

Schedule of Presentations

NTC	Ted Carnevale
MLH	Michael Hines
WWL	Bill Lytton
GMS	Gordon Shepherd

Morning session

Time	Speaker	Title	Page
9:00 AM	MLH	Welcome	3
9:05	NTC	NEURON: a brief tour	5
		The basics	9
		Construction and use of models	19
		Using the CellBuilder to make a stylized model	20
		Creating and using an interface for running simulations	32
10:15	NTC	The Linear Circuit Builder	43
10:30		Coffee Break	
10:45	MLH	Using NMODL to add new biophysical mechanisms	51
11:15	MLH	Numerical methods: accuracy, stability, speed	59
11:30 AM	NTC	Networks: spike-triggered synaptic transmission, events, and artificial spiking cells	65
12:15 PM		Lunch	

Afternoon session

1:15 PM	MLH	Numerical methods: adaptive integration and events	75
1:30	MLH	Parallelizing network simulations	79

2:00	MLH	Python + NEURON	95
3:15		Coffee Break	
3:30	GMS	Databases for computational neuroscience	103
4:00	WWL	Reaction-diffusion	supplement
4:45	MLH	Future directions	
5:00		End of afternoon session	

Receipt and Survey**last two pages**

We value your opinions and suggestions for improving this course. Please take a moment to fill out and hand in the survey.

Satellite Symposium, Society for Neuroscience

USING NEURON TO MODEL CELLS AND NETWORKS

San Diego, CA

Friday, November 8, 2013

Ted Carnevale
Michael Hines
Bill Lytton
Gordon Shepherd

Supported by NINDS

NEURON

<http://neuron.yale.edu/>

NEURON: a brief tour

A tool for empirically-based models of neurons
and neural circuits

Open source project directed by Michael Hines

Active development and user support

Documentation, tutorials, and forum at
<http://www.neuron.yale.edu/>

Courses

SFN meetings

summer course at UCSD

other courses

The NEURON user community

Used by experimentalists, theoreticians, and educators
for neuroscience research and teaching

As of October 2012

- more than 1180 publications
- more than 1500 subscribers to mailing list and forum
<http://www.neuron.yale.edu/phpBB/>
- source code for 355 published models at ModelDB
<http://modeldb.yale.edu/>

Specifying and using models with NEURON

Model specifications written in hoc and/or Python
and/or

created with GUI tools (work via hoc)

CellBuilder, Channel Builder,
Network Builder, Linear Circuit Builder

Add new functionality with NMODL (compiled)
new density mechanisms and point processes
described by ODEs, kinetic schemes,
algebraic equations
events, state machines, artificial spiking cells

Not model specification, but necessary

Instrumentation

stimulators, current or voltage clamps
plotting and recording variables

Simulation control

default and custom initializations
integration methods
fixed time step
adaptive integration
event system useful for implementing
"experimental protocols"

User interface

Other features

- Parallel simulation
 - multithreaded execution
 - embarrassingly parallel problems
 - distributed models
- Optimization tools
- Model analysis
 - Impedance tools
 - ModelView
- Import3D for detailed morphometric data

Where to learn more

- The NEURON Book
- The WWW page <http://www.neuron.yale.edu/>
 - Documentation
 - hints and tutorials
 - link to FAQ list
 - links to key papers about NEURON
 - Programmer's Reference
 - Courses
- The Forum <http://www.neuron.yale.edu/phpBB/>
 - Getting started
 - Hot tips

The What and the Why of Neural Modeling

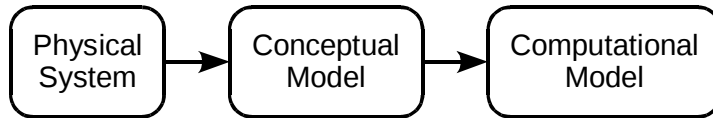
The moment-to-moment processing of information in the nervous system involves the propagation and interaction of electrical and chemical signals that are distributed in space and time.

Empirically-based modeling is needed to test hypotheses about the mechanisms that govern these signals and how nervous system function emerges from the operation of these mechanisms.

Topics

1. How to create and use models of neurons and networks of neurons
 - How to specify anatomical and biophysical properties
 - How to control, display, and analyze models and simulation results
2. How NEURON works
3. How to add user-defined biophysical mechanisms

From Physical System to Computational Model



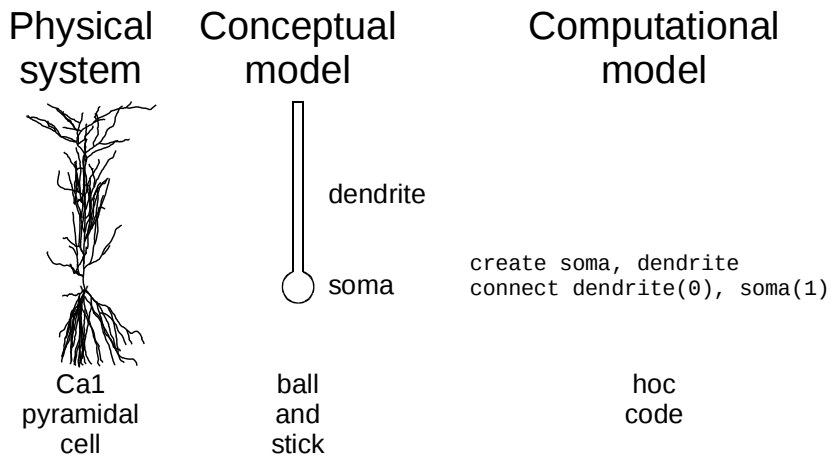
Conceptual model

a simplified representation of the physical system

Computational model

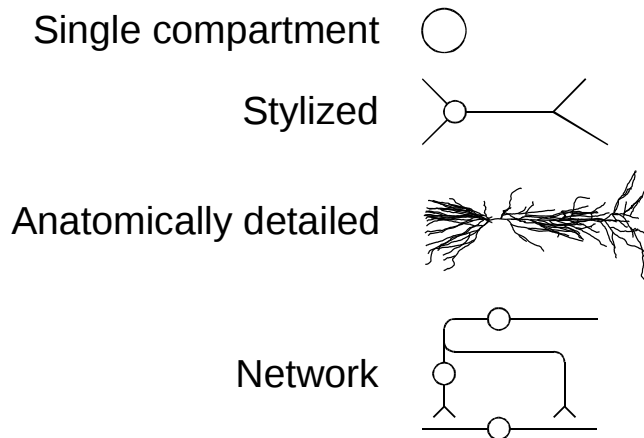
an accurate representation of the conceptual model

From Physical System to Computational Model



Hierarchies of Complexity

Structure



Hierarchies of Complexity

Mechanism

Passive and Active currents

HH-style
kinetic scheme

Synaptic transmission

continuous
spike-triggered

Gap junctions

Extracellular fields, Linear circuits

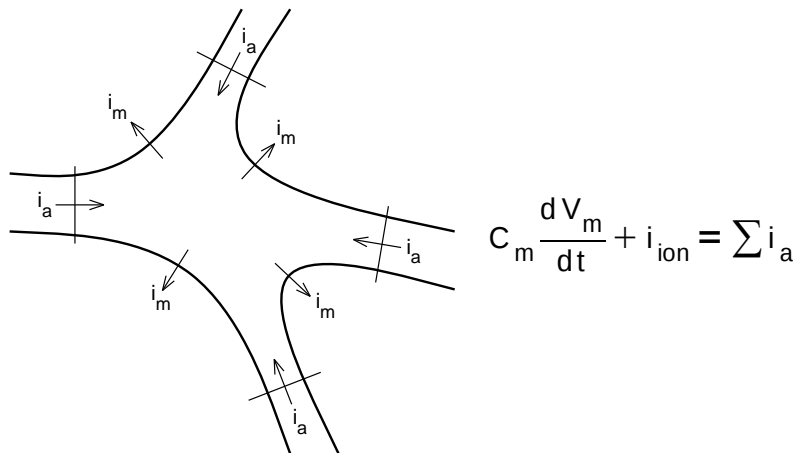
Diffusion, buffers, transport & exchange

Artificial spiking cells ("integrate & fire")

Fundamental Concepts in NEURON

Signals	What moves	Driving force	What is conserved
Electrical	charge carriers	voltage gradient	charge
Chemical	solute	concentration gradient	mass

Conservation of Charge



The Model Equations

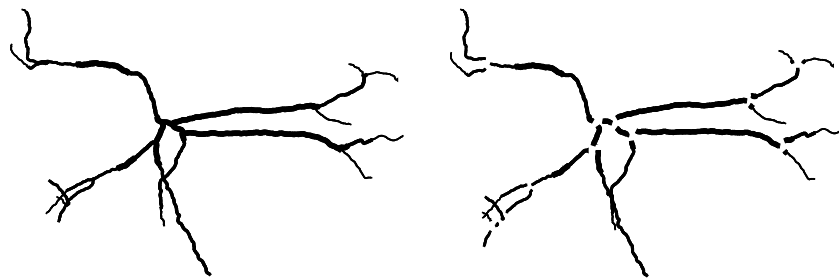
$$c_j \frac{dv_j}{dt} + i_{ion_j} = \sum_k \frac{v_k - v_j}{r_{jk}}$$

- v_j membrane potential in compartment j
 i_{ion_j} net transmembrane ionic current in compartment j
 c_j membrane capacitance of compartment j
 r_{jk} axial resistance between the centers of compartment j and adjacent compartment k

Separating Anatomy and Biophysics from Purely Numerical Issues

section

a continuous length of unbranched cable



Anatomical data from A.I. Gulyás

Mathematical description of a section

What we want:

$$c_j \frac{dv_j}{dt} + i_{ion_j} = \sum_k \frac{v_k - v_j}{r_{jk}}$$

What a new section gives us:

$$c_j \frac{dv_j}{dt} = \sum_k \frac{v_k - v_j}{r_{jk}}$$

i.e. membrane capacitance and axial resistance,
but no ionic current.

How can we put ion channels in the membrane?

Adding mechanisms to sections

Density mechanisms
distributed channels
ion accumulation

Point processes
electrodes, synapses

Described by
differential equations
kinetic schemes
algebraic equations

Constructed with
NMODL
Channel Builder

```

create soma, dend
connect dend(0), soma(1)

soma {
  L = 50 // [um] length
  diam = 50 // [um] diameter
  insert hh // Hodgkin-Huxley mechanism
  nseg = 1
}

dend {
  L = 200
  diam = 2
  insert pas // passive channels
  nseg = 3
}

```

Range Variables

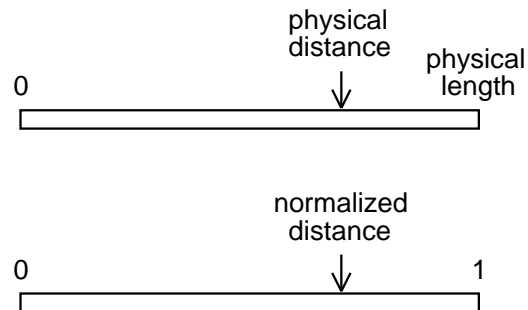
Name	Meaning	Units
diam	diameter	[μm]
cm	specific membrane capacitance	[$\mu\text{f}/\text{cm}^2$]
g_pas	specific conductance of the pas mechanism	[siemens/ cm^2]
v	membrane potential	[mV]

range

normalized position along the length of a section

$$0 \leq \text{range} \leq 1$$

any variable name can be used for range, e.g. x

**Syntax:**

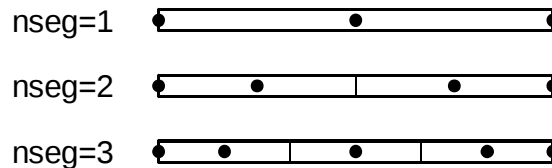
```
sectionname.rangevar(range)
  returns or sets value of rangevar
  at location that corresponds to range
```

Examples:

```
dend.v(0.5)
  returns v at middle of dend
  Shortcut: dend.v
dend for (x) print x*L, v(x)
  prints physical distance and v
  at each point in dend where v was calculated
```


nseg

the number of points in a section where membrane current and potential are computed



Example: axon nseg = 3

To test spatial resolution
 forall nseg = nseg*3
 and repeat the simulation

Category	Variable	Units
Time	t	[ms]
Distance	diam, L	[μm]
Voltage	v	[mV]
Current		
specific	i	[mA/cm ²] (density)
absolute		[nA] (point process)
Capacitance		
specific	cm	[$\mu\text{f/cm}^2$]
absolute		[nf] (point process)
Conductance		
specific	g	[S/cm ²] (density)
absolute		[μS] (point process)
Cytoplasmic resistivity	Ra	[$\Omega\text{ cm}$]
Resistance	SEClamp.rs	[10 ⁶ Ω]
Concentration	cai, nao, etc.	[mM]

Model specification summary

Topology: create and connect sections

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

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

Network models

Create cells

Connect cells

Construction and Use of Models

1. Specify the model ("virtual organism").
2. Specify the user interface ("virtual lab rig").
3. Tests
 - structural integrity
 - spatial grid
 - time steps

Example: using the GUI to build and exercise a stylized model

1. How to use the CellBuilder to create and manage a model cell.
2. How to use NEURON's graphical tools to make an interface for running simulations.

Step 0: Conceptualize the task

Shape

stick figure / detailed

Channel distribution

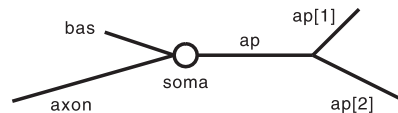
uniform / nonuniform

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 μm	20 μm	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

* - gnabar_hh and gkbar_hh reduced to 10%, el_hh = - 64 mV

§ - e_pas = - 65 mV

Throughout the cell Ra = 160 Ω cm, cm = 1 $\mu\text{f} / \text{cm}^2$

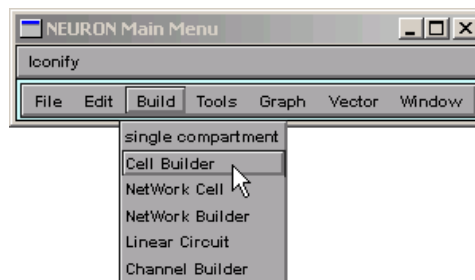
Launch NEURON with its library of graphical tools

UNIX/Linux `nrngui`

MSWin or OS X

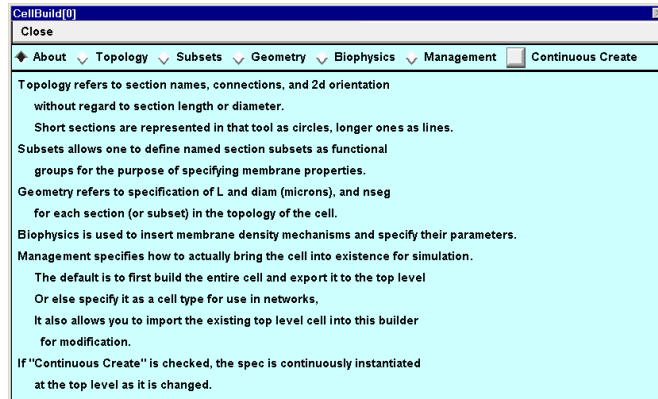


Bring up a CellBuilder



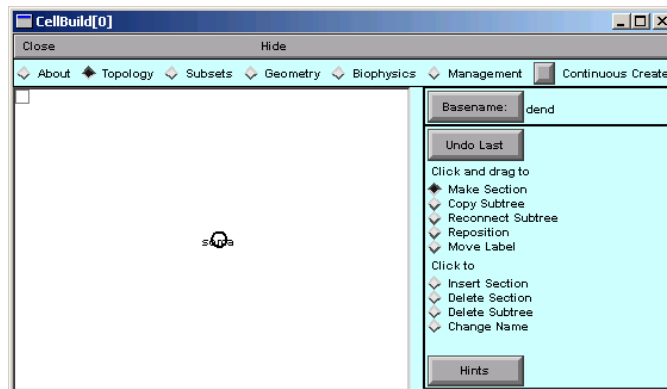
NEURON Main Menu / Build / Cell Builder

The CellBuilder



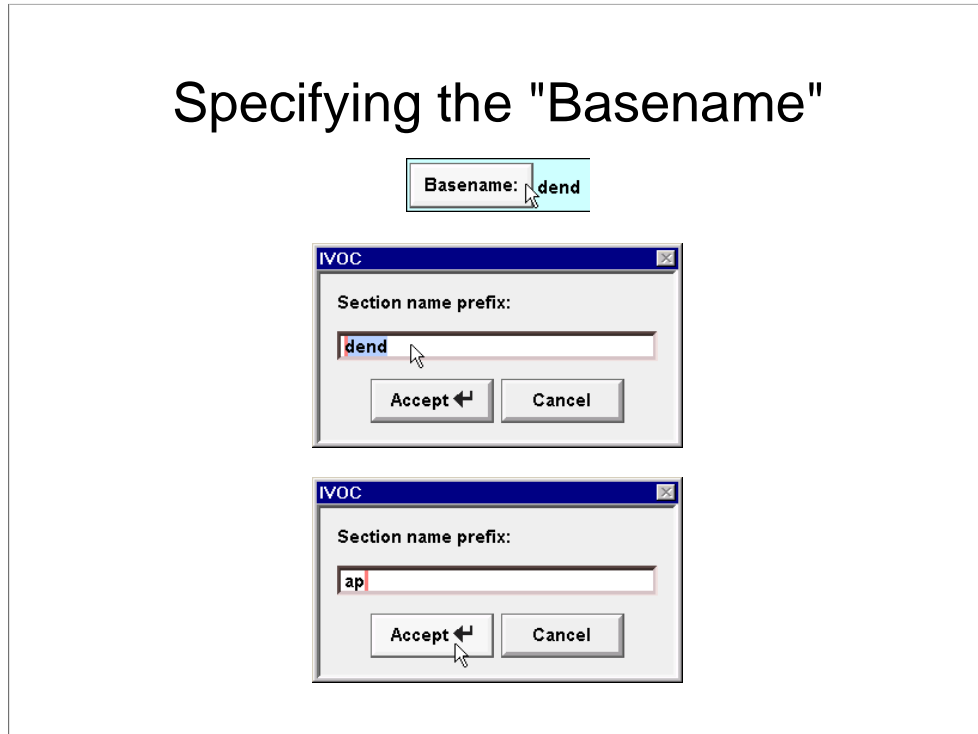
Use buttons from left to right.

Topology



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

Specifying the "Basename"



Making a new section

Place cursor near end
of existing section



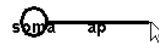
Click to start new section



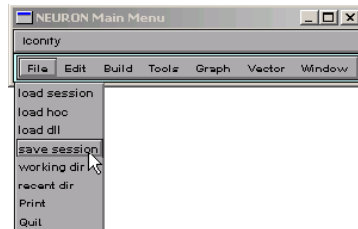
Drag to desired length



Release mouse button

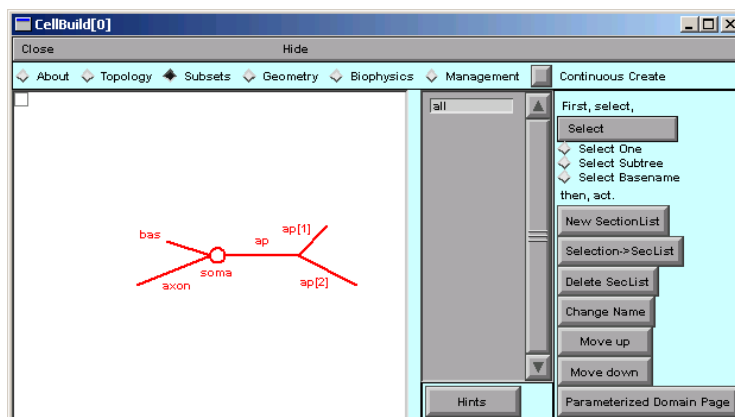


Save your work as you make progress!



NEURON Main Menu / File / save session

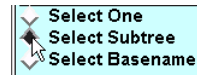
Subsets



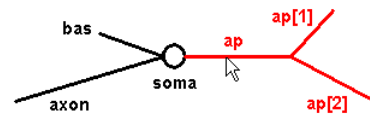
Group sections that have shared properties.
We want to make an "apicals" subset.

Making a new subset

Click "Select Subtree"



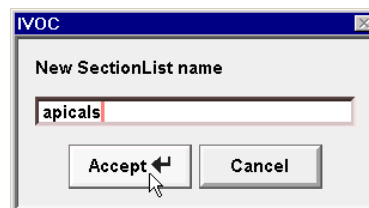
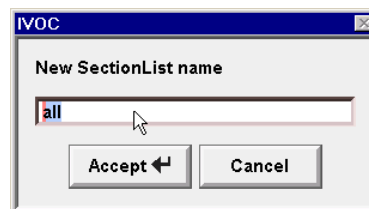
Click root of apical tree . . .



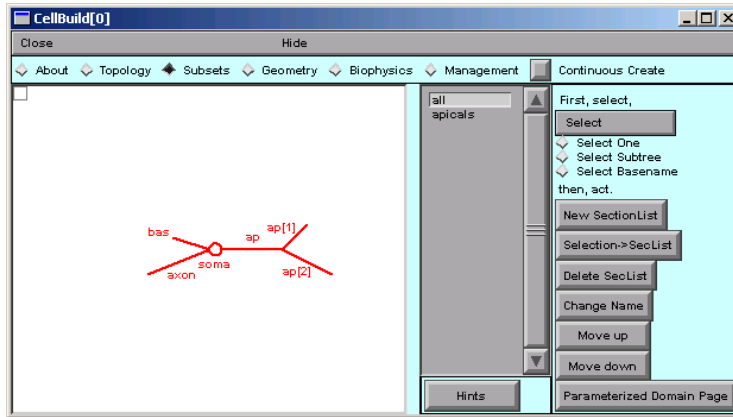
. . . then "New SectionList"



Making a new subset *continued*



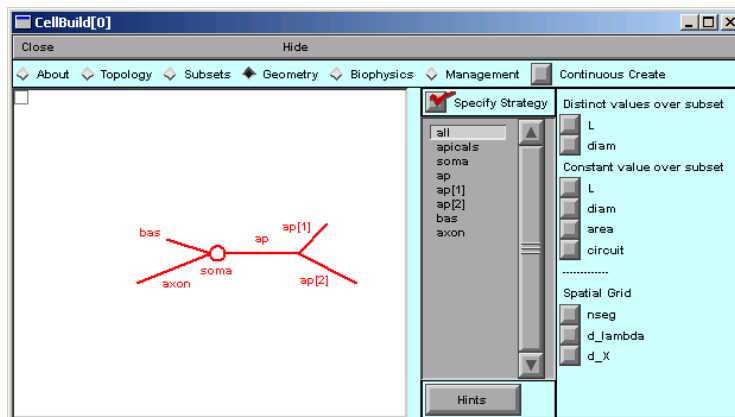
Subsets finished



Note "apicals".

Time to save a new session file.

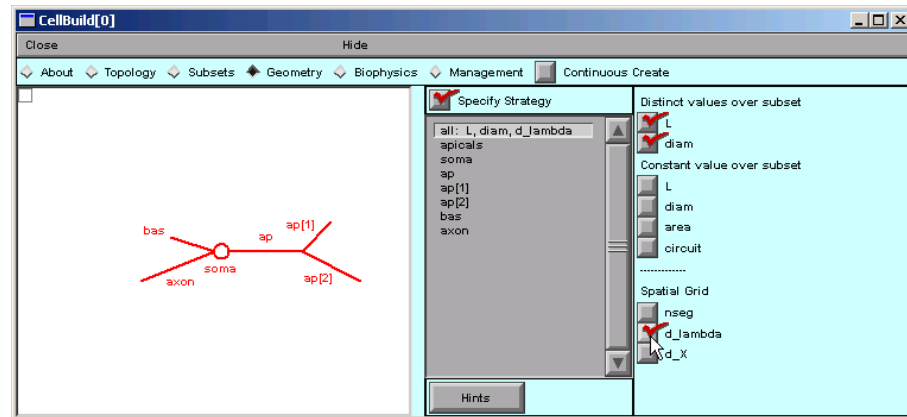
Geometry



"Specify Strategy" is ON.

A good strategy is a concise strategy.

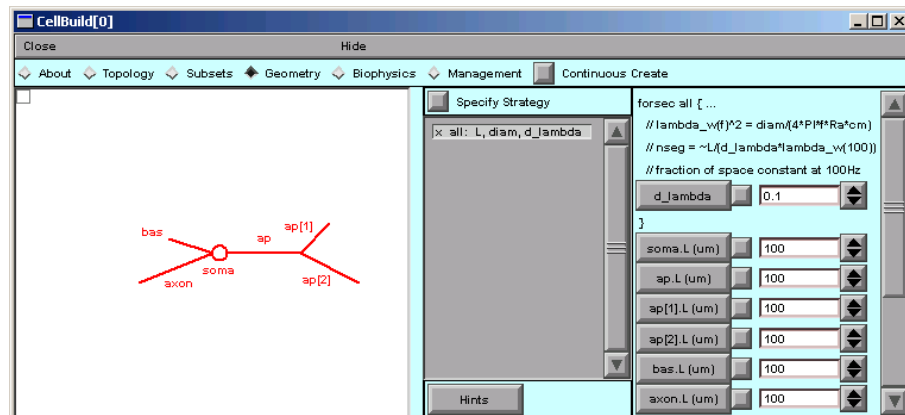
Geometry strategy



Each section has a different L and diam.

Compartmentalize according to λ_{100} Hz (d_lambda rule).

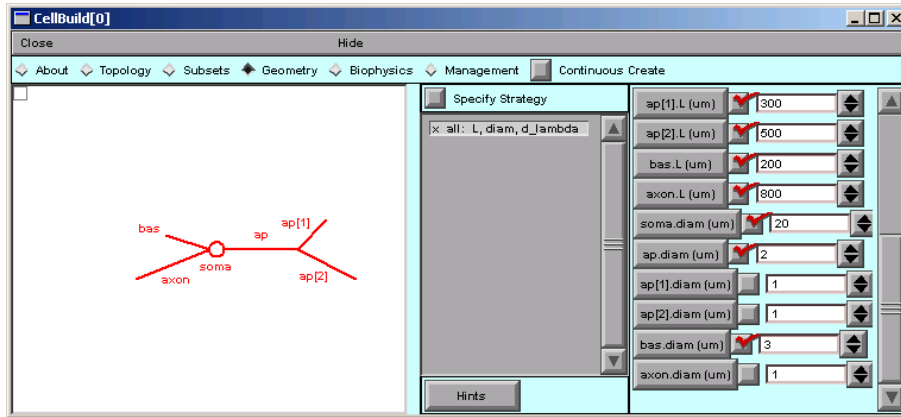
Implementing geometry strategy



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

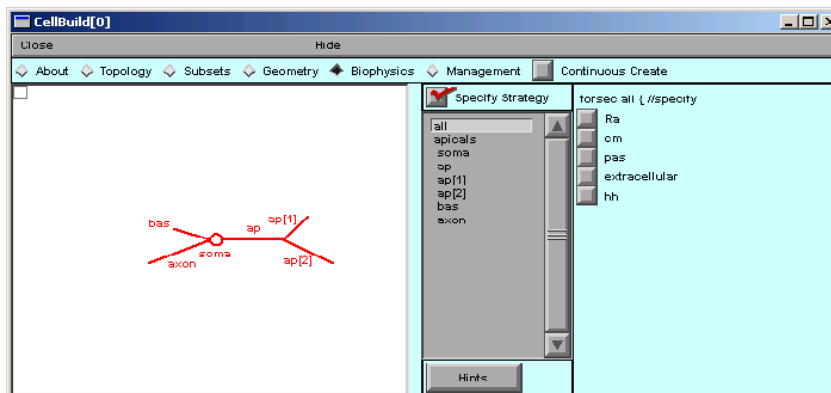
d_lambda = 0.1 at 100 Hz usually gives good spatial accuracy.

Implementing geometry *continued*



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

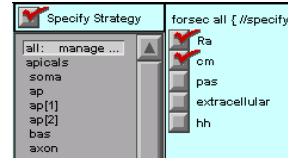
Biophysics



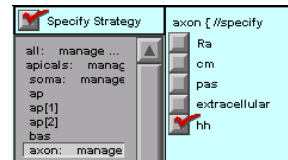
"Specify Strategy" is ON.
 Base the plan on shared properties.

Biophysics strategy

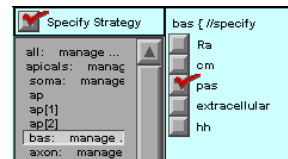
Ra and cm are homogeneous



apicals, soma and axon have hh

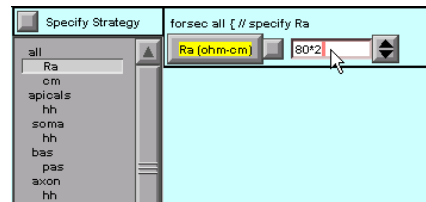


bas has pas

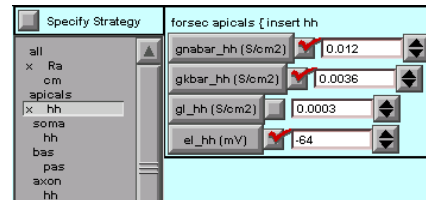


Implementing biophysics strategy

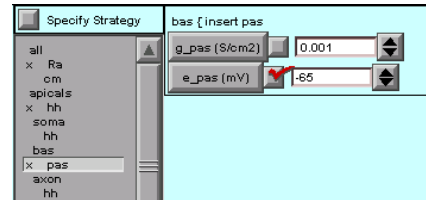
Double Ra



Fix apicals hh params



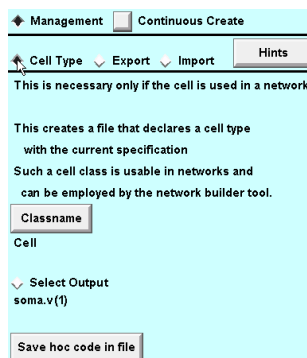
Shift e_pas in bas



Save another session file!!

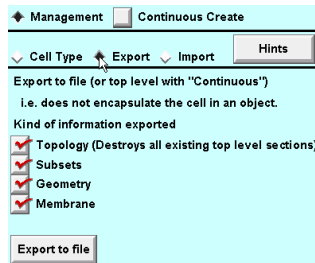
Management

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



Management *continued*

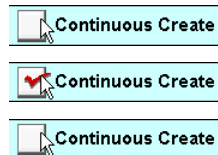
Option 2: save as hoc file



Management *continued*

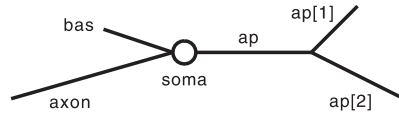
Option 3: export to interpreter

Toggle Continuous Create ON and OFF



or just leave it ON all the time.

Step 2: creating and using an interface for running simulations



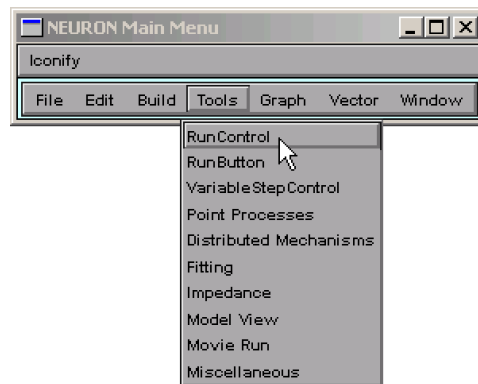
We want to

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

We need

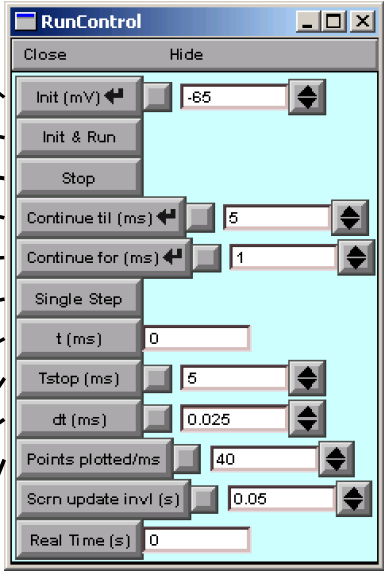
- a "Run" button
- graphs to plot results
- a stimulator

Get a "Run" button



NEURON Main Menu / Tools / RunControl

RunControl panel



The RunControl panel is a window with a light blue background. It contains several controls: 'Init (mV)' with a value of -65; 'Init & Run' button; 'Stop' button; 'Continue til (ms)' with a value of 5; 'Continue for (ms)' with a value of 1; 'Single Step' button; 't (ms)' with a value of 0; 'Tstop (ms)' with a value of 5; 'dt (ms)' with a value of 0.025; 'Points plotted/ms' with a value of 40; 'Scrn update invl (s)' with a value of 0.05; and 'Real Time (s)' with a value of 0.

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 $1/(\text{Points plotted/ms})$

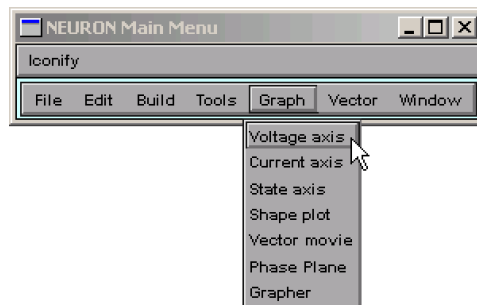
t numeric field shows model time

Tstop specifies when simulation ends

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

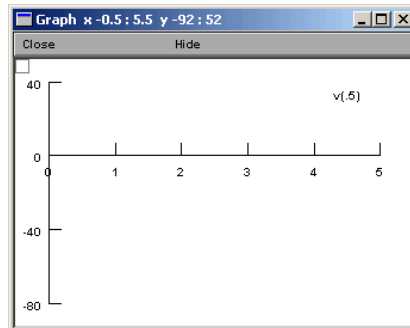
Points plotted/ms is plotting interval

We need to plot Vm(t) at soma



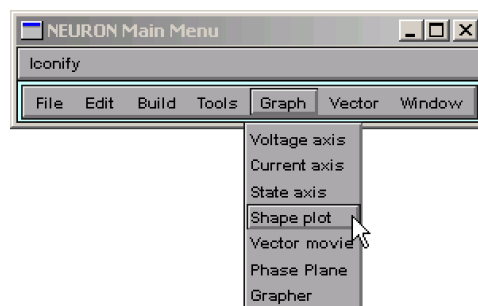
NEURON Main Menu / Graph / Voltage axis

Graph window



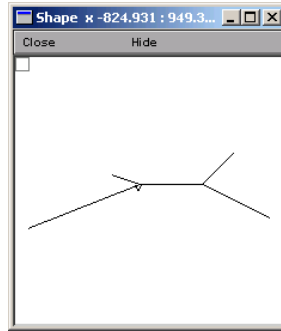
$v(.5)$ is V_m at middle of default section
(soma in this example)

We need to plot V_m along a path



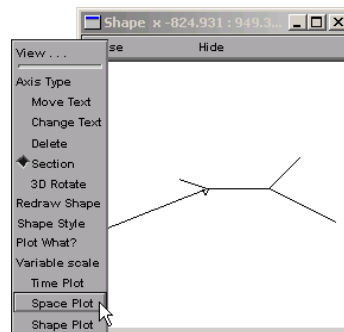
NEURON Main Menu / Graph / Shape plot

Bringing up a space plot



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

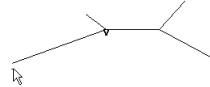
Bringing up a space plot *continued*



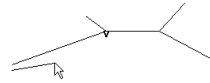
. . . and scroll down to "Space Plot".

Bringing up a space plot *continued*

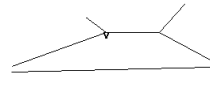
Click just left of the shape



Hold button down while dragging from left . . .



. . . to right . . .

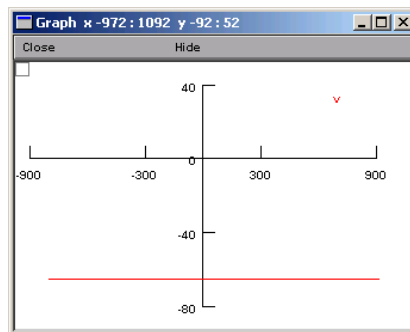


. . . then release button.



This pops up a . . .

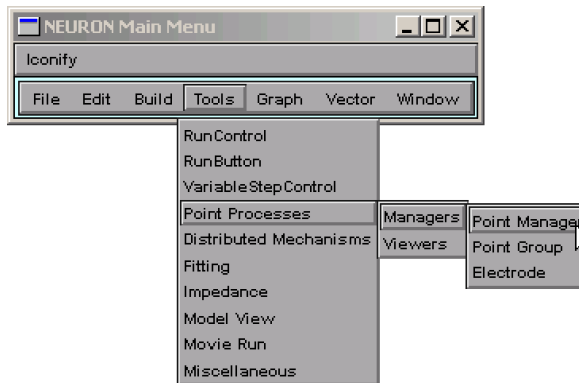
Space plot



A plot of V_m vs. distance along a path.

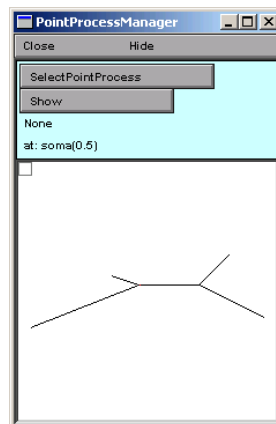
Better save a session file.

We need a stimulator



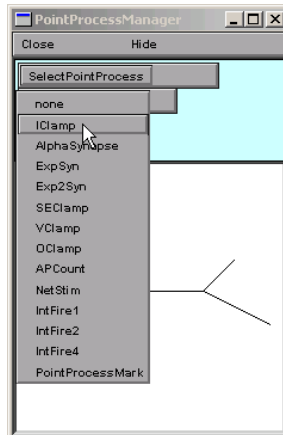
NEURON Main Menu / Tools / Point Processes
/ Managers / Point Manager

PointProcessManager window



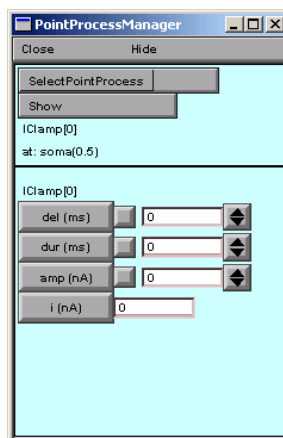
To make this an IClamp . . .

Creating an IClamp



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

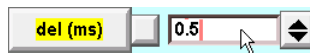
IClamp parameter panel



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

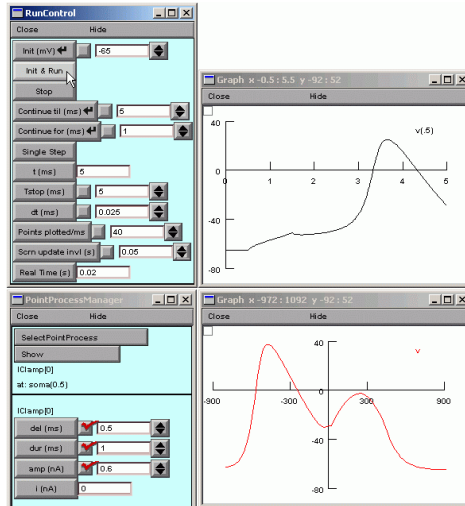


Our user interface

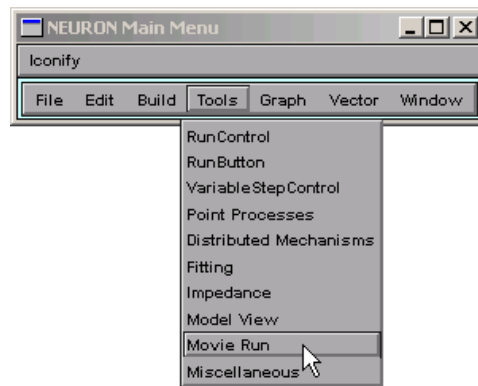


Time to save to a new session file!

It works!

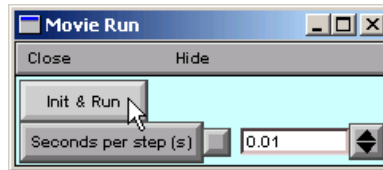


How to get nice space plot "movies"



NEURON Main Menu / Tools / Movie Run

Space plot "movies" *continued*



Movie Run / Init & Run

What if channel density in the apical tree varies systematically with position, e.g. distance from the soma?

See "Specifying parameterized variation of biophysical properties" in the CellBuilder tutorial at <http://neuron.yale.edu/neuron/docs>

The Linear Circuit Builder

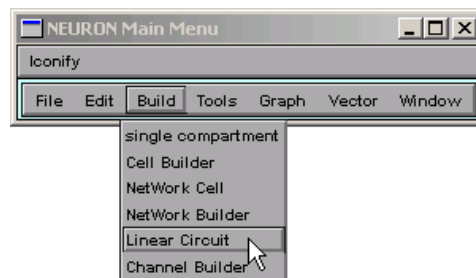
For building models that have linear circuit elements and may also involve neurons

Circuit elements include ground, current & voltage source, R, C, op amp

Potential applications include

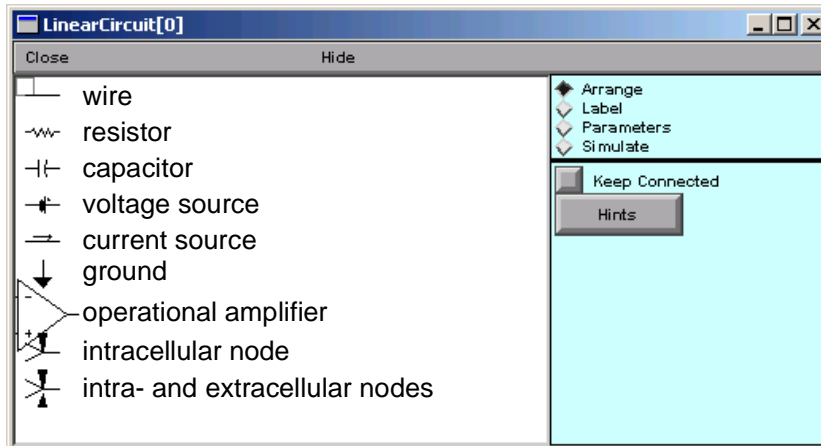
- effects and compensation of electrode R & C
- two-electrode voltage clamp
- ohmic and nonlinear gap junctions

1. Bring up a Linear Circuit Builder



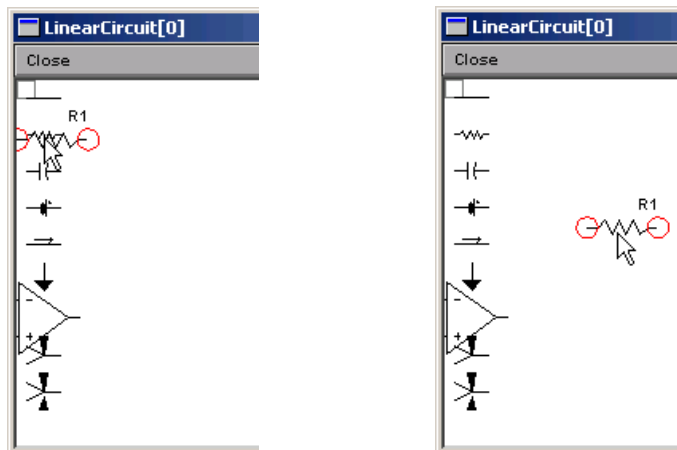
NEURON Main Menu / Build / Linear Circuit

The Linear Circuit Builder



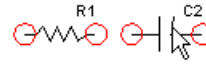
Arrange: spawn components

Click on palette and drag onto canvas

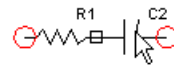


Arrange: connect components

Click and drag to overlap red circles



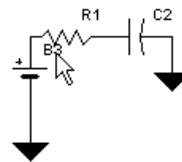
Black square is "solder joint"



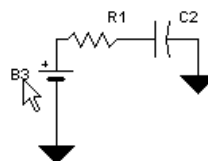
Pull apart to break connection

Label: move labels

Click and drag to new location



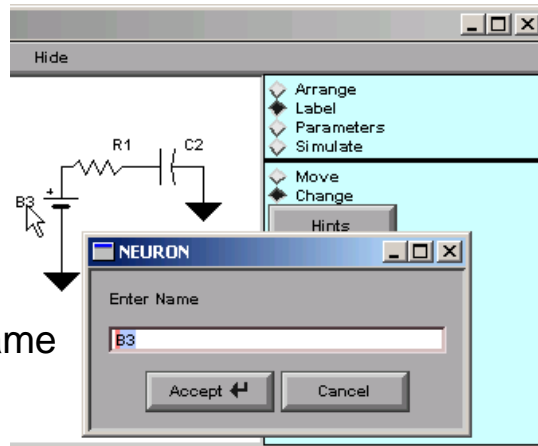
- ◇ Arrange
- ◆ Label
- ◇ Parameters
- ◇ Simulate
- ◆ Move
- ◇ Change
- Hints



- ◇ Arrange
- ◆ Label
- ◇ Parameters
- ◇ Simulate
- ◆ Move
- ◇ Change
- Hints

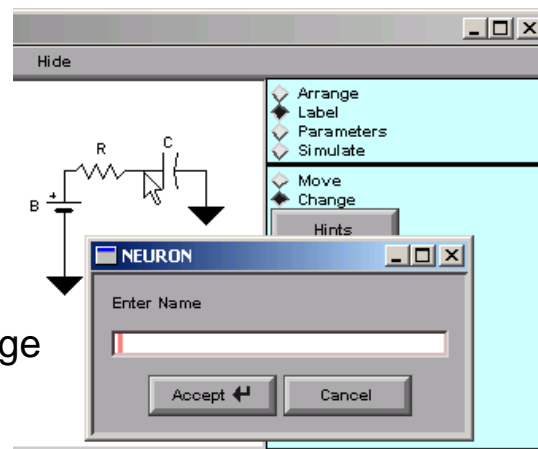
Label: change labels 1

Click on a label . . .
 . . . to change its name



Label: change labels 2

Click on a node . . .
 . . . to label a voltage



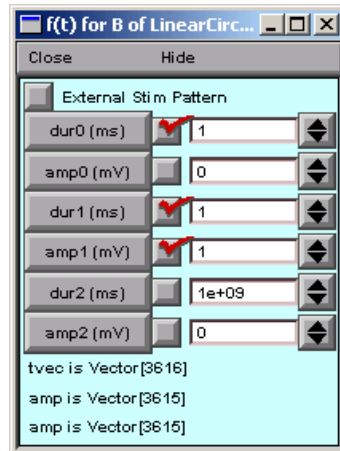
Parameters: non-source elements

Click on "Parameters"

Parameters: signal sources

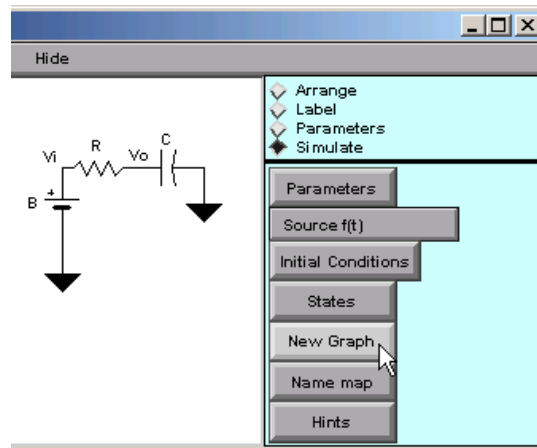
Source $f(t)$ / B

Parameters: signal sources *continued*



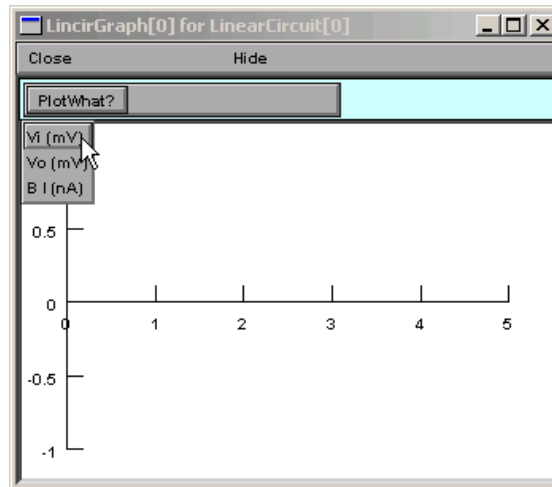
Configured

Simulate: creating a graph



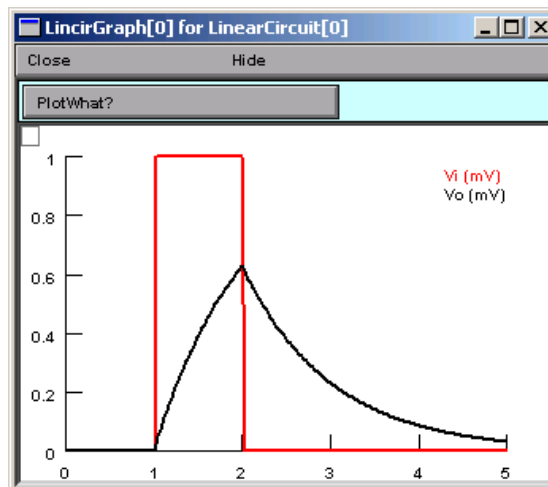
New Graph

Simulate: specifying what to plot



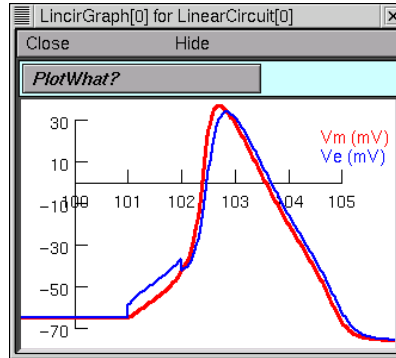
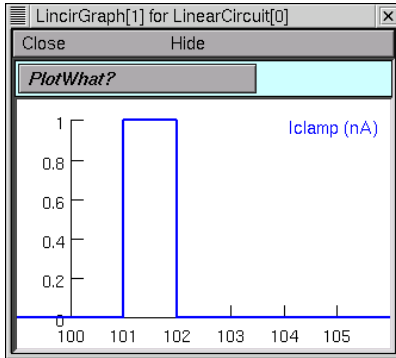
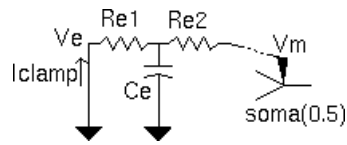
PlotWhat? / *variable_label*

Simulate: simulation results

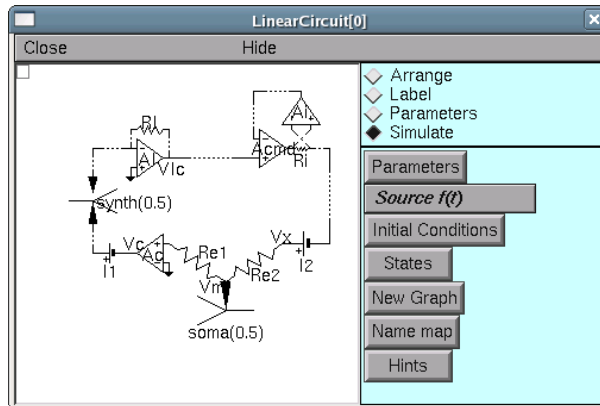


After minor cosmetic changes

Patch clamp with electrode R and C



NEURON demo: dynamic clamp



NMODL

NEURON Model Description Language

Add new membrane mechanisms to NEURON

Density mechanisms

- Distributed Channels
- Ion accumulation

Point Processes

- Electrodes
- Synapses

Described by

- Differential equations
- Kinetic schemes
- Algebraic equations

Benefits

- Specification only -- independent of solution method.
- Efficient -- translated into C.
- Compact
 - One NMODL statement → many C statements.
 - Interface code automatically generated.
- Consistent ion current/concentration interactions.
- Consistent Units

NMODL general block structure

What the model looks like from outside

```
NEURON {
    SUFFIX kchan
    USEION k READ ek WRITE ik
    RANGE gbar, ...
}
```

What names are manipulated by this model

```
UNITS { (mV) = (millivolt) ... }
PARAMETER { gbar = .036 (mho/cm2) <0, 1e9>... }
STATE { n ... }
ASSIGNED { ik (mA/cm2) ... }
```

Initial default values for states

```
INITIAL {
    rates(v)
    n = ninf
}
```

Calculate currents (if any) as function of v, t, states

(and specify how states are to be integrated)

```
BREAKPOINT {
    SOLVE deriv METHOD cnexp
    ik = gbar * n^4 * (v - ek)
}
```

State equations

```
DERIVATIVE deriv {
    rates(v)
    n' = (ninf - n)/ntau
}
```

Functions and procedures

```
PROCEDURE rates(v(mV)) {
    ...
}
```

UNIX

nrnivmodl
nrngui

MSWIN



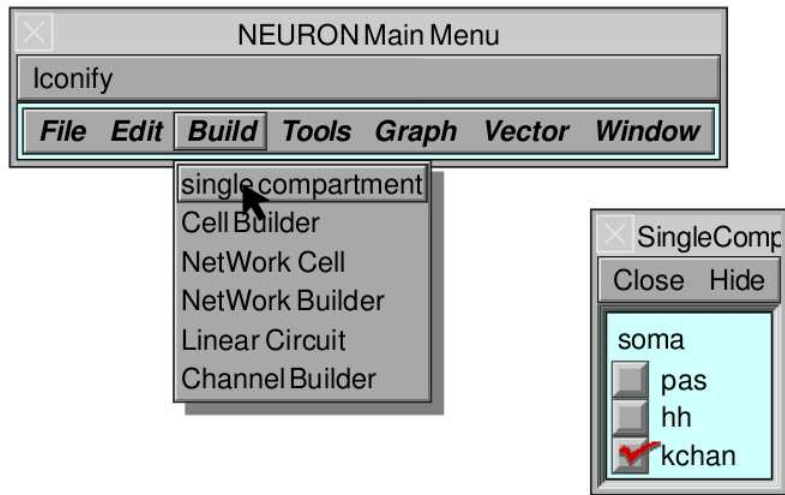
mknrndll



nrngui



Select NEURON Main Menu / Build / single compartment



Density mechanism

```
NEURON {
  SUFFIX leak
  NONSPECIFIC_CURRENT i
  RANGE i, e, g
}

PARAMETER {
  g = .001 (mho/cm2) <0, 1e9>
  e = -65 (millivolt)
}

ASSIGNED {
  i (milliamp/cm2)
  v (millivolt)
}

BREAKPOINT {
  i = g*(v - e)
}
```

Point Process

```
NEURON {
  POINT_PROCESS Shunt
  NONSPECIFIC_CURRENT i
  RANGE i, e, r
}

PARAMETER {
  r = 1 (gigaohm) <1e-9,1e9>
  e = 0 (millivolt)
}

ASSIGNED {
  i (nanoamp)
  v (millivolt)
}

BREAKPOINT {
  i = (.001)*(v - e)/r
}
```

Density mechanism

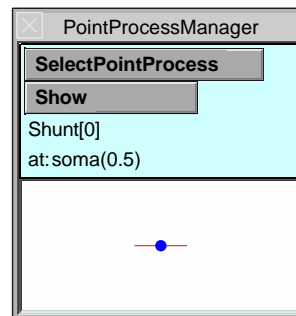
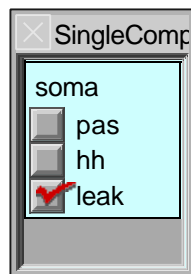
Point Process

NMODL

```
NEURON {
  SUFFIX leak
  NONSPECIFIC_CURRENT i
  RANGE i, e, g
}
```

```
NEURON {
  POINT_PROCESS Shunt
  NONSPECIFIC_CURRENT i
  RANGE i, e, r
}
```

GUI



Interpreter

```
soma {
  insert leak
  g_leak = .0001
}
print soma.i_leak(.5)
```

```
objref s
soma s = new Shunt(.5)
s.r = 2
```

Ion Channel

```

NEURON {
  USEION k READ ek WRITE ik
}
BREAKPOINT {
  SOLVE states METHOD cnexp
  ik = gbar*n*n*n*n*(v - ek)
}
DERIVATIVE states {
  rate(v*1(/mV))
  n' = (inf - n)/tau
}

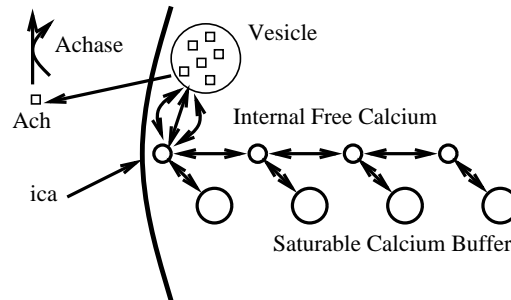
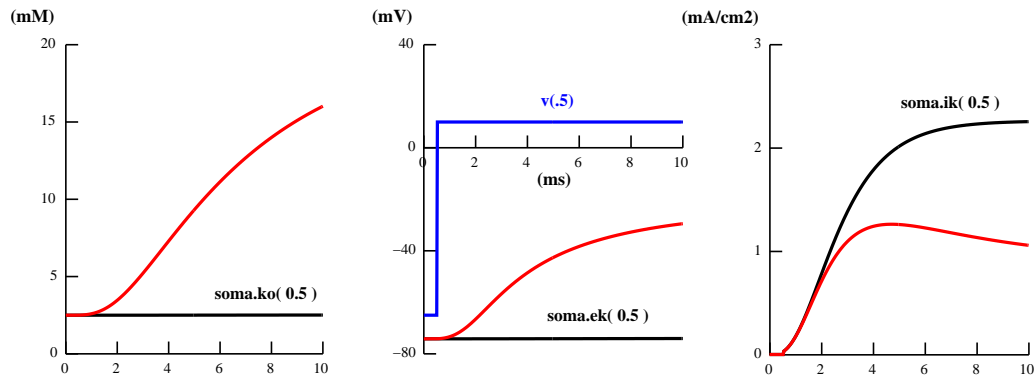
```

Ion Accumulation

```

NEURON {
  USEION k READ ik WRITE ko
}
BREAKPOINT {
  SOLVE state METHOD cnexp
}
DERIVATIVE state {
  ko' = ik/fhspace/F*(1e8)
      + k*(kbath - ko)
}

```



```

STATE {
  Vesicle Ach Achase Ach2ase X Buffer[N] CaBuffer[N] Ca[N]
}
KINETIC calcium_evoked_release {
  : release
  ~ Vesicle + 3Ca[0] <-> Ach (Agen, Arev)
  ~ Ach + Achase <-> Ach2ase (Aase2, 0) : idiom for enzyme reaction
  ~ Ach2ase <-> X + Achase (Aase2, 0) : requires two reactions
  : Buffering
  FROM i = 0 TO N-1 {
    ~ Ca[i] + Buffer[i] <-> CaBuffer[i] (kCaBuffer, kmCaBuffer)
  }
  : Diffusion
  FROM i = 1 TO N-1 {
    ~ Ca[i-1] <-> Ca[i] (Dca*a[i-1], Dca*b[i])
  }
  : inward flux
  ~ Ca[0] << (ica)
}

```

UNITS Checking

```

NEURON { POINT_PROCESS Shunt ... }
PARAMETER {
    e = 0 (millivolt)
    r = 1 (gigaohm) <1e-9,1e9>
}
ASSIGNED {
    i (nanoamp)
    v (millivolt)
}
BREAKPOINT {
    i = (v - e)/r
}

```

Units are incorrect in the "i = ..." current assignment.

```

BREAKPOINT {
    i = (v - e)/r
}

```

**The output from
modlunit shunt
is:**

```

Checking units of shunt.mod
The previous primary expression with units: 1-12 coul/sec
is missing a conversion factor and should read:
(0.001)*()
at line 14 in file shunt.mod
i = (v - e)/r<>

```

To fix the problem replace the line with:

```
i = (.001)*(v - e)/r
```

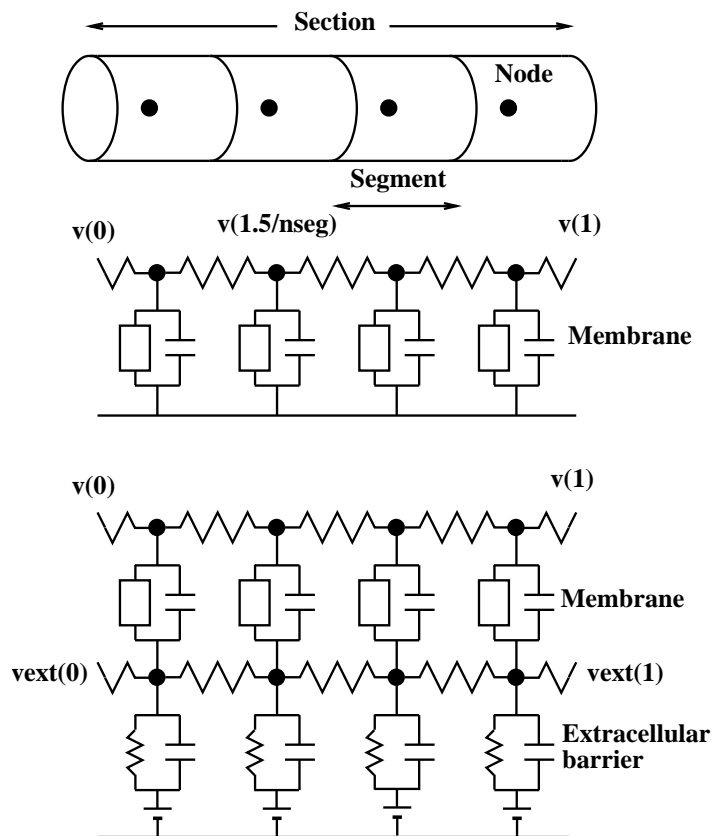
What conversion factor will make the following consistent?

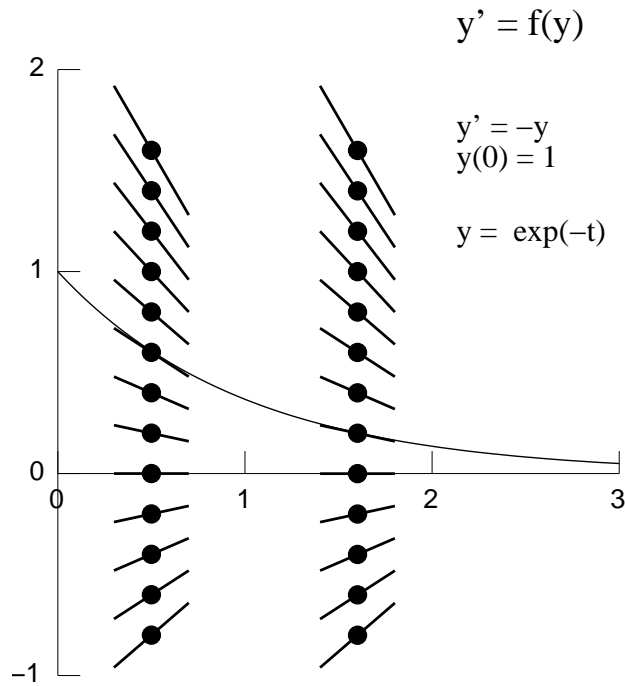
$$\text{na}i' = \text{ina} \quad / \quad \text{FARADAY} \quad * \quad (\text{c/radius}) \\
 (\text{uM/ms}) \quad (\text{mA/cm}^2) \quad / \quad (\text{coulomb/mole}) \quad \quad \quad / \quad (\text{um})$$

Compartmental Modeling

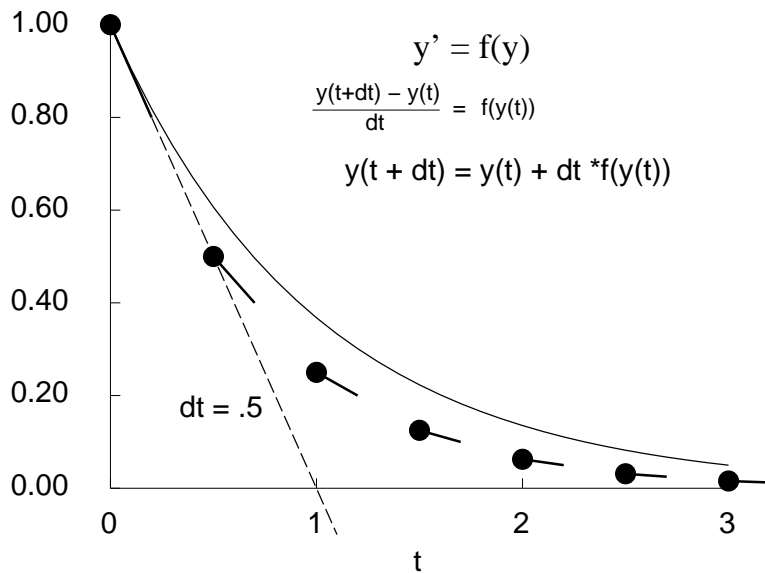
Not much mathematics required.

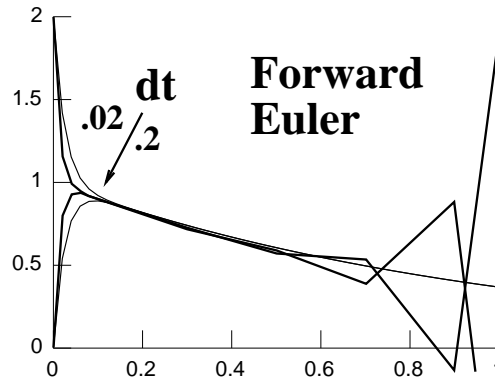
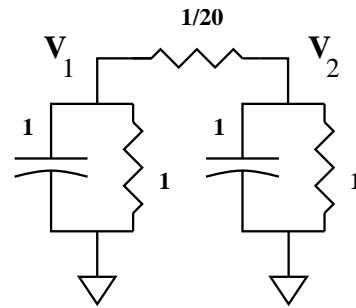
Good judgment essential!



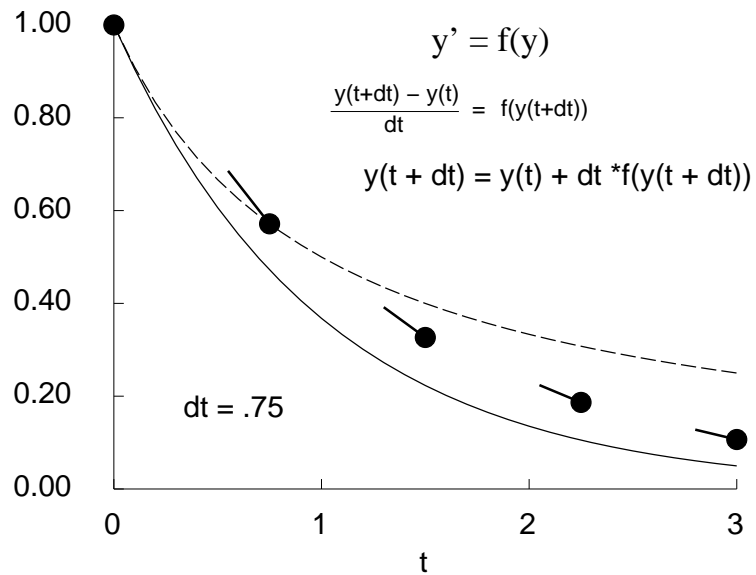


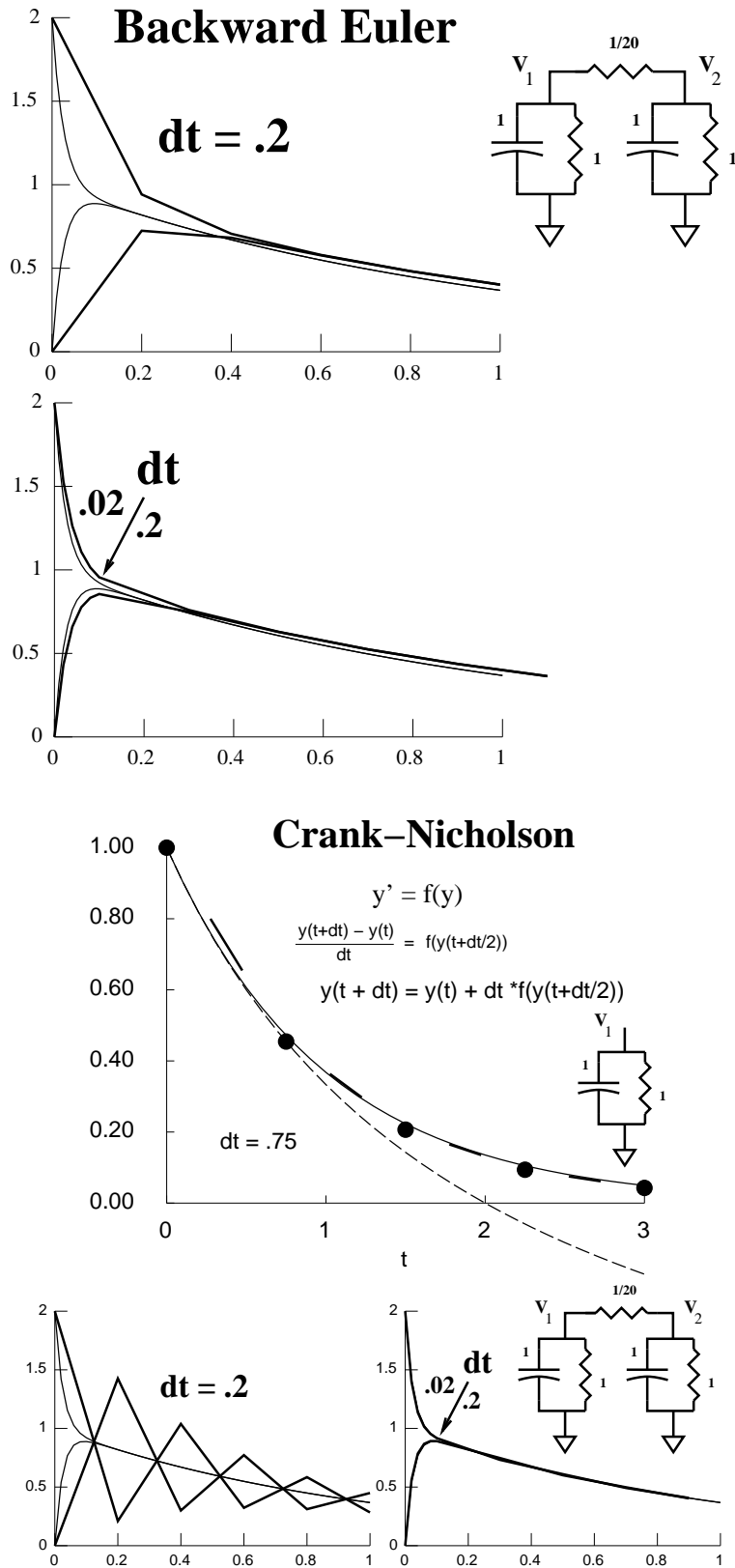
Forward Euler

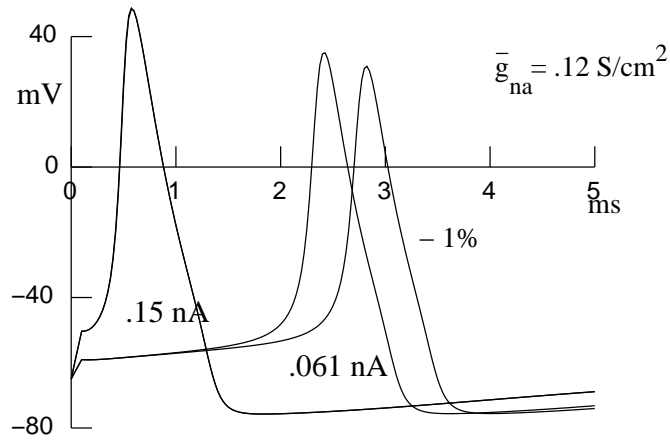
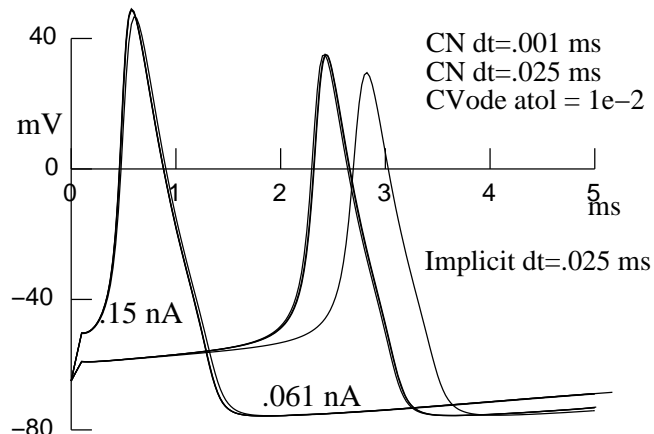
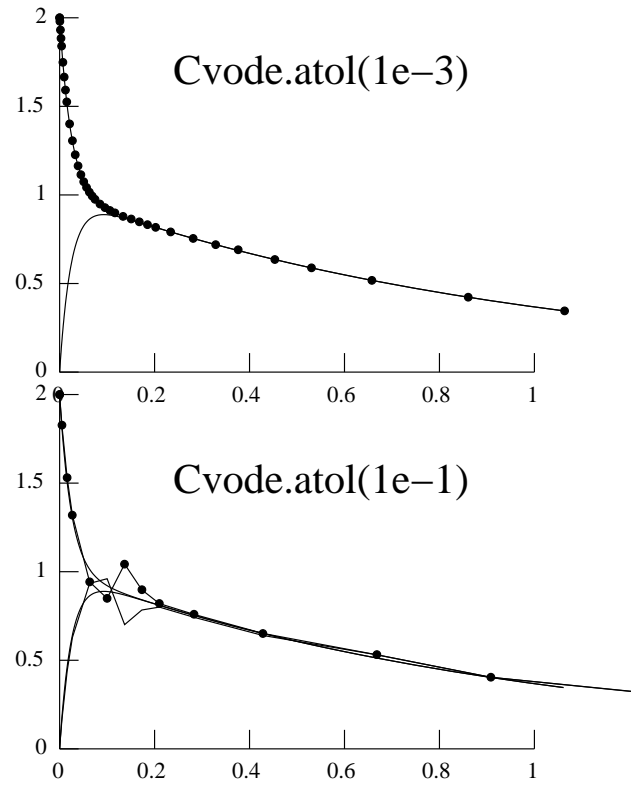




Backward Euler







Networks: spike-triggered synaptic transmission, events, and artificial spiking cells

1. Define the types of cells
2. Create each cell in the network
3. Connect the cells

Communication between cells

Gap junctions
Synaptic transmission
 graded
 spike-triggered

Spike-triggered synaptic transmission

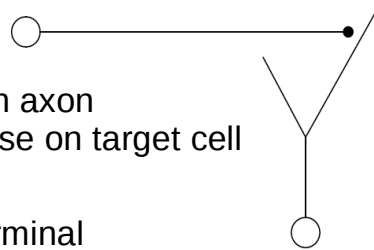
Physical system:

Presynaptic neuron with axon that projects to synapse on target cell

Conceptual model:

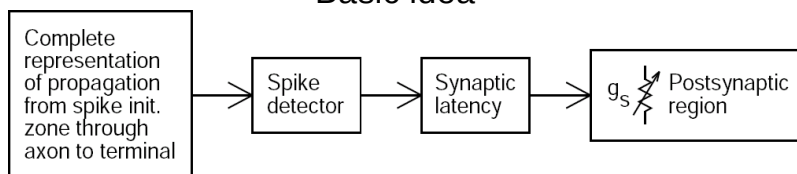
Spike in presynaptic terminal triggers transmitter release; presynaptic details unimportant

Postsynaptic effect described by DE or kinetic scheme that is perturbed by occurrence of a presynaptic spike

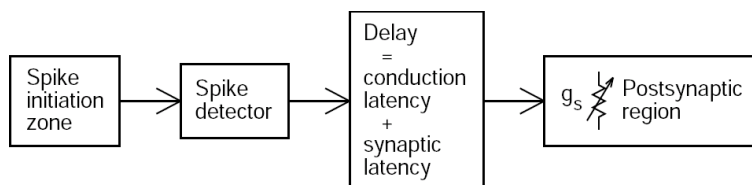


Spike-triggered transmission: computational implementation

Basic idea



More efficient: "virtual spike propagation"



The NetCon class

hoc usage

```
netcon = new NetCon(source, target)
presection netcon = new NetCon(&v(x), \
    target, threshold, delay, weight)
```

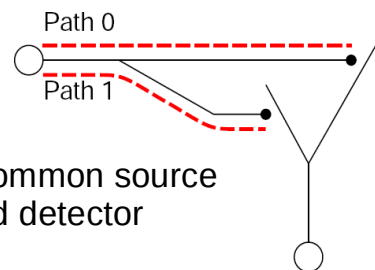
Defaults

```
threshold = 10
delay = 1 // must be >= 0
weight = 0
```

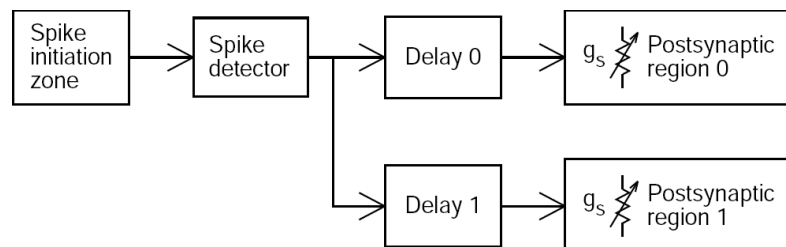
NMODL specification of synaptic mechanism

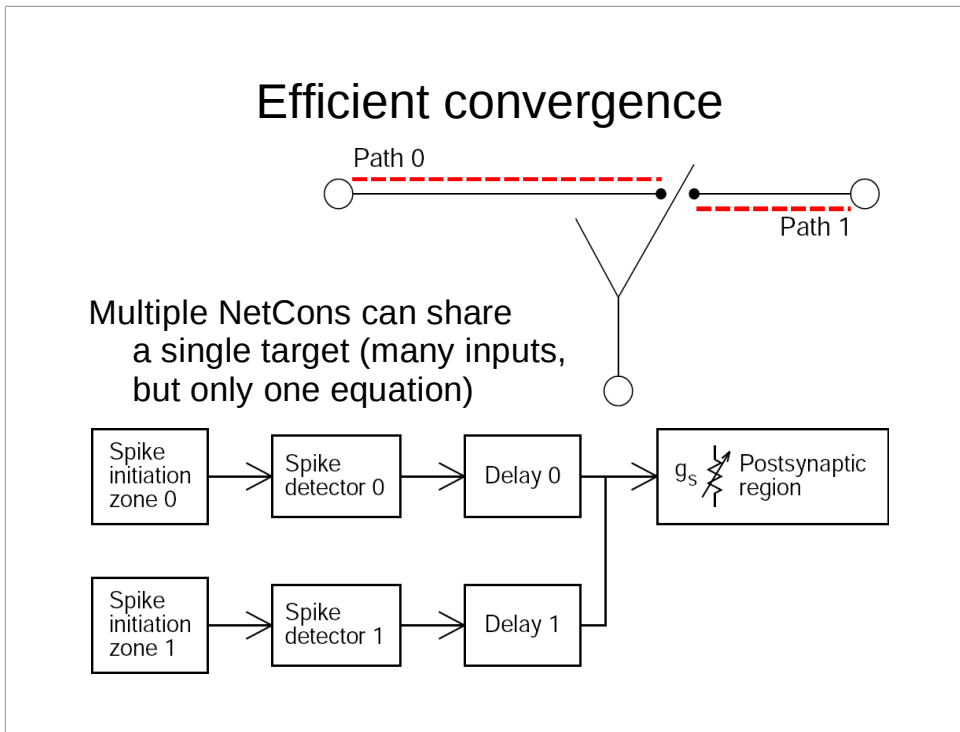
```
NET_RECEIVE(weight(microsiemens)) {
    . . .
}
```

Efficient divergence



Multiple NetCons with a common source
share a single threshold detector





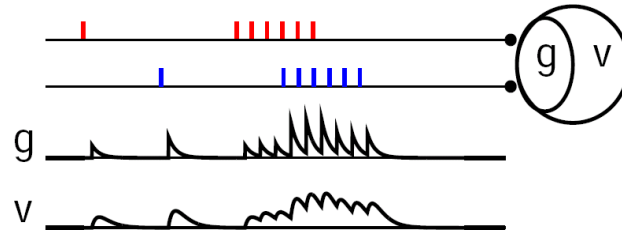
Example: g_s with fast rise and exponential decay

```

NEURON {
  POINT_PROCESS ExpSyn
  RANGE tau, e, i
  NONSPECIFIC_CURRENT i
}
... declarations ...
INITIAL { g = 0 }
BREAKPOINT {
  SOLVE state METHOD cnexp
  i = g*(v-e)
}
DERIVATIVE state { g' = -g/tau }
NET_RECEIVE(w (uS)) { g = g + w }

```

g_s with fast rise and exponential decay *continued*

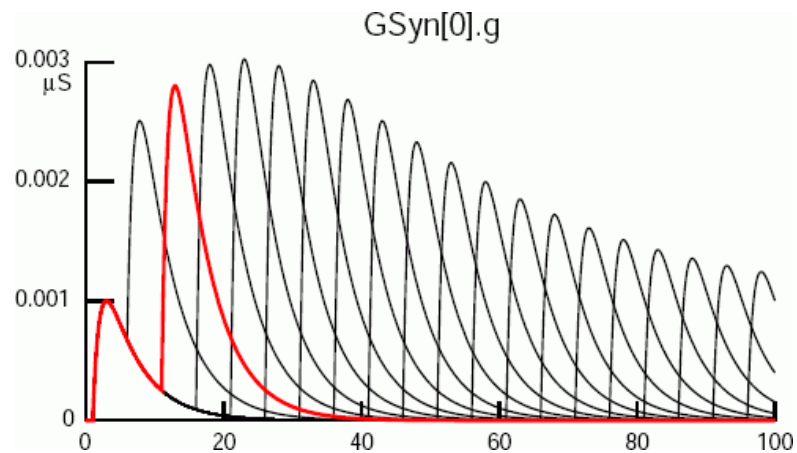


```

BREAKPOINT {
  SOLVE state METHOD cnexp
  i = g*(v-e)
}
DERIVATIVE state { g' = -g/tau }
NET_RECEIVE(w (uS)) { g = g + w }

```

Example: use-dependent synaptic plasticity

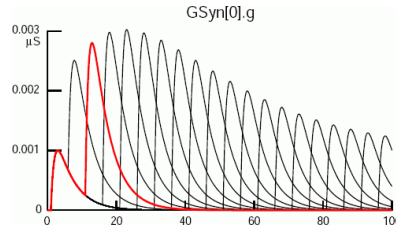


Use-dependent synaptic plasticity *continued*

```

BREAKPOINT {
  SOLVE state METHOD cnexp
  g = B - A
  i = g*(v-e)
}
DERIVATIVE state {
  A' = -A/tau1
  B' = -B/tau2
}
NET_RECEIVE(weight (uS), w, G1, G2, t0 (ms)) {
  INITIAL {w=0 G1=0 G2=0 t0=t}
  G1 = G1*exp(-(t-t0)/Gtau1)
  G2 = G2*exp(-(t-t0)/Gtau2)
  G1 = G1 + Ginc*Gfactor
  G2 = G2 + Ginc*Gfactor
  t0 = t
  w = weight*(1 + G2 - G1)
  g = g + w
  A = A + w*factor
  B = B + w*factor
}

```



Artificial spiking cells

"Integrate and fire" cells

Prerequisite: all state variables must be
analytically computable from a new initial condition

Orders of magnitude faster than numerical integration

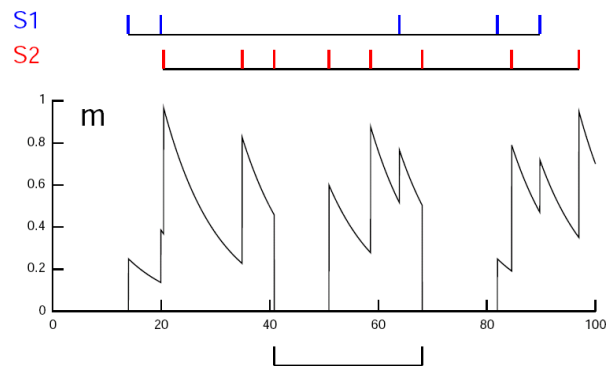
Event-driven simulation run time is

proportional to # of received events

independent of # of cells, # of connections,
and problem time

Hybrid networks

Example: leaky integrate and fire model

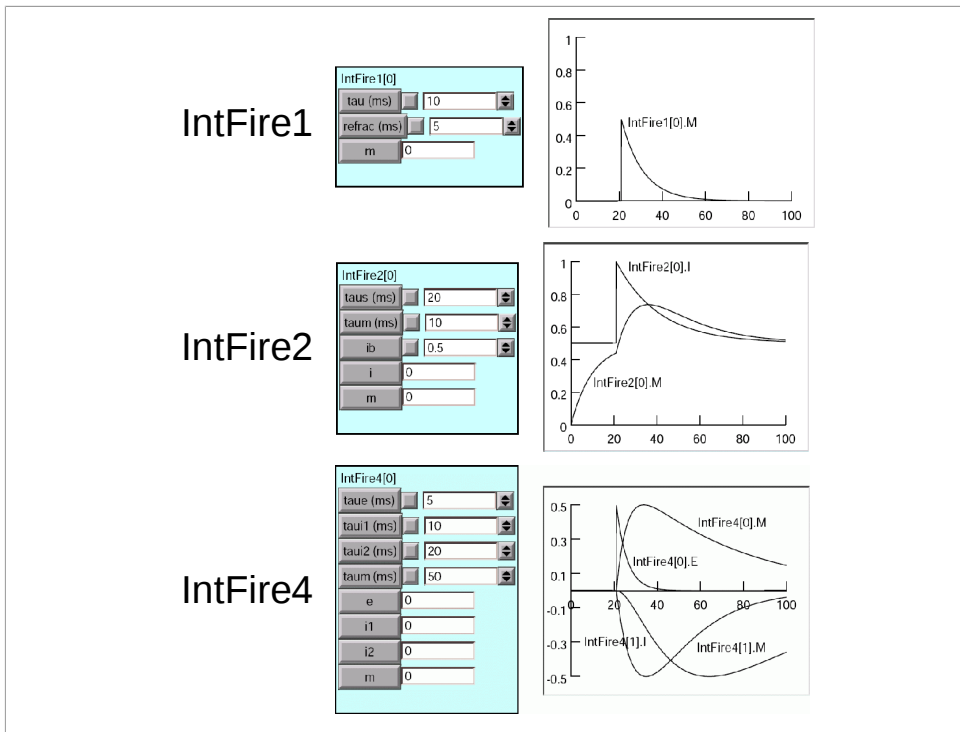


Leaky integrate and fire model *continued*

```

NEURON {
  ARTIFICIAL_CELL IntFire
  RANGE tau, m
}
. . . declarations . . .
INITIAL { m = 0   t0 = t }
NET_RECEIVE (w) {
  m = m*exp(-(t-t0)/tau)
  t0 = t
  m = m + w
  if (m > 1) {
    net_event(t)
    m = 0
  }
}

```



Defining the types of cells

Artificial spiking cells

ARTIFICIAL_CELL with a NET_RECEIVE block that calls net_event

NetStim, IntFire1, IntFire2, IntFire4

Biophysical model cells

"Real" model cells

Sections and density mechanisms

Synapses are POINT_PROCESSES that affect membrane current and have a NET_RECEIVE block, e.g. ExpSyn, Exp2Syn

Defining types of biophysical model cells

Encapsulate in a class

```

begintemplate Cell
  public soma, E, I
  create soma
  objref E, I
  proc init() {
    soma {
      insert hh
      E = new ExpSyn(0.5)
      I = new Exp2Syn(0.5)
      I.e = -80
    }
  }
endtemplate Cell

objref bag_of_cells
bag_of_cells = new List()
for i = 1,1000 bag_of_cells.append(new Cell())

```

Connecting cells

Which setup strategy is more efficient?

Iterate over sources

```

for each cell {
  connect this cell to its targets
}

```

or iterate over targets?

```

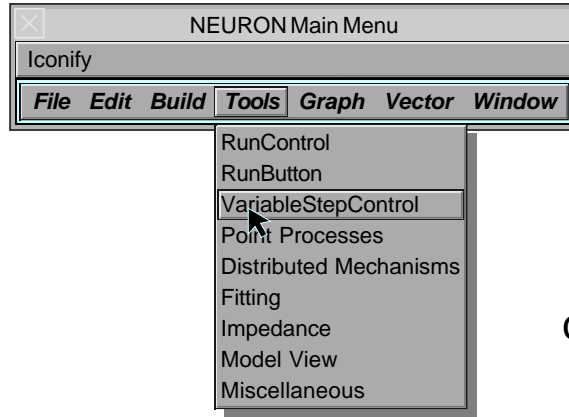
for each cell {
  connect sources to this cell
}

```

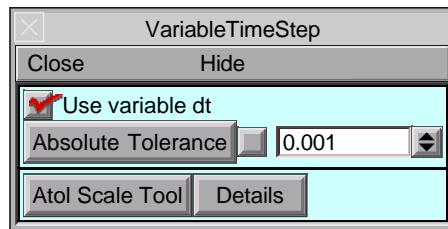
Connecting cells

For a net distributed over multiple CPUs,
it is most efficient to iterate over targets first.

```
for each cell {  
    connect sources to this cell  
}
```



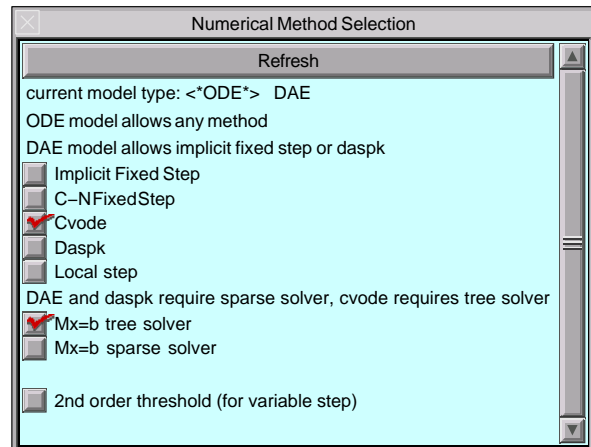
`cvode_active(1)`

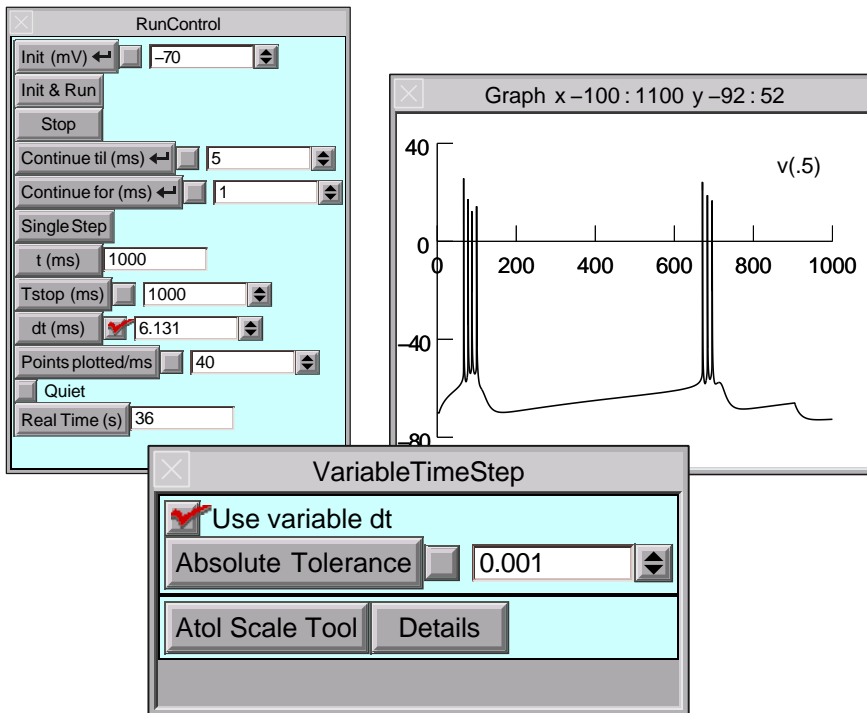
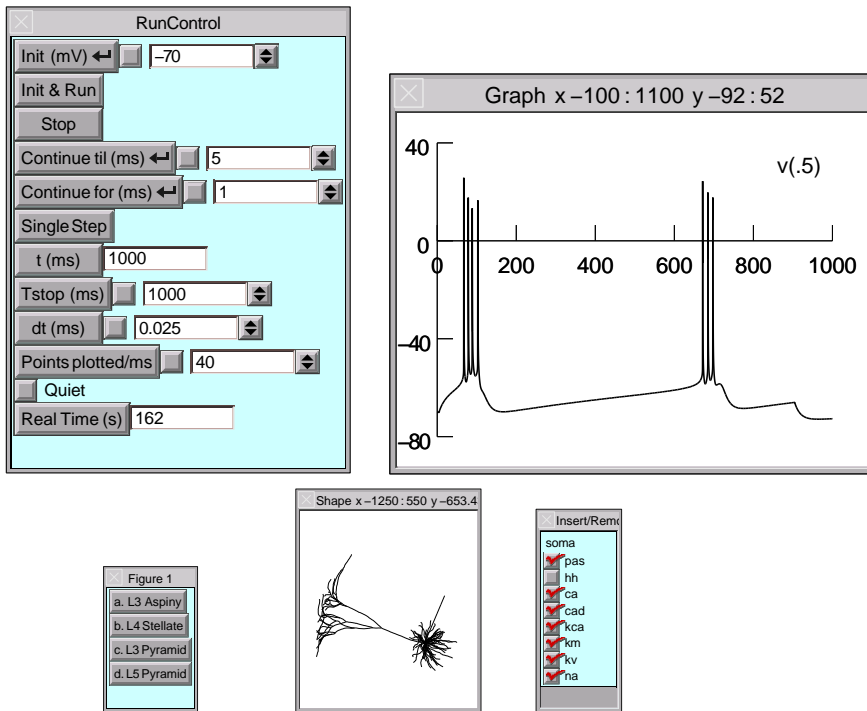


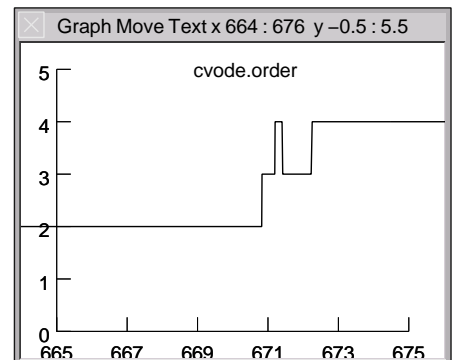
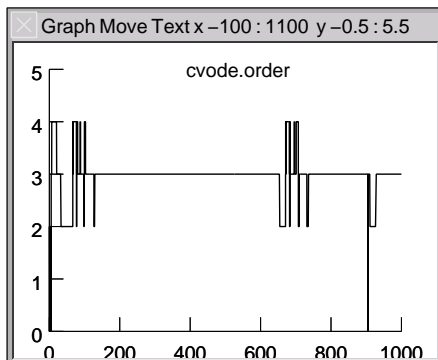
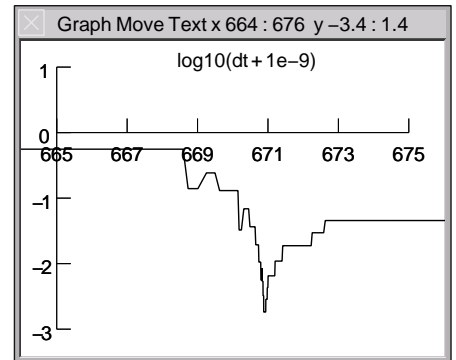
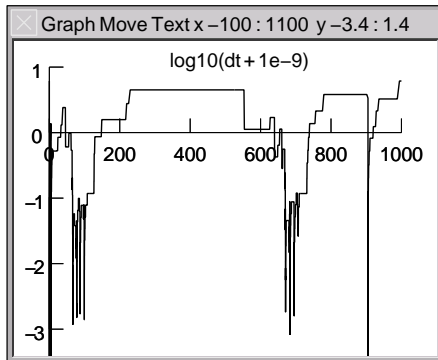
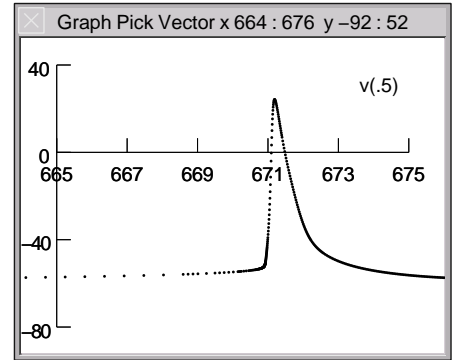
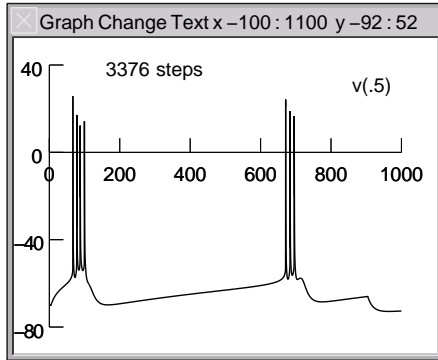
Absolute Tolerance Scale Factors

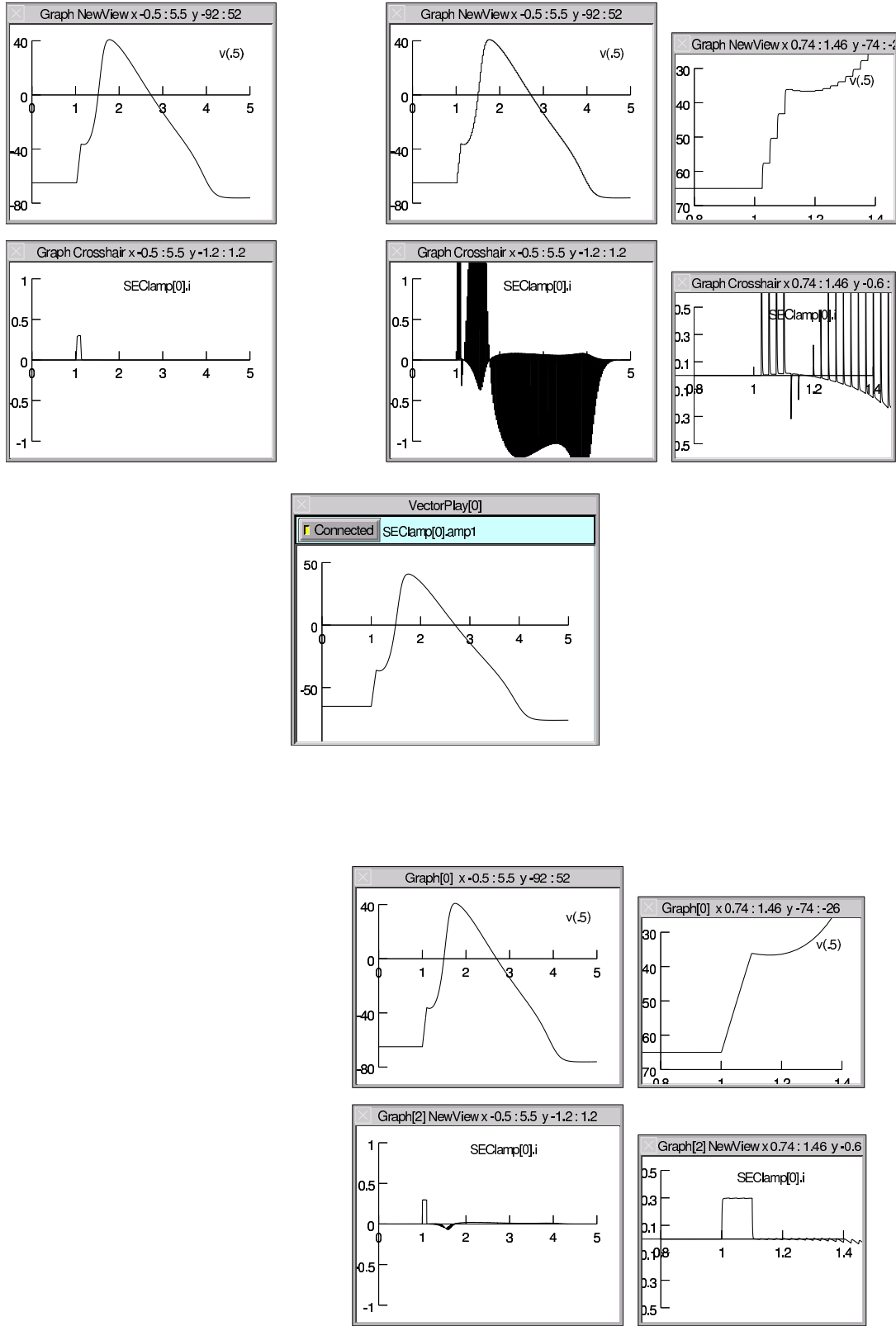
Analysis Run Rescale Original

	*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









`soma vvec.play(&SEClamp[0].amp1, tvec, 1)`

Parallel Computation

"Faster" is the only reason

But...

greater programming complexity
new kinds of bugs
...and not much help for fixing them.

Can the day or week of user effort be recovered?

16384 core EPFL IBM BlueGene/P
1 hour at 850MHz
6 months at 3GHz

Parallel Computation

A simulation run takes about a second

want to do 1000's of them,
varying a dozen or so parameters.

- Screensaver Calin-Jageman and Katz, 2006
- Bulletin-board (Linda)

A simulation run takes hours.

want to spread the problem over several machines.

Parallel Computation

A simulation run takes hours.

want to spread the problem over several machines.

Network

Subnets on different machines

Cells communicate by:

logical spike events with significant
axonal, synaptic delay.

postsynaptic conductance depends
continuously on presynaptic voltage.

gap junctions

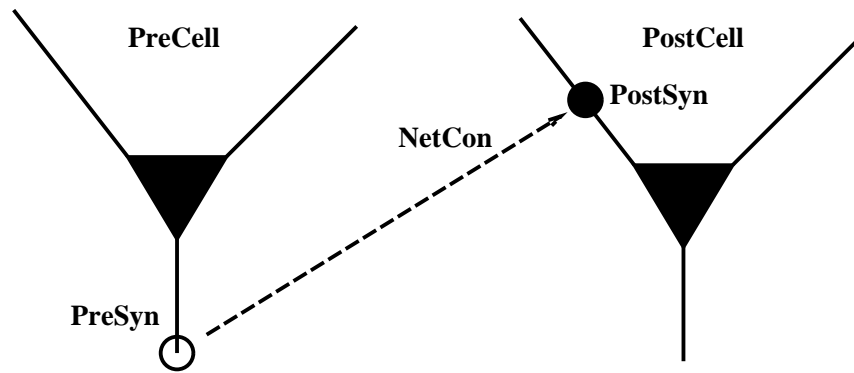
Parallel Computation

A simulation run takes hours.

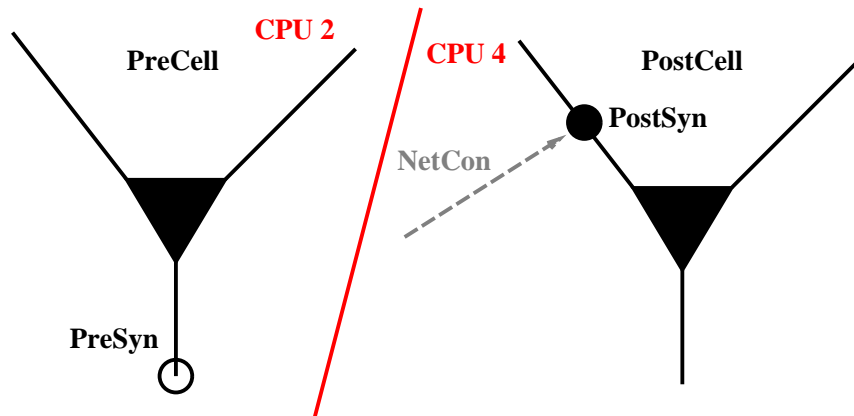
want to spread the problem over several machines.

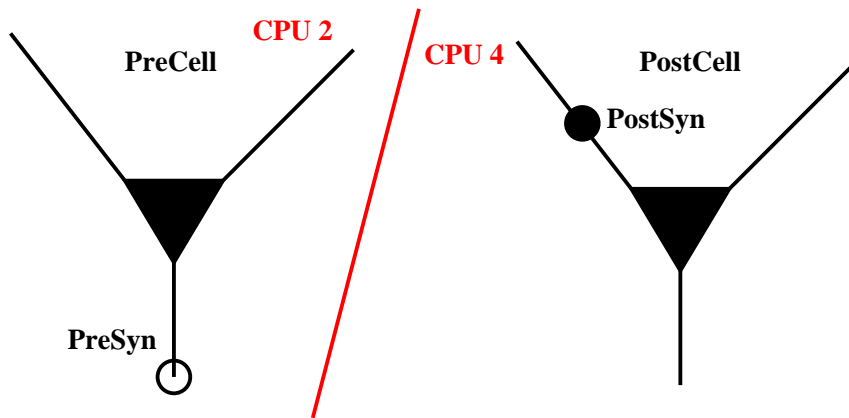
Single cells

portions of the tree cable equation on
different machines.

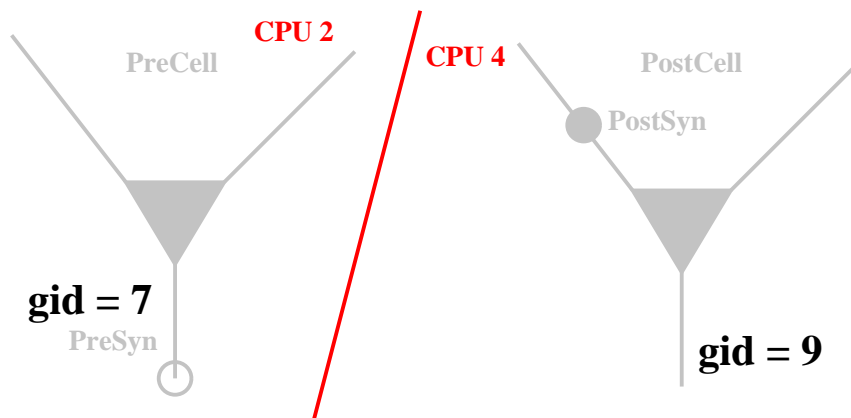


```
nc = new NetCon(PreSyn, PostSyn)
```





```
pc = new ParallelContext()
```



Every spike source (cell) must have a global id number.

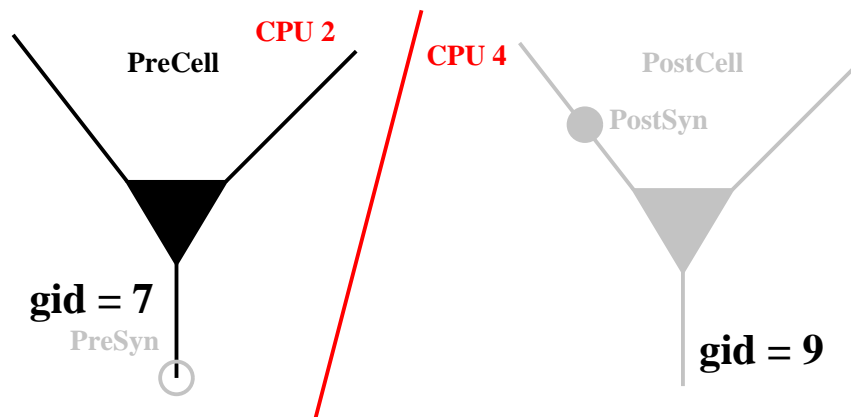
CPU 0	...	CPU 3	CPU 4
pc.id 0		pc.id 3	pc.id 4
pc.nhost 5		pc.nhost 5	pc.nhost 5
ncell 14		ncell 14	ncell 14
gid		gid	gid
0		3	4
5		8	9
10		13	

An efficient way to distribute:

```

for (gid = pc.id; gid < ncell; gid += pc.nhost)
  pc.set_gid2node(gid, pc.id)
  ...
}
body executed only ncell/nhost times, not ncell.

```

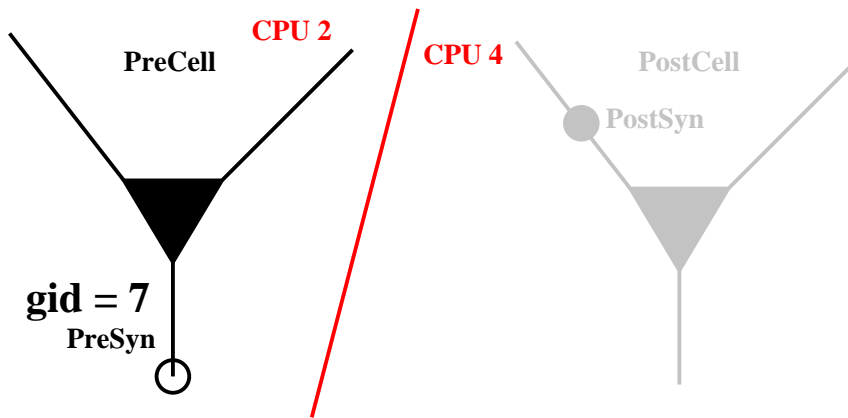


Create cell only where the gid exists.

```

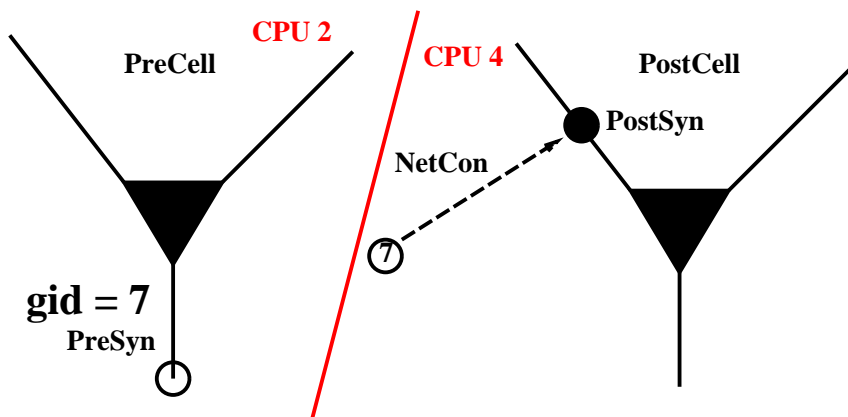
if (pc.gid_exists(7)) {
  PreCell = new Cell()
}

```



Associate gid with spike source.

```
nc = new NetCon(PreSyn, nil)
pc.cell(7, nc)
```



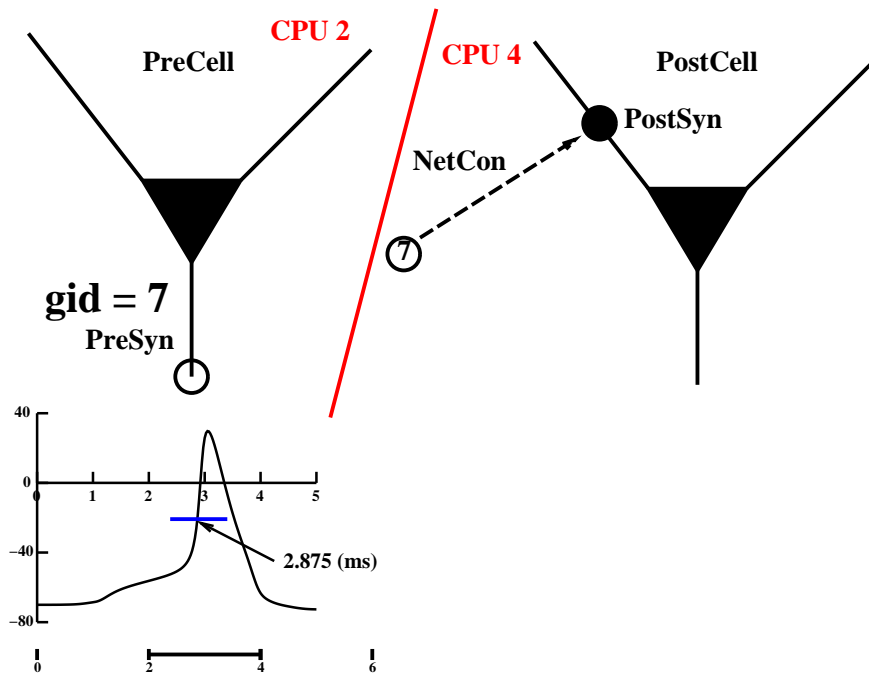
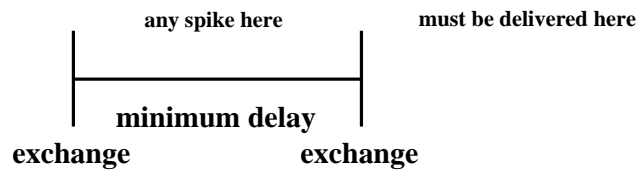
Create NetCon on CPU where target exists.

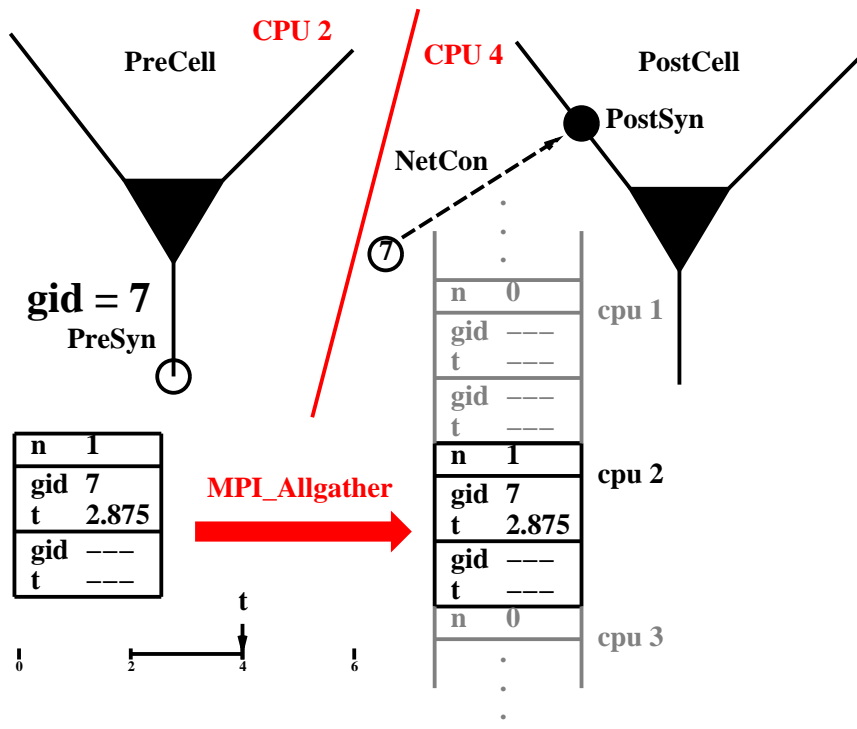
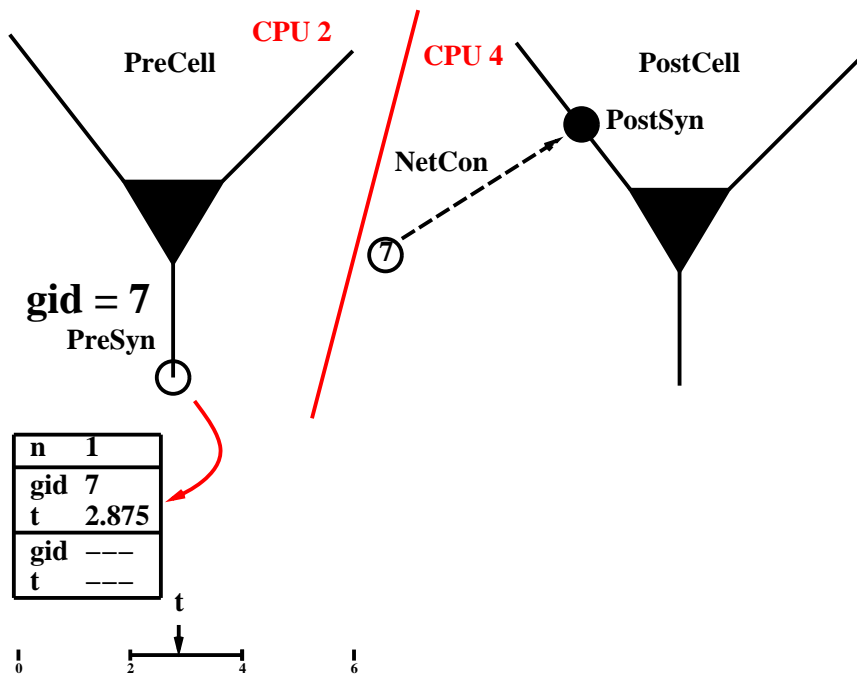
```
nc = pc.gid_connect(7, PostSyn)
```

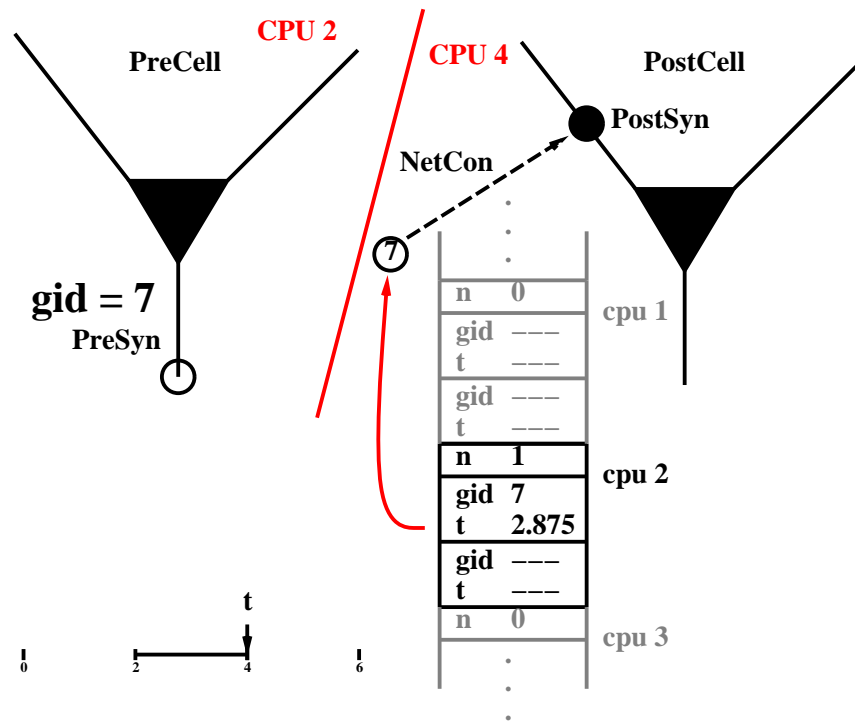
Run using the idiom

```
pc.set_maxstep(10)
stdinit()
pc.solve(tstop)
```

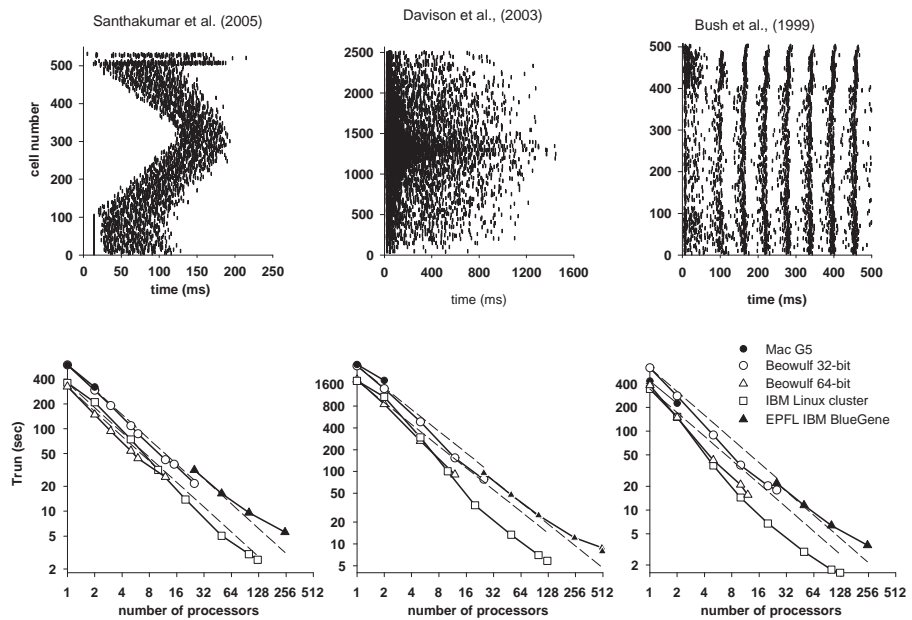
`pc.set_maxstep()` uses
MPI_Allreduce
to determine minimum delay.

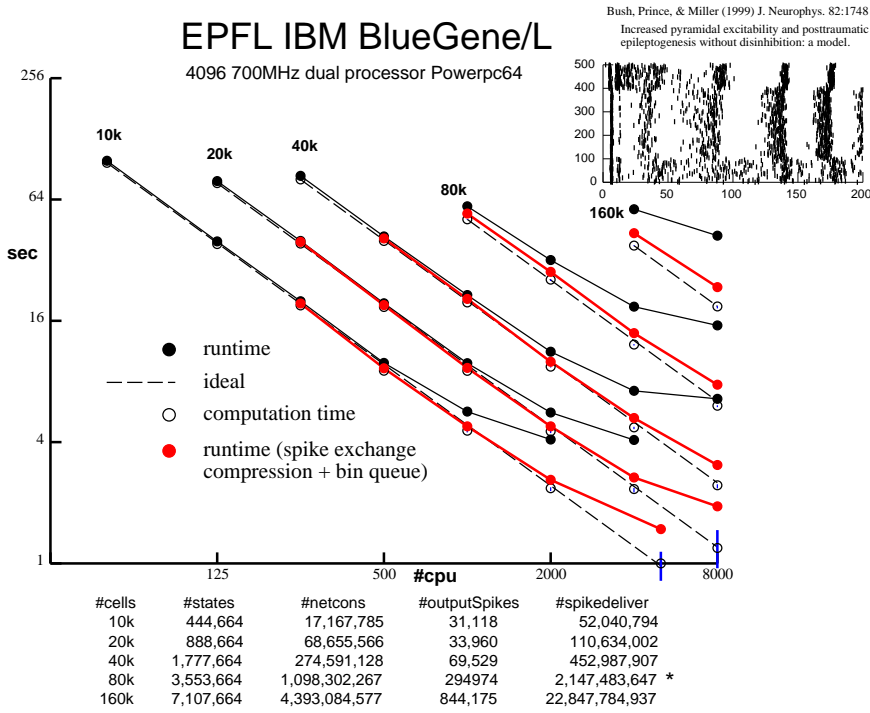






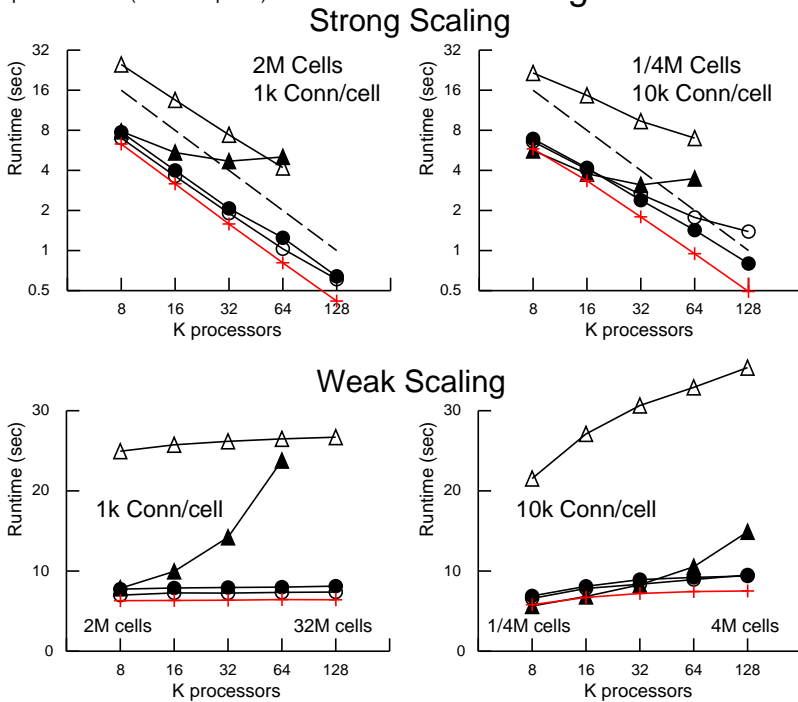
Migliore et al (2006) J. Comput. Neurosci. 21(2):119



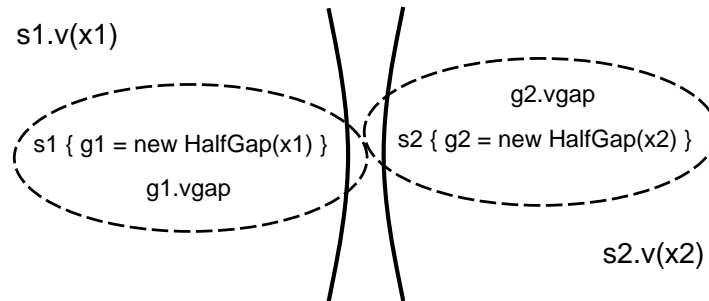


- △ MPI_ISeSend – Two Phase, Two Subinterval
- ▲ Allgather
- DCMF_Multicast – Two Phase, Two Subinterval
- Record-Replay – One Subinterval
- + Computation Time (includes queue)

Artificial Spiking Net Blue Gene/P Argonne National Lab



Continuous Voltage Exchange



gap.mod

```

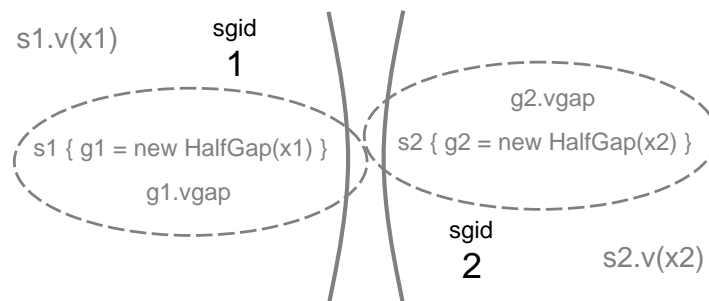
NEURON {
  POINT_PROCESS HalfGap
  ELECTRODE_CURRENT i
  RANGE r, i, vgap
}
PARAMETER { r = 1e9 (megohm) }

ASSIGNED {
  v (millivolt)
  vgap (millivolt)
  i (nanoamp)
}
CURRENT { i = (vgap - v)/r }

```

Continuous Voltage Exchange

`pc.source_var(&source_var, sgid)`



gap.mod

```

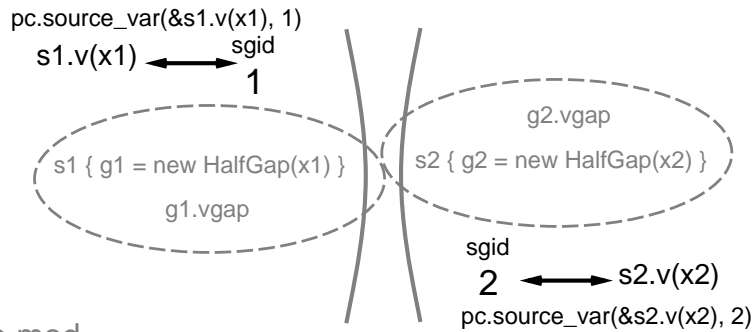
NEURON {
  POINT_PROCESS HalfGap
  ELECTRODE_CURRENT i
  RANGE r, i, vgap
}
PARAMETER { r = 1e9 (megohm) }

ASSIGNED {
  v (millivolt)
  vgap (millivolt)
  i (nanoamp)
}
CURRENT { i = (vgap - v)/r }

```

Continuous Voltage Exchange

pc.source_var(&source_var, sgid)



gap.mod

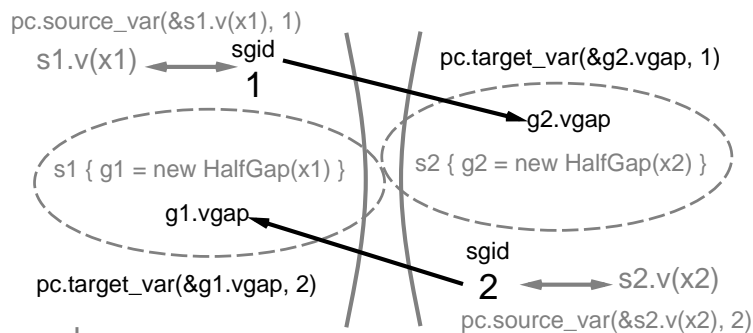
```
NEURON {
    POINT_PROCESS HalfGap
    ELECTRODE_CURRENT i
    RANGE r, i, vgap
}
PARAMETER { r = 1e9 (megohm) }

ASSIGNED {
    v (millivolt)
    vgap (millivolt)
    i (nanoamp)
}
CURRENT { i = (vgap - v)/r }
```

Continuous Voltage Exchange

pc.source_var(&source_var, sgid)

pc.target_var(&target_var, sgid)

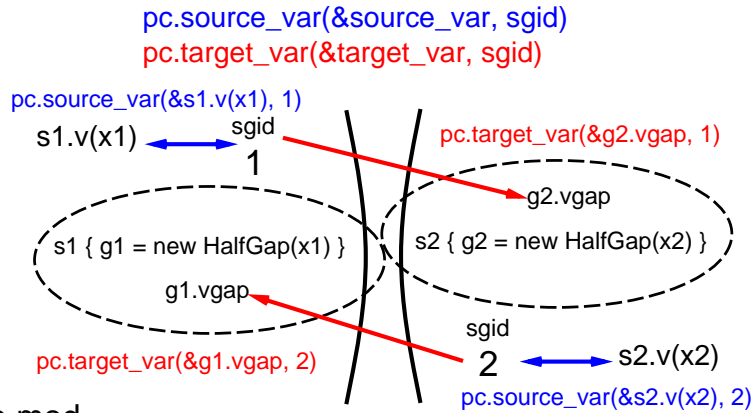


gap.mod

```
NEURON {
    POINT_PROCESS HalfGap
    ELECTRODE_CURRENT i
    RANGE r, i, vgap
}
PARAMETER { r = 1e9 (megohm) }

ASSIGNED {
    v (millivolt)
    vgap (millivolt)
    i (nanoamp)
}
CURRENT { i = (vgap - v)/r }
```

Continuous Voltage Exchange



gap.mod

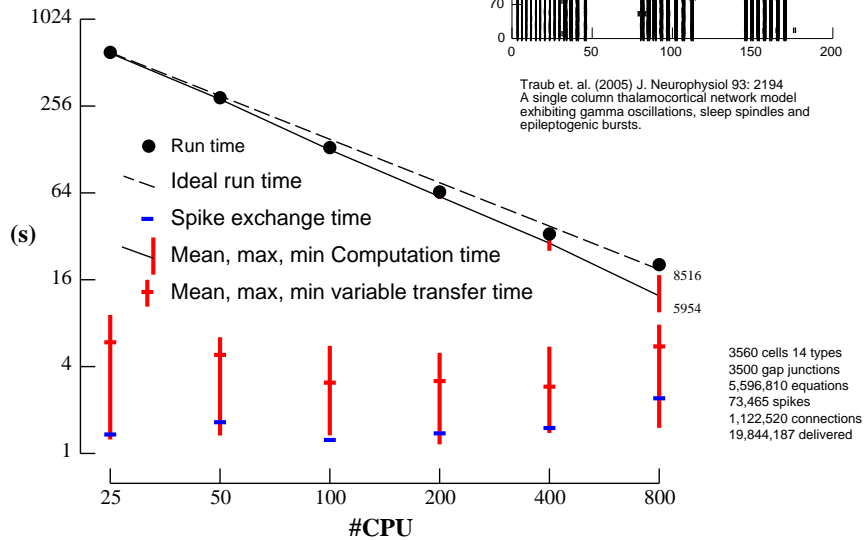
```

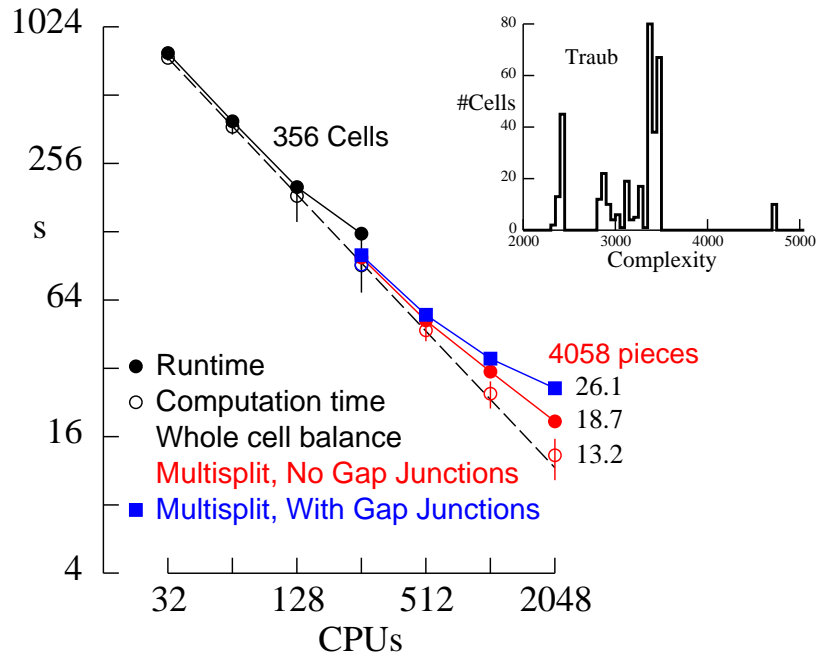
NEURON {
    POINT_PROCESS HalfGap
    ELECTRODE_CURRENT i
    RANGE r, i, vgap
}
PARAMETER { r = 1e9 (megohm) }
ASSIGNED {
    v (millivolt)
    vgap (millivolt)
    i (nanoamp)
}
CURRENT { i = (vgap - v)/r }
    
```

Pittsburgh Supercomputing Center

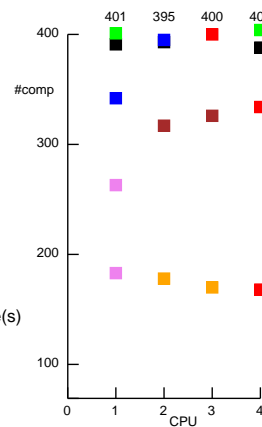
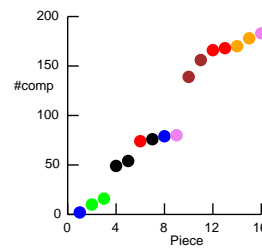
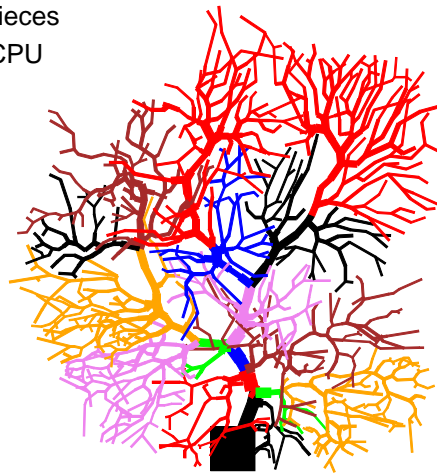
Bigben Cray XT3

2068 2.4 GHz Optron Processors

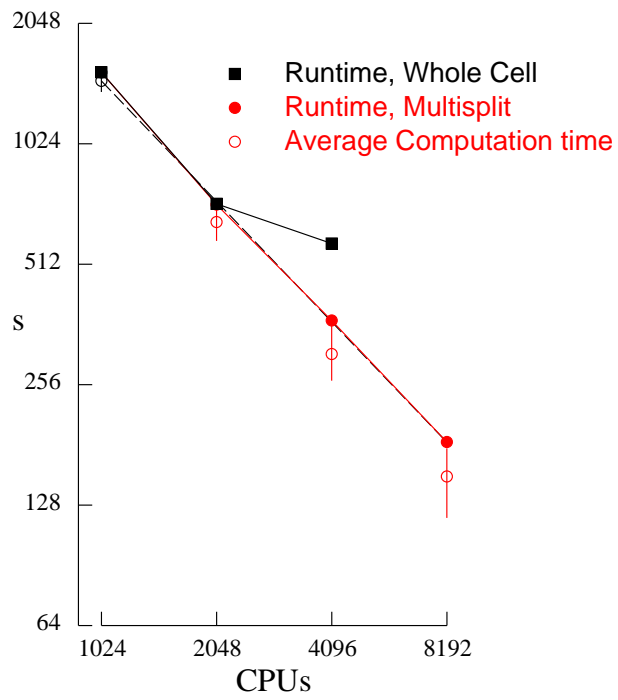
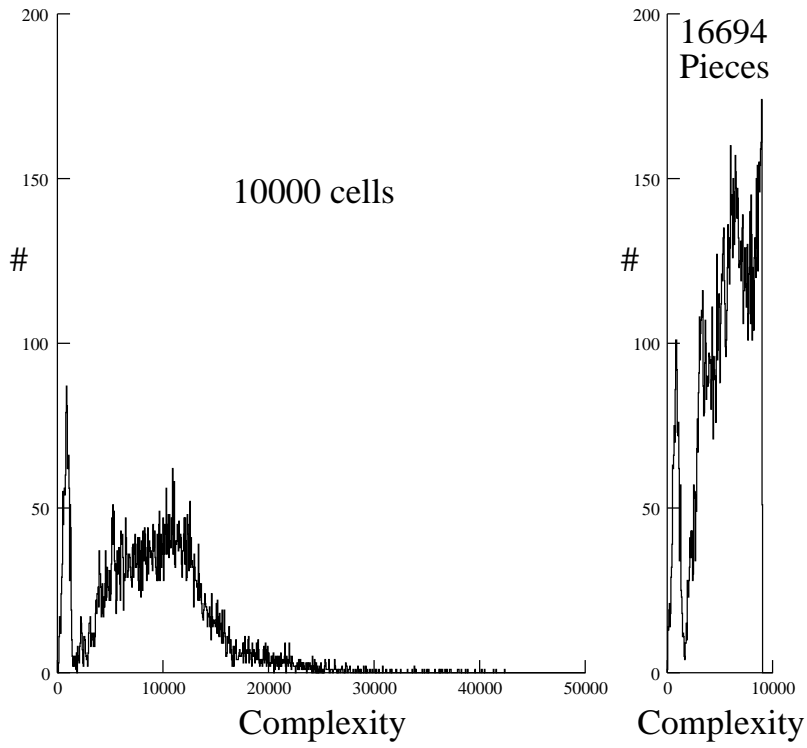




16 Pieces
4 CPU



CPU	Time (s)			Runtime(s)
	Computation	Exchange		
0	13.82	0.56		
1	13.35	1.03	16 pieces, 1 cpu	55.0
2	13.47	0.90	wholecell, 1 cpu	56.2
3	13.56	0.82	16 pieces, 4 cpu	14.4

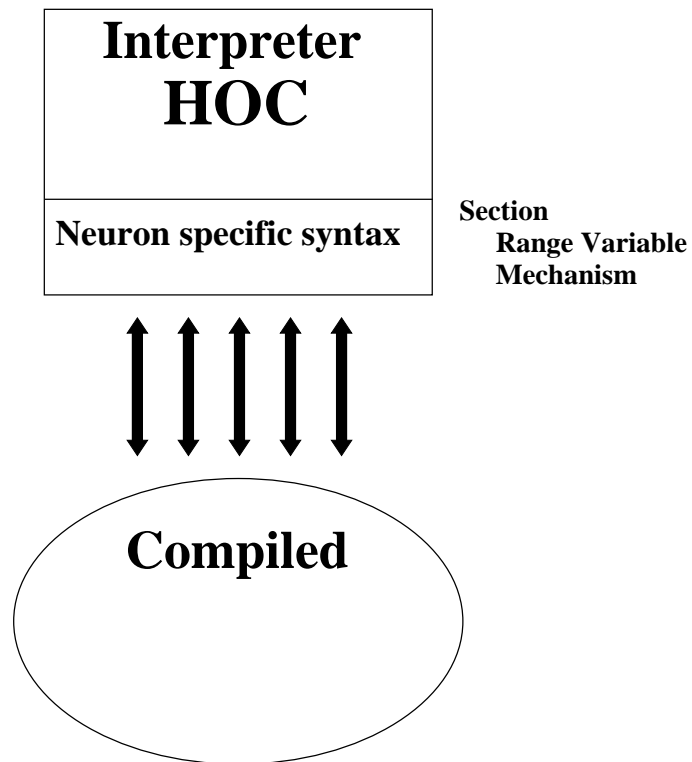


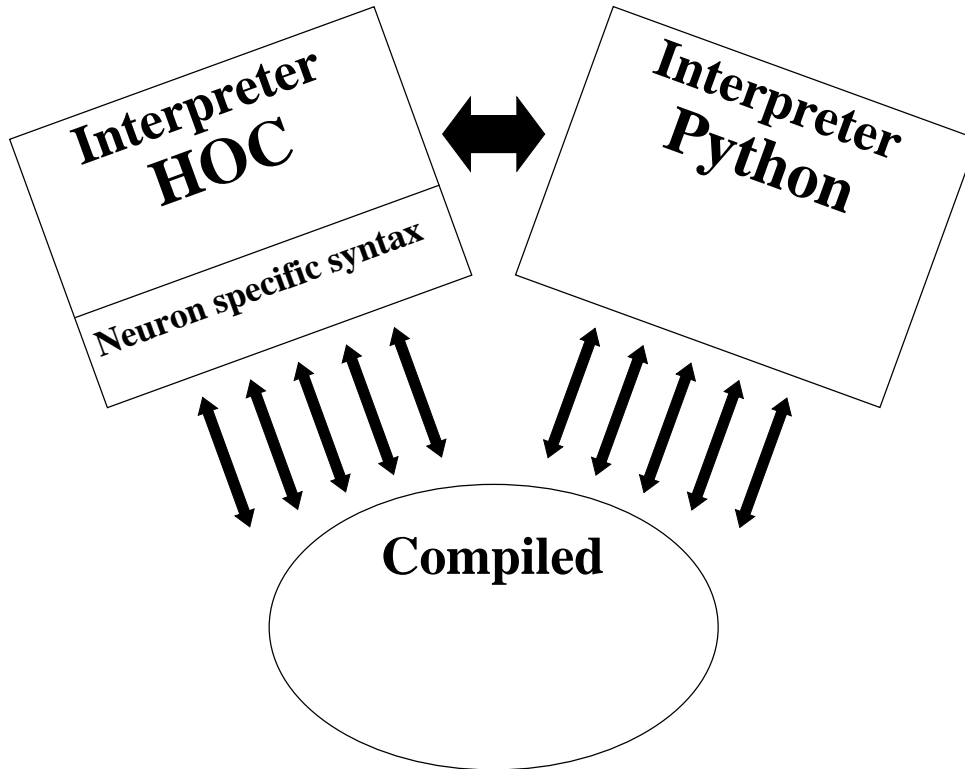
Python + NEURON

All legacy models must work.

Superior representation of
underlying concepts.

No extra installation difficulty.





Installation

```

Linux  i686      >>> import neuron
       x86_64

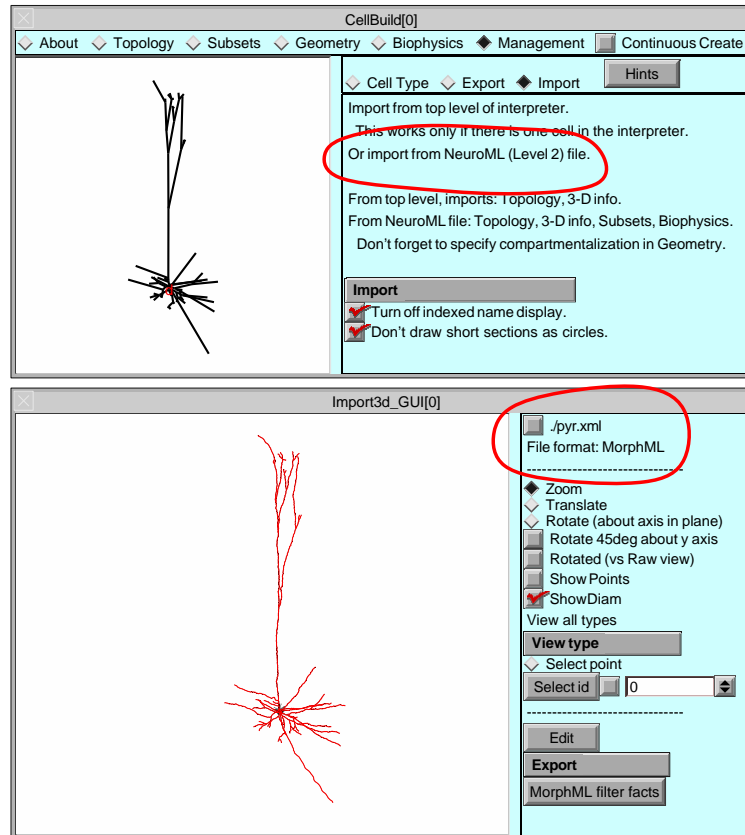
Mac    OS X 10.5-8 Python 2.3-4
       Python 2.5-7
       Python 3.0-2

MSWin  Cygwin
       MinGW

Launch NEURON
       Python

       NumPy

```

```

$ nrniv -python
NEURON -- VERSION 7.3 ...

>>> from neuron import h
>>> print h
<hoc.HocObject object at 0x2b4f1b81e030>

>>> print h.hname()
TopLevelHocInterpreter

>>> h('''
... x = 5
... strdef s
... s = "hello"
... func square() { return $1*$1 }
... ''')
1
>>> print h.x, h.s, h.square(4)
5.0 hello 16.0

```

```

>>> v = h.Vector(4).indgen().add(10)
>>> print v.hname(), len(v), v.size(), v.x[2], v[2]
Vector[1] 4 4.0 12.0 12.0
>>> v.printf()
10      11      12      13
4.0
>>> for x in v: print x
...
10.0
11.0
12.0
13.0
>>>

>>> import numpy
>>> na = numpy.arange(0, 10, 0.00001) # 0.0131
>>> v = h.Vector(na) # 0.0197
>>> v.size()
1000000.0
>>> nb = numpy.array(v) # 0.0125
>>> nb[999999]
9.999990000000000004
>>> b = list(v) # 0.0717
>>> for i in xrange(0, len(nb)):
...     v.x[i] = na[i]
... # 3.7497
>>> nc = v.as_numpy()
>>> v.x[20] = 50.0
>>> nc[20]
50.0

```

```

>>> def callback(a = 1, b = 2):
...     print "callback: a=%d b=%d" % (a, b)
...
>>> fih = h.FInitializeHandler(callback)
>>> h.finitialize()
callback: a=1 b=2
1.0
>>> fih = h.FInitializeHandler((callback,\
... (4, 5)))
>>> h.finitialize()
callback: a=4 b=5
1.0
>>>

```

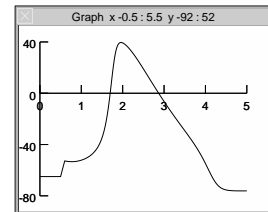
```
# assume hh soma model
```

```
vvec = h.Vector()
vvec.record(soma(.5)._ref_v, sec=soma)
```

```
tvec = h.Vector()
tvec.record(h._ref_t, sec=soma)
```

```
h.run()
```

```
g = h.Graph()
g.size(0, 5, -80, 40)
vvec.line(g, tvec)
```



```

>>> from neuron import h
>>> soma = h.Section(name = 'soma')
>>> axon = h.Section()
>>> axon.connect(soma(1))
>>> axon.nseg = 5
>>> h.topology()

|-|          soma(0-1)
  `-----|          PySec_2b371cd17190(0-1)

1.0
>>> axon.L = 1000
>>> axon.diam = 1

>>> for sec in h.allsec():
...     sec.cm = 1
...     sec.Ra = 100
...     sec.insert('hh')
...
>>> axon.gnabar_hh = .1
>>> axon(.5).hh.gnabar = .09
>>> for seg in axon:
...     print seg.x, seg.hh.gnabar
...
0.1 0.1
0.3 0.1
0.5 0.09
0.7 0.1
0.9 0.1

```

```
>>> stim = h.IClamp(soma(.5))
>>> stim.delay = .5
>>> stim.dur = .1
>>> stim.amp = .4
```

```
class Cell(object):
    def __init__(self):
        self.topology()
        self.subsets()
        ...
    def topology(self):
        self.soma = h.Section(cell = self)
        self.dend = h.Section(cell = self)
        self.dend.connect(self.soma)
        ...
    def subsets(self):
        self.all = h.SectionList()
        self.all.wholetree(sec=self.soma)
```


SenseLab

Neuron Course SfN 2013

Gordon Shepherd

Friday November 8th

[Login](#)

The SenseLab Project is a long-term effort to build integrated, multidisciplinary models of neurons and neural systems. It was founded in 1993 as part of the original Human Brain Project, which began the development of neuroinformatics tools in support of neuroscience research. It is now part of the Neuroscience Information Framework (NIF) and the International Neuroinformatics Coordinating Facility (INCF). The SenseLab project involves novel informatics approaches to constructing databases and database tools for collecting and analyzing neuroscience information, using the olfactory system as a model, with extension to other brain systems.

- [Overview](#)
- [Membrane Properties Resource](#)
- [Read about recent changes in SenseLab](#)

Brain Database Research

Neuronal Databases	CellPropDB	NeuronDB	ModelDB	MicrocircuitDB
Olfactory Databases	ORDB	dorDB	OdorMapDB	DBModelDB
Disease Databases	BrainPharm			


Neuroscience Information Framework

[Help & Introduction](#) |
 [Labs & People](#) |
 [Links](#) |
 [Publications](#) |
 [Architecture](#) |
 [Teaching](#)

Total site hits in the past 12 months: **2,368,283**

This database was supported by the Human Brain Project (NIDCD, NIH, NIA, NICD, NINDS) and MURI (Multidisciplinary University Research Initiative). It is now supported by R01 DC 009577 from the National Institute for Deafness and other Communication Disorders.

Questions, comments, problems? Email the [SenseLab Administrator](#).
 This site is Copyright 2013 Shepherd Lab, Yale University



NeuronDB

Back to [SenseLab](#) User: Public

NeuronDB provides a dynamically searchable database of three types of neuronal properties: voltage gated conductances, neurotransmitter receptors, and neurotransmitter substances. It contains tools that provide for integration of these properties in a given type of neuron and compartment, and for comparison of properties across different types of neurons and compartments. Read the tutorial for [searching for Neuron Properties in NeuronDB](#)

This resource is intended to:

- Support the genomics and proteomics of neuron types
- Support research on neuron properties
- Facilitate the creation of computational neuronal models
- Identify receptors across neuron types to aid in drug development
- Serve as a teaching aid

Search the Database By:


- Neuron List [Alphabetically](#)
- Neuron List [By Brain Regions](#)
- [Membrane Properties Comprehensive Inventory: Channels, Receptors, Neurotransmitters/Neuromodulators](#)
- [Membrane Properties for NeuronDB: Currents, Receptors, Neurotransmitters/Neuromodulators](#)
- Canonical forms of neurons ([see explanation](#))
- [Bibliographic citations](#)

- Give us your [feedback](#)
- [Deposit](#) to the Database
- [FAQ](#) and related [Links](#)
- [NeuronDB Login](#)

This database is being developed by [Luis N. Marengo](#)¹, [Rixin Wang](#)¹, [Thomas M. Morse](#)², [Perry L. Miller](#)¹ and [Gordon M. Shepherd](#)², ¹*Center for Medical Informatics, Department of Neurobiology, Yale University School of Medicine, New Haven, CT 06510.*

Some of the data, together with the graphics on the NeuronDB banner, are taken from *The Synaptic Organization of the Brain*, edited by G.M. Shepherd, New York: Oxford University Press (Second to Fourth Editions: 1979, 1990, 1998).

This database was supported by the Human Brain Project (NICHD, NIMH, NIA, NICD, NINDS) and MURI (Multidisciplinary University Research Initiative). It is now supported by ROI DC 009977 from the National Institute for Deafness and other Communication Disorders.



NeuronDB

Back User: Public

Olfactory bulb mitral cell

Mode: [Overview](#) [Data/Search](#) [plus Connectivity](#) [plus Classical References/Notes](#) [Models](#) [BrainPharm](#)




Region: [Distal apical dendrite](#) [Middle apical dendrite](#) [Proximal apical dendrite](#) [Distal basal dendrite](#) [Middle basal dendrite](#) [Proximal basal dendrite](#) [Soma](#) [Axon hillock](#) [Axon fiber](#) [Axon terminal](#) [All Compartments](#)

Properties: [Receptors](#) [Channels](#) [Transmitters](#) [All Properties](#)

Are: Present Absent

Neuron Type: principal
 Organism: Vertebrates
 ElectroPhysiology: [NeuroElectro.org](#)
 Genes: [Allen Brain Atlas - Links](#)

	Input Receptors	Intrinsic Currents	Output Transmitters
Distal apical dendrite	Glutamate from olfactory receptor neuron axon terminals AMPA Intracellular recordings: CNQX blocks early component of EPSP elicited by olfactory nerve volley nerve volley (Berkowicz D and Trombley PQ and Shepherd GM, 1994 [turtle] ¹⁰). Electrophysiology data: DNQX attenuates early and late excitatory components in peristimulus time histograms of mitral cell unit responses to olfactory nerve volleys (Ernis and Zimmer LA and Shipley MT, 1996 [rat] ²⁰). Intracellular recordings: CNQX blocks early component of EPSP response to olfactory nerve volley (Chen WR and Shepherd GM, 1997 [rat] ¹⁶). Paired whole-cell recording revealed reciprocal excitatory connections between mitral cells. Pharmacological analysis suggested that it could be mediated by both AMPA and NMDA receptors (Irshah NN and Sakmann B, 2002 ¹⁶⁹). (autoreceptors) mitral cell glomerular tuft (Dad) mGluR1 Auto-activation from glutamate released by mitral cell secondary dendrites (van den Pol AN, 1995 [rat] ¹).	I_h (Angelo K and Margrie TW, 2011 ²⁶⁸) report the presence and function of I _h . I_A (Bischofberger J and Jonas P, 1997 ³²²). I_{Na,t} Implied by recording of fast prepotential. Dual patch recordings provide evidence for both backpropagating and forward-propagating impulses in the primary dendrite (Mori K, Nowycky M and Shepherd GM, 1982 [turtle] ¹⁸ ; Chen et al 1997). Dendritic patch recordings showed an even density of Na channels (120pS um ⁻²) up to 350 um from the soma along the primary dendrite to the origin of the glomerular tuft (Bischofberger J and Jonas P, 1997 ³²²). By	Mitral cell glomerular tuft and PG Glutamate cell dendrites in the glomerulus (presumably) Implied by Glu released by other compartments of the mitral cell (Dale's law). Target (destination) is presumably PG cell dendrites in the glomerulus (van den Pol AN, 1995 [rat] ¹).




Models that contain the Neuron : *Olfactory bulb mitral cell*

Models

[A two-layer biophysical olfactory bulb model of cholinergic neuromodulation \(Li and Cleland 2013\)](#)
[Compartmental model of a mitral cell \(Popovic et al. 2005\)](#)
[Dynamical model of olfactory bulb mitral cell \(Rubin, Cleland 2006\)](#)
[Functional structure of mitral cell dendritic tuft \(Djurisic et al. 2008\)](#)
[I&F models of ACh modulation in the olfactory bulb and piriform cortex \(de Almeida et al. 2012\)](#)
[Large scale model of the olfactory bulb \(Yu et al., 2013\)](#)
[Lateral dendrodendritic inhibition in the Olfactory Bulb \(David et al. 2008\)](#)
[Olfactory Bulb Network \(Davison et al 2003\)](#)
[Olfactory Computations in Mitral-Granule cell circuits \(Migliore & McTavish 2013\)](#)
[Olfactory Mitral Cell \(Bhalla, Bower 1993\)](#)
[Olfactory Mitral Cell \(Davison et al 2000\)](#)
[Olfactory Mitral Cell \(Shen et al 1999\)](#)
[Olfactory Mitral Cell: I-A and I-K currents \(Wang et al 1996\)](#)
[Olfactory Mitral cell: AP initiation modes \(Chen et al 2002\)](#)
[Olfactory bulb cluster formation \(Migliore et al. 2010\)](#)
[Olfactory bulb granule cell: effects of odor deprivation \(Saghatelyan et al 2005\)](#)
[Olfactory bulb mitral and granule cell column formation \(Migliore et al. 2007\)](#)
[Olfactory bulb mitral and granule cell: dendrodendritic microcircuits \(Migliore and Shepherd 2008\)](#)
[Olfactory bulb mitral cell gap junction NN model: burst firing and synchrony \(O'Connor et al. 2012\)](#)
[Olfactory bulb mitral cell: synchronization by gap junctions \(Migliore et al 2005\)](#)
[Olfactory bulb network model of gamma oscillations \(Rathellier et al. 2006; Lagier et al. 2007\)](#)
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[Synchrony by synapse location \(McTavish et al. 2012\)](#)



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Models that contain the Neuron : *Olfactory bulb mitral cell*

Models	Description
A two-layer biophysical olfactory bulb model of cholinergic neuromodulation (Li and Cleland 2013)	This is a two-layer biophysical olfactory bulb (OB) network model to study cholinergic neuromodulation. Simulations show that nicotinic receptor activation sharpens mitral cell receptive field, while muscarinic receptor activation enhances network synchrony and gamma oscillations. This general model suggests that the roles of nicotinic and muscarinic receptors in OB are both distinct and complementary to one another, together regulating the effects of ascending cholinergic inputs on olfactory bulb transformations.
Compartmental model of a mitral cell (Popovic et al. 2005)	Usage of a morphologically realistic compartmental model of a mitral cell and data obtained from whole-cell patch-clamp and voltage-imaging experiments in order to explore passive parameter space in which reported low EPSP attenuation is observed.
Dynamical model of olfactory bulb mitral cell (Rubin, Cleland 2006)	This four-compartment mitral cell exhibits endogenous subthreshold oscillations, phase resetting, and evoked spike phasing properties as described in electrophysiological studies of mitral cells. It is derived from the prior work of Davison et al (2000) and Bhalla and Bower (1993). See readme.txt for details.
Functional structure of mitral cell dendritic tuft (Djurisic et al. 2008)	The computational modeling component of Djurisic et al. 2008 addressed two primary questions: whether amplification by active currents is necessary to explain the relatively mild attenuation suffered by tuft EPSPs spreading along the primary dendrite to the soma; what accounts for the relatively uniform peak EPSP amplitude throughout the tuft. These simulations show that passive spread from tuft to soma is sufficient to yield the low attenuation of tuft EPSPs, and that random distribution of a biologically plausible number of excitatory synapses throughout the tuft can produce the experimentally observed uniformity of depolarization.
I&F models of ACh modulation in the olfactory bulb and piriform cortex (de Almeida et al. 2012)	This matlab code was used in the paper "A model of cholinergic modulation in olfactory bulb and piriform cortex" (de Almeida, Idiart and Linster, 2013). This work uses a computational model of the OB and PC and their common cholinergic inputs to investigate how bulbar cholinergic modulation affects cortical odor processing.
Large scale model of the olfactory bulb (Yu et al., 2013)	The readme file currently contains links to the results for all the 72 odors investigated in the paper, and the movie showing the network activity during learning of odor k3-3 (an aliphatic ketone).

A single column thalamocortical network model (Traub et al 2005)

Accession: 45539

To better understand population phenomena in thalamocortical neuronal ensembles, we have constructed a preliminary network model with 3,560 multicompartment neurons (containing soma, branching dendrites, and a portion of axon). Types of neurons included superficial pyramids (with regular spiking [RS] and fast rhythmic bursting [FRB] firing behaviors); RS spiny stellates; fast spiking (FS) interneurons, with basket-type and axoaxonic types of connectivity, and located in superficial and deep cortical layers; low threshold spiking (LTS) interneurons, that contacted principal cell dendrites; deep pyramids, that could have RS or intrinsic bursting (IB) firing behaviors, and endowed either with non-tufted apical dendrites or with long tufted apical dendrites; thalamocortical relay (TCR) cells; and nucleus reticularis (nRT) cells. To the extent possible, both electrophysiology and synaptic connectivity were based on published data, although many arbitrary choices were necessary.

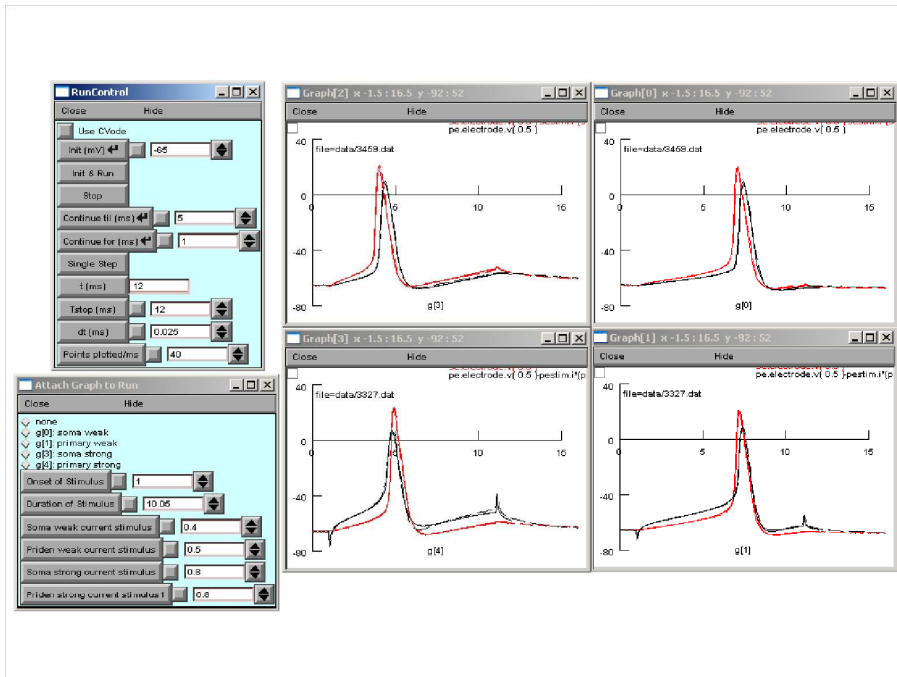
References:
 1. Traub RD, Contreras D, Cunningham MO, Murray H, Lebeau FE, Roopun A, Bibbig A, et al (2005) A single-column thalamocortical network model exhibiting gamma oscillations, sleep spindles and epileptogenic bursts. Appendix B. *J Neurophysiol* **93**(4):2194-232 [PubMed]
 2. Traub RD, Contreras D, Whittington MA (2005) Combined experimental-simulation studies of cellular and network mechanisms of epileptogenesis in vitro and in vivo. *J Clin Neurophysiol* **22**:330-42 [PubMed]


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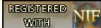
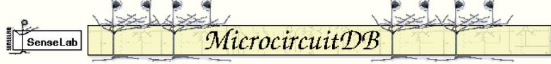
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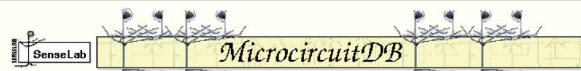
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