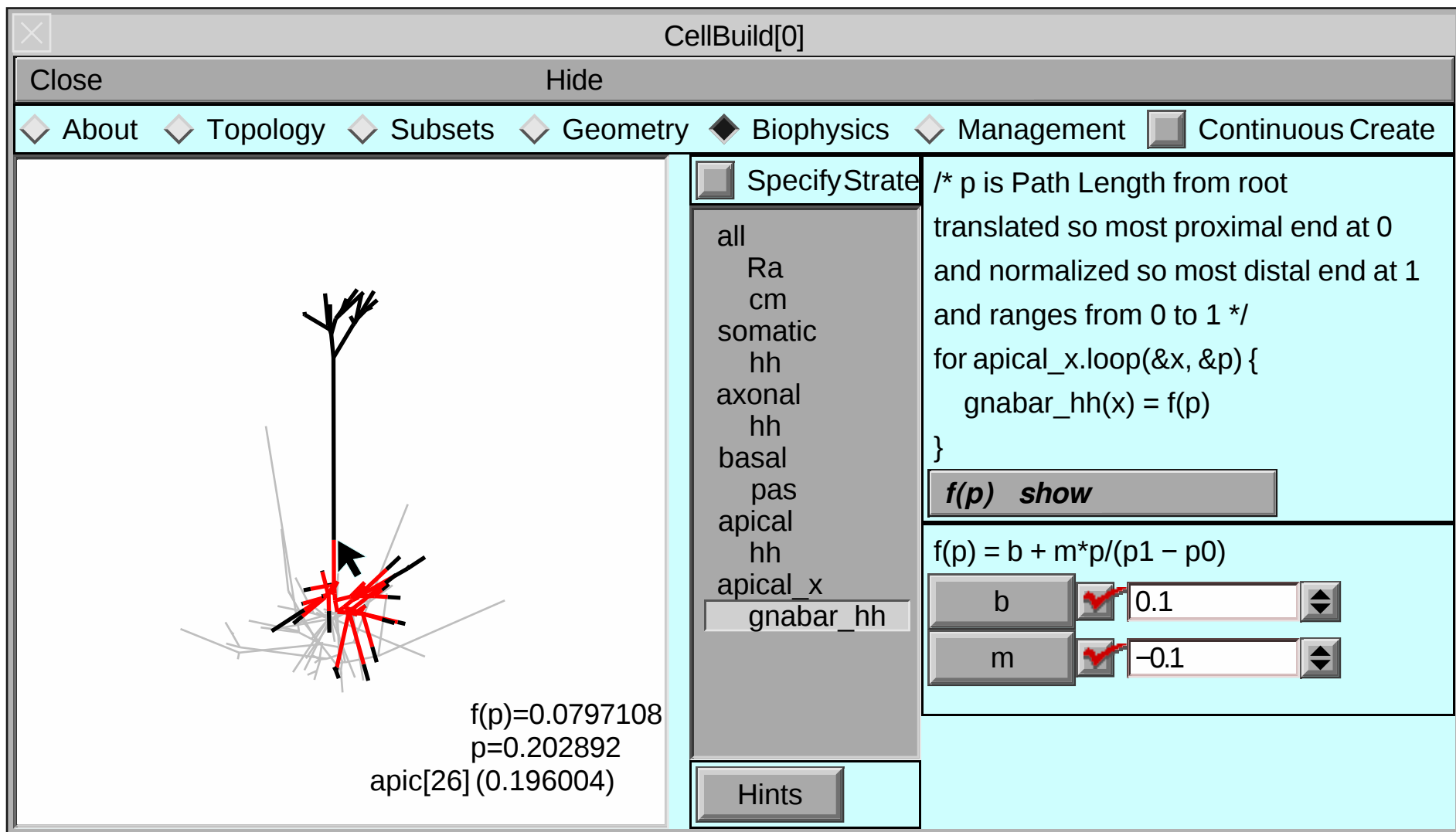
Path Length from root
translated so most proximal end at 0
and normalized so most distal end at 1
ranges from 0 to 1

Show domain value

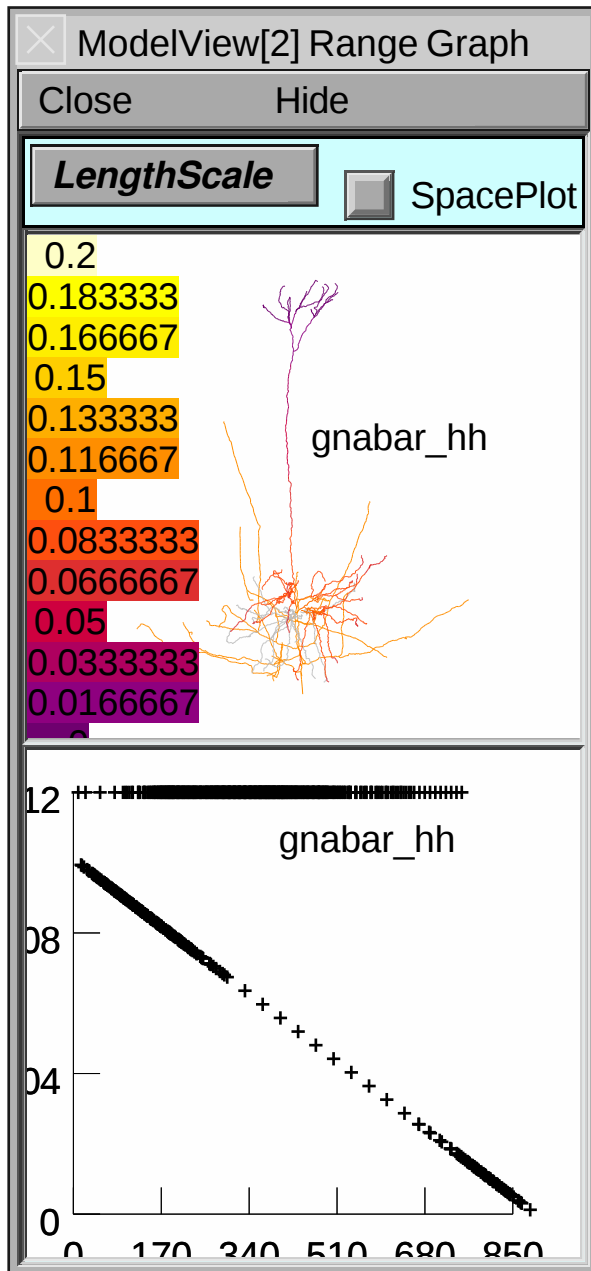
metric proximal distal

Remove

...and arbitrary functions of that parameter can be used to specify a range variable.



It's always a good idea to check that expectations are met.



ModelView[2]

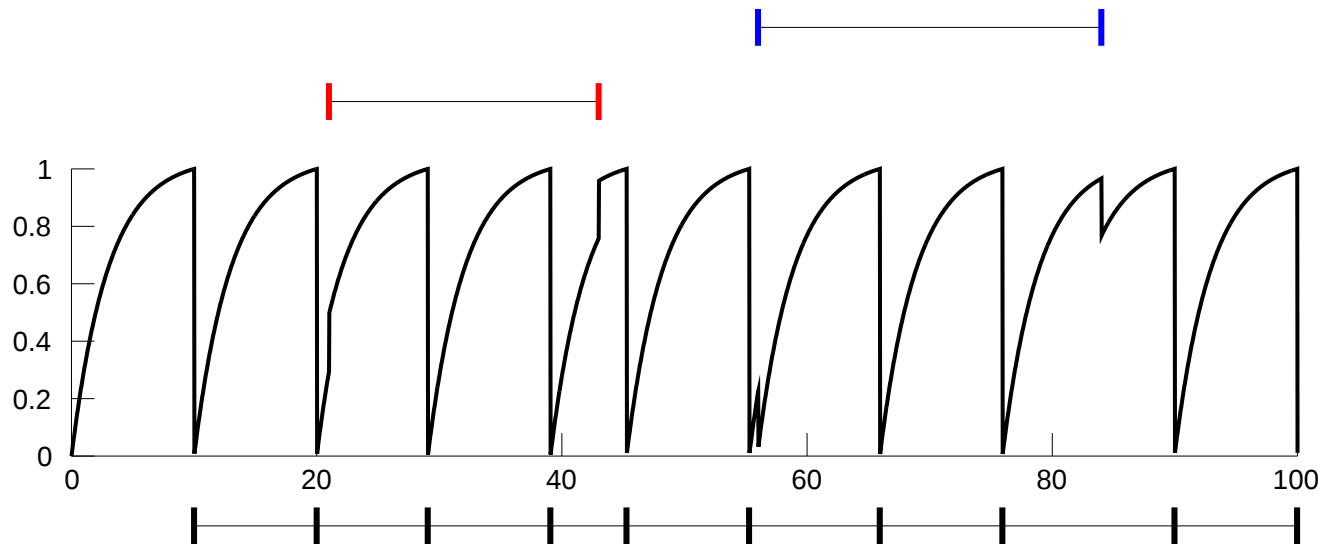
Close Hide

File

167 sections; 945 segments

- * 1 real cells
 - * root soma
 - 167 sections; 945 segments
 - * 15 distinct values of nseg
 - * 6 inserted mechanisms
 - Ra = 80
 - cm = 1
 - * pas
 - ena = 50
 - ek = -77
 - * hh
 - * 80 gnabar_hh
 - 80 or more distinct values
 - gkbar_hh = 0.036
 - gl_hh = 0.0003
 - el_hh = -54.3
- * 4 subsets with constant parameters
- * 79 sections with unique parameters

Networks (Inhibitory Synchronization).

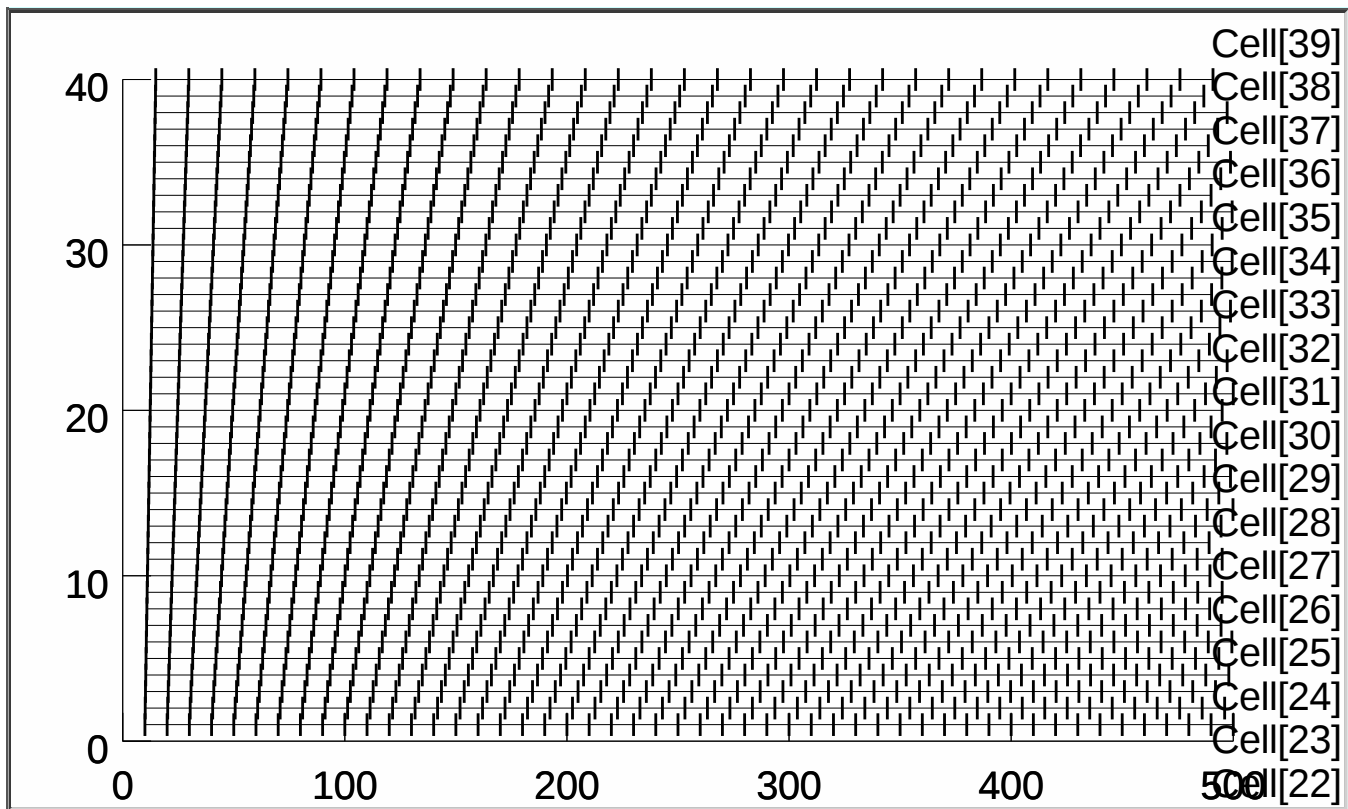


```
: dm/dt = (minf - m)/tau
: input event adds w to m
: when m = 1, or event
:   makes m >= 1, cell fires
: minf is calculated so
:   that the natural interval
:   between spikes is invl
```

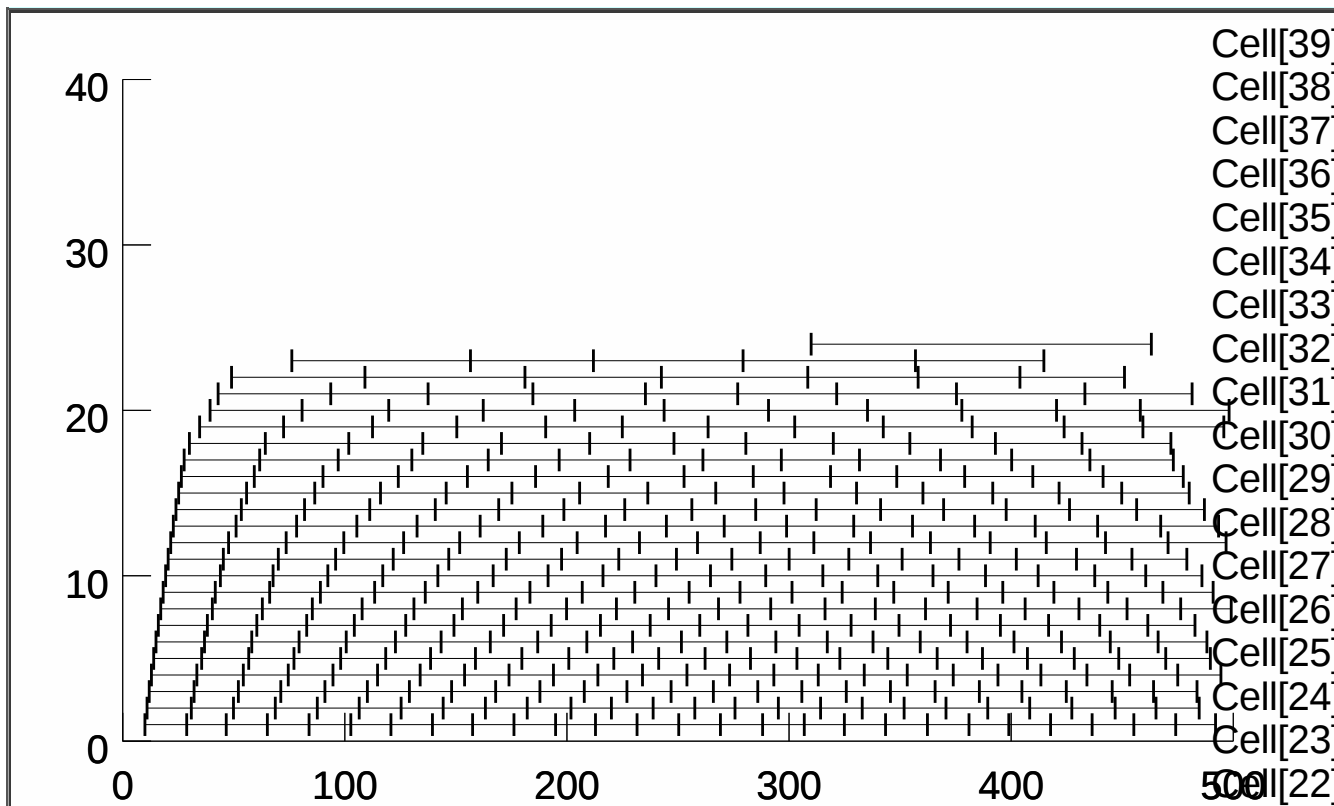
```
INITIAL {
  minf = 1/(1 - exp(-invl/tau))
  m = 0
  t0 = t
  net_send(firetime(), 1)
}
```

```
NET_RECEIVE (w) {
  m = minf + (m - minf)*exp(-(t - t0)/tau)
  t0 = t
  if (flag == 0) {
    m = m + w
    if (m > 1) {
      m = 0
      net_event(t)
    }
    net_move(t+firetime())
  }else{
    net_event(t)
    m = 0
    net_send(firetime(), 1)
  }
}
```

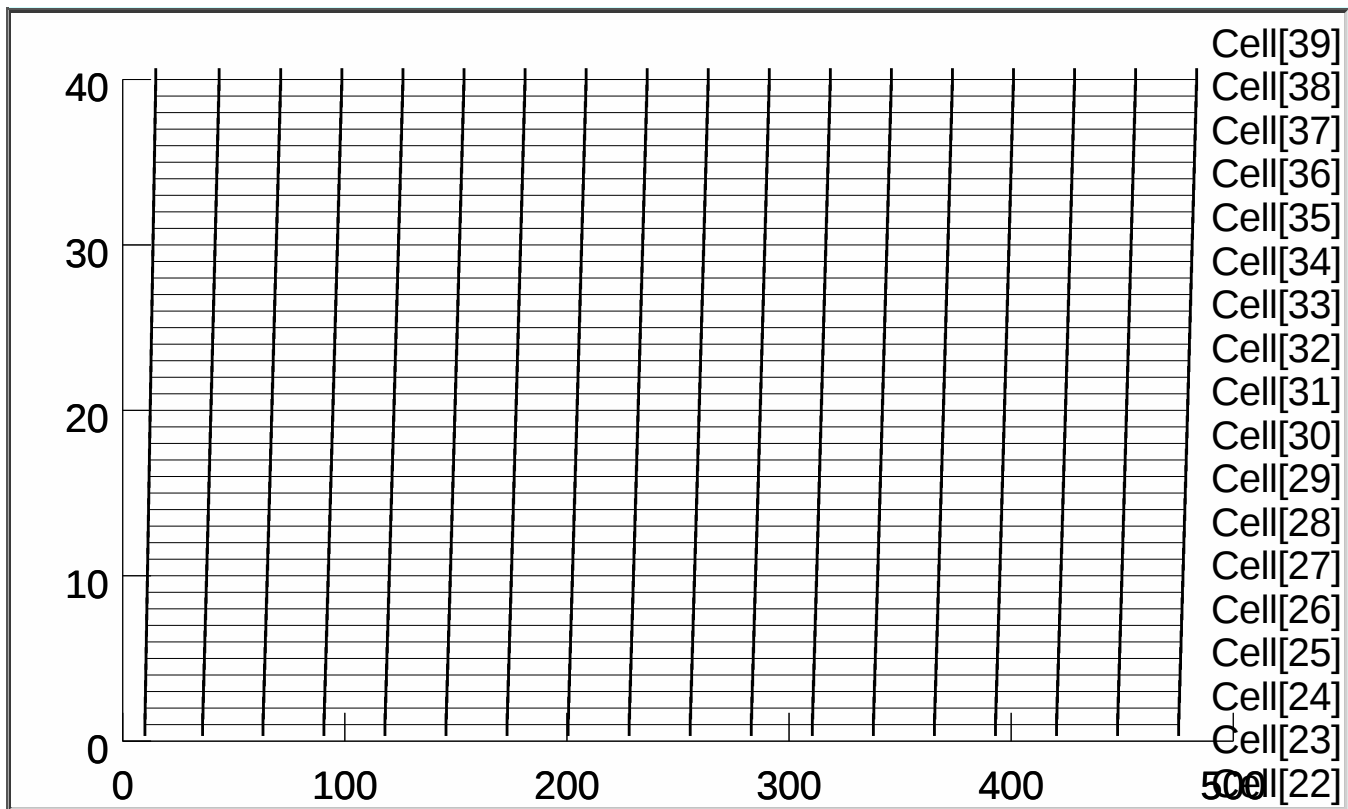
```
FUNCTION firetime() { : m < 1 < minf
  firetime = tau*log((minf-m)/(minf - 1))
}
```



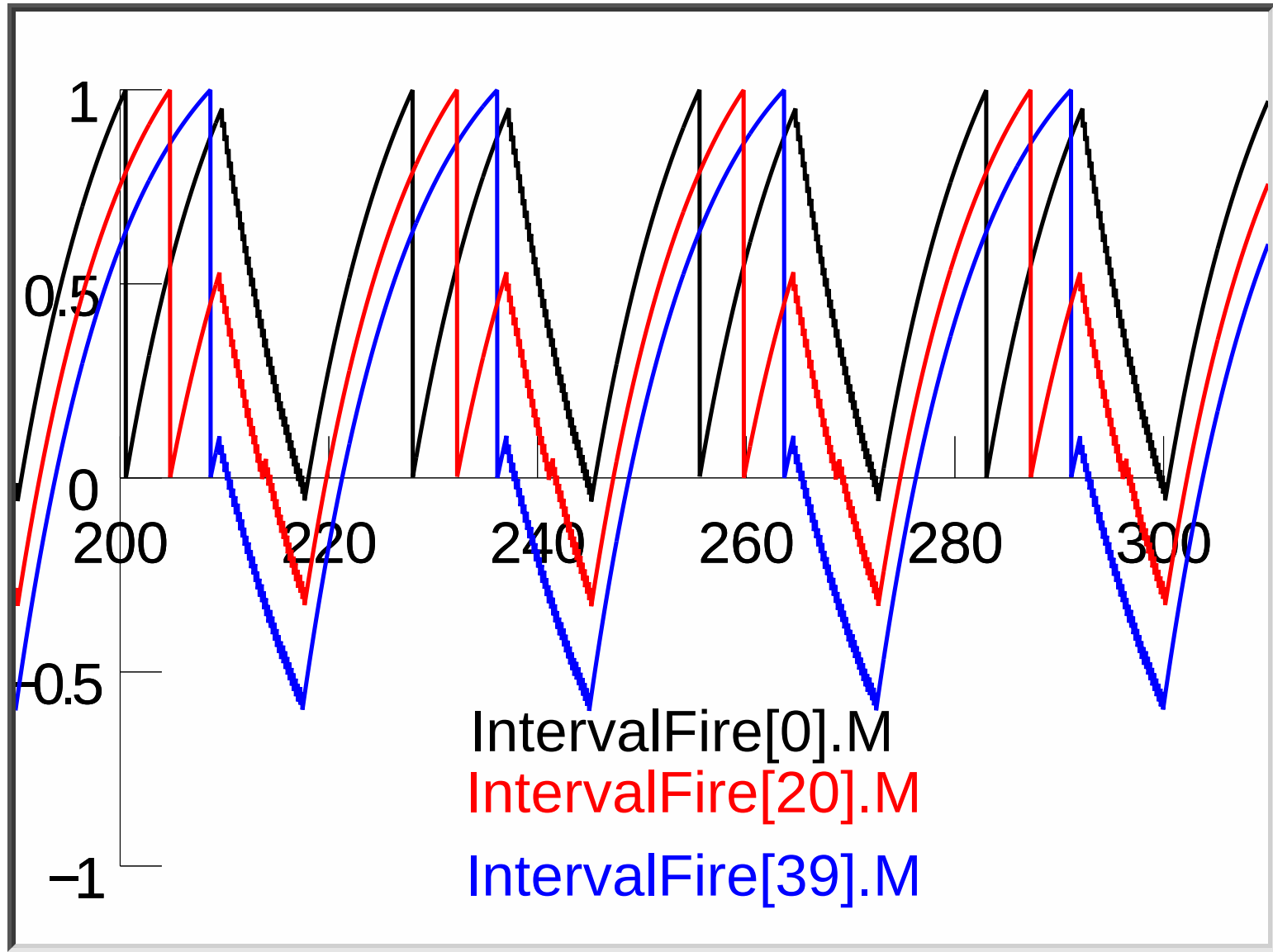
Number of all to all cells	☐	40	◀▶
All to all connection weight	☒	0	◀▶
Delay (ms)	☒	0	◀▶
Cell time constant (ms)	☐	10	◀▶
Lowest natural interval	☐	10	◀▶
Highest natural interval	☐	15	◀▶



Number of all to all cells	40
All to all connection weight	-0.05
Delay (ms)	☒ 0
Cell time constant (ms)	10
Lowest natural interval	10
Highest natural interval	15



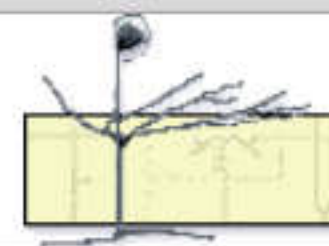
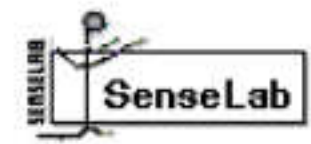
Number of all to all cells	40
All to all connection weight	-0.05
Delay (ms)	9
Cell time constant (ms)	10
Lowest natural interval	10
Highest natural interval	15



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ModelDB provides an accessible location for storing and efficiently retrieving computational neuroscience models. ModelDB is tightly coupled with [NeuronDB](#). Models can be coded in any language for any environment. Model code can be viewed before downloading and browsers can be set to auto-launch the models. For further information, see [model sharing in general](#) and [ModelDB in particular](#).

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mai

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Mainen ZF

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Mai Z

Maier J

Maidana JP

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Cell Type

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Olfactory bulb main granule MC cell

Olfactory bulb main periglomerular cell

3 more...

Concept

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Kinetic synaptic models applicable to building networks (Destexhe et al 1998)

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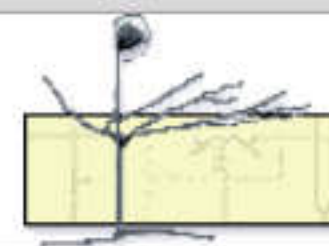
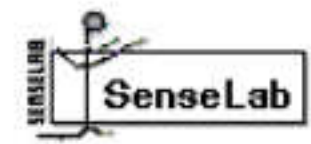
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Pyramidal Neuron Deep, Superficial; Aspiny, Stellate (Mainen and Sejnowski 1996)

Accession:2488

This package contains compartmental models of four reconstructed neocortical neurons (layer 3 Aspiny, layer 4 Stellate, layer 3 and layer 5 Pyramidal neurons) with active dendritic currents using NEURON. Running this simulation demonstrates that an entire spectrum of firing patterns can be reproduced in this set of model neurons which share a common distribution of ion channels and differ only in their dendritic geometry. The reference paper is: Z. F. Mainen and T. J. Sejnowski (1996) Influence of dendritic structure on firing pattern in model neocortical neurons. Nature 382: 363-366. See also <http://www.cnl.salk.edu/~zach/methods.html> and <http://www.cnl.salk.edu/~zach/> More info in readme.txt file below made visible by clicking on the patdemo folder and then on the readme.txt file.

Reference:

- 1 . Mainen ZF, Sejnowski TJ (1996) Influence of dendritic structure on firing pattern in model neocortical neurons. [Nature](#) 382:363-6 [\[PubMed\]](#)

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Model Information (Click on a link to find other models with that property)

Model Type:	Neuron or other electrically excitable cell;
Brain Region(s)/Organism:	
Cell Type(s):	Neocortex layer 5-6 pyramidal cell; Neocortex layer 2-3 pyramidal cell; Myelinated neuron; Neocortex spiny stellate cell;

ModelDB: Pyramidal Neuron Deep, Superficial; Aspiny, Stellate (Mainen and Sejnowski 1996) - Mozilla Firefox

ModelDB: Pyramida... x

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~/zach/methnods.html and http://www.cnl.salk.edu/~zach/ More info in readme.txt file below made visible by clicking on the patdemo folder and then on the readme.txt file.

Reference: Mainen ZF, Sejnowski TJ (1996) Influence of dendritic structure on firing pattern in model neocortical neurons. *Nature* 382:363-6 [PubMed]

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Model Information (Click on a link to find other models with that property)

Model Type: [Neuron or other electrically excitable cell](#);

Brain

Region(s)/Organism:

Cell Type(s): [Neocortex pyramidal layer 5-6 cell](#); [Neocortex pyramidal layer 2-3 cell](#); [Myelinated neuron](#); [Spiny stellate cell](#);

Channel(s): [I Na,t](#); [I K](#); [I M](#); [I K,Ca](#); [I Sodium](#); [I Calcium](#); [I Potassium](#);

Gap Junctions:

Receptor(s):

Gene(s):

Transmitter(s):

Simulation Environment: [NEURON](#);

Model Concept(s): [Activity Patterns](#); [Active Dendrites](#); [Influence of Dendritic Geometry](#); [Detailed Neuronal Models](#);

Implementer(s): [Mainen, Zach](#) [Mainen at cshl.edu];

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downloading and running models

\

 patdemo

 cells

 README.txt

 cad.mod *

 kca.mod *

This readme file gives usage instructions for (essentially patdemo.zip at http://www.cnl.salk.edu/~zach/ by Z. F. Mainen and T. J. Sejnowski) (see bottom of this file includes)

This model contains compartmental models of for 2 neocortical neurons (Layer 3 Aspiny, layer 4 Stellate) and active dendritic currents using a wide range of ion channel parameters to generate a wide spectrum of firing patterns

1a. L3 Aspiny

1b. L4 Stellate

1c. L3 Pyramidal

1d. L5 Pyramidal

https://senselab.med.yale.edu/modeldb/modelview/modelview.html#2488_4

