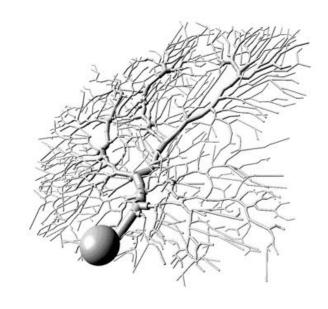
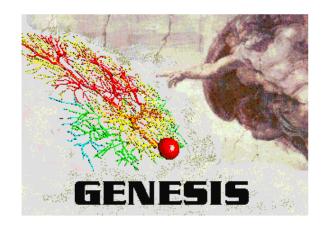
Built-in solvers de neuronas detalladas

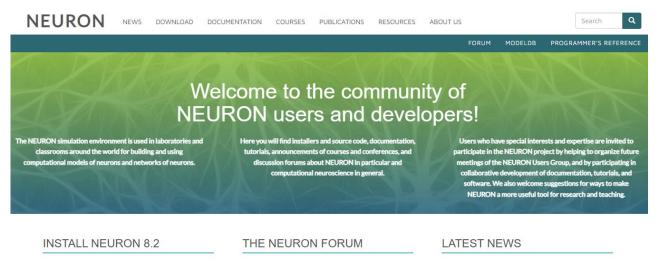
- NEURON's CVODE: NEURON provides the CVODE solver, which is an adaptive, variable-order solver designed for stiff and non-stiff systems. It allows accurate time-stepping while adapting to the system's needs.
- GENESIS Solvers: GENESIS also provides several solvers optimized for neural simulations, including implicit methods and adaptive time-stepping.



GENESIS 2.4 Reference Manual



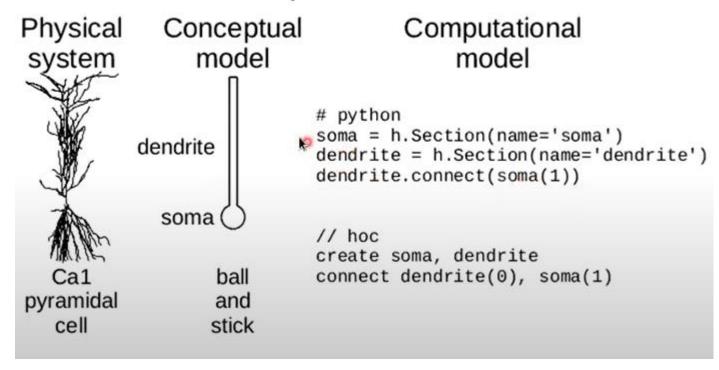
May 2019 Update



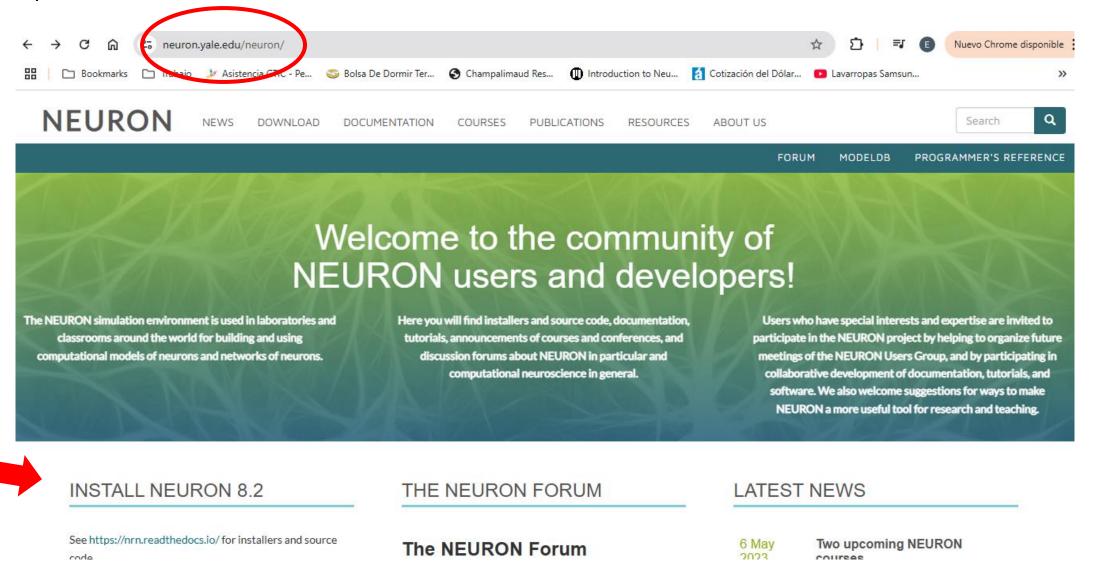
Buscamos modelos de neuronas / circuitos neuronales donde:

- Hay propiedades morfológicas y biofísicas complejas en juego
- Hay comunicación eléctrica y/o química
- Los modelos están fuertemente asociados a observaciones experimentales

From Physical System to Computational Model



Python y NEURON instalados



Python y NEURON instalados



/ The NEURON Simulator O Edit on GitHub

The NEURON Simulator

NEURON is a simulator for neurons and networks of neurons that runs efficiently on your local machine, in the cloud, or on an HPC, Build and simulate models using Python, HOC, and/or NEURON's graphical interface. From this page you can watch recorded NEURON classes, read the Python or HOC programmer's references, browse the NEURON forum, explore the source code for over 750 NEURON models on ModelDB, and more (use the links on the side or search).



Installation

macOS Linux Windows Cloud Source code

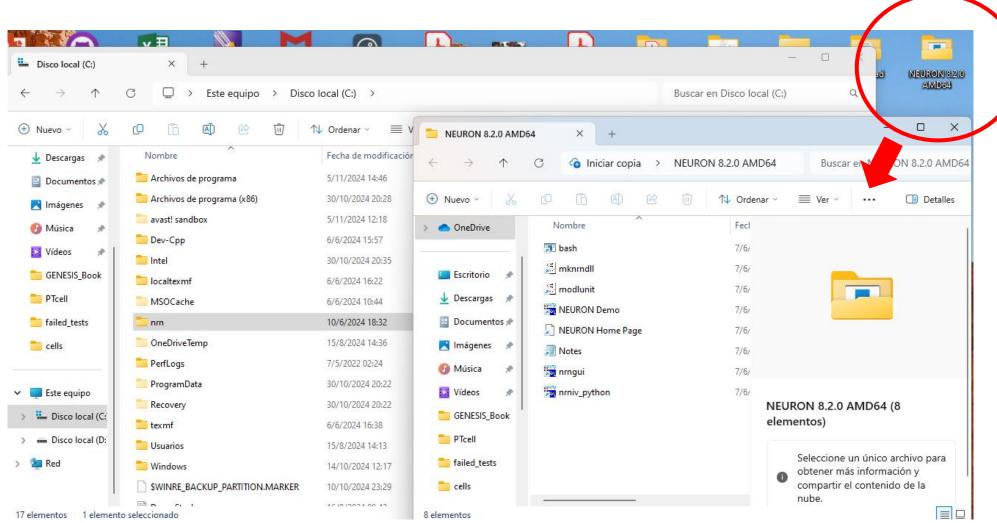
Download the Windows Installer.

You can also install the Linux wheel via the Windows Subsystem for Linux (WSL). See instructions.

For troubleshooting, see the detailed installation instructions.

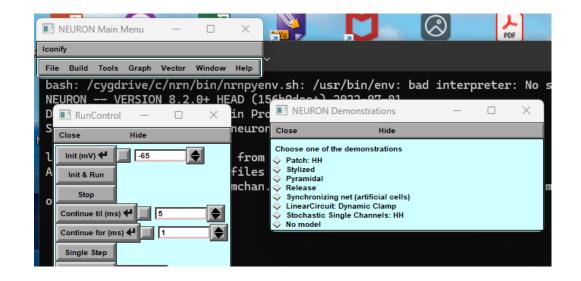
See also the NEURON documentation index and the NEURON forum.

Python y NEURON instalados





- -> Anaconda Python terminal + "neuron": Ejecuta y carga NEURON GUI (graphical user interface)
- -> NEURON Folder: Ejecutar "NEURON Demo" -> Carga modelos ya implementados (Demostraciones)

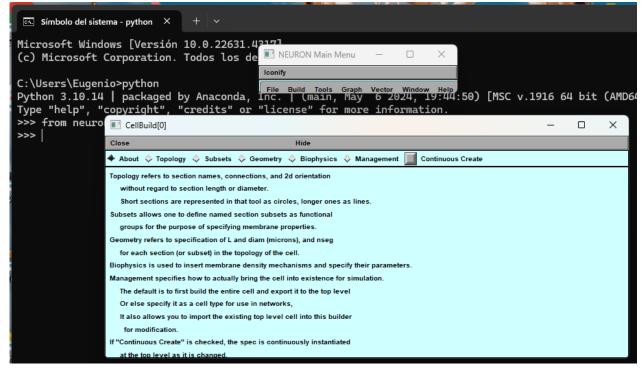


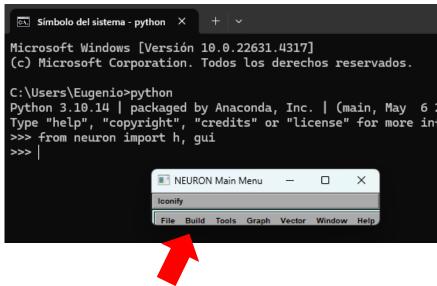
Mas fácil para construir modelos rápidos y tener feedback

-> NEURON as a Python module. System prompt + "python". Then, >>> from neuron import h, gui

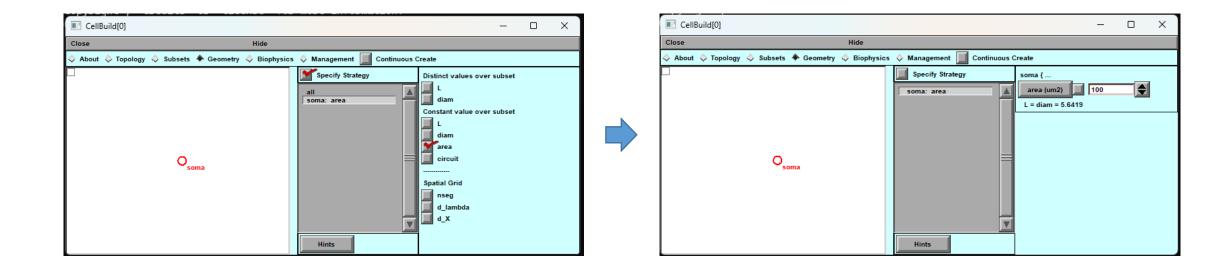
Acceso desde Python a toda la maquinaria computacional de NEURON

- -> Construyendo un modelo simple de compartimiento único (soma)
 - System prompt + "python" . Then, >>> from neuron import h, gui
 - Hacer un modelo de célula: Main menú -> Build -> CellBuilder

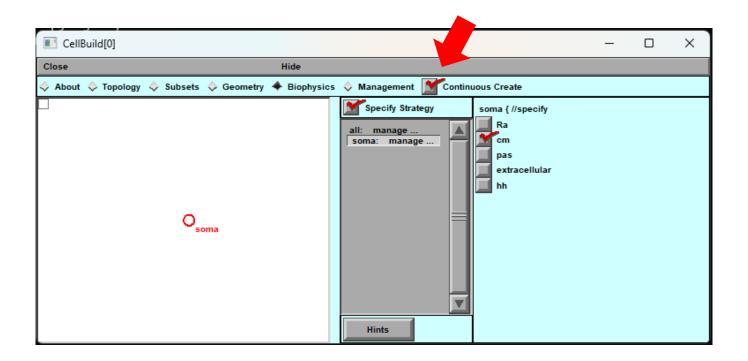




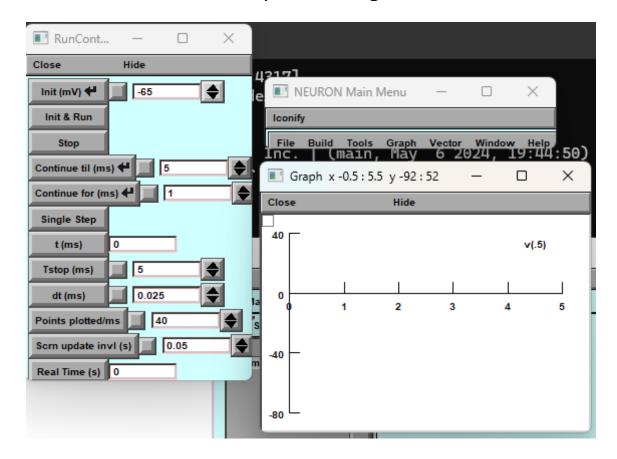
- -> Construyendo un modelo simple de compartimiento único (soma)
 - Topology -> Hay un elemento/sección (no está creado todavía, está "pedido")
 - Geometry -> Cliqueamos en "soma". Cliqueamos en la propiedad que queramos definir (por ejemplo, área). Para modificarla, (des)cliquear "Specify Strategy"



- -> Construyendo un modelo simple de compartimiento único (soma)
 - Biophysics -> Cliqueando "cm" -> crea sólo la membrana como un capacitor
 - Continuous create -> Cliqueando, instanciamos en memoria el modelo especificado

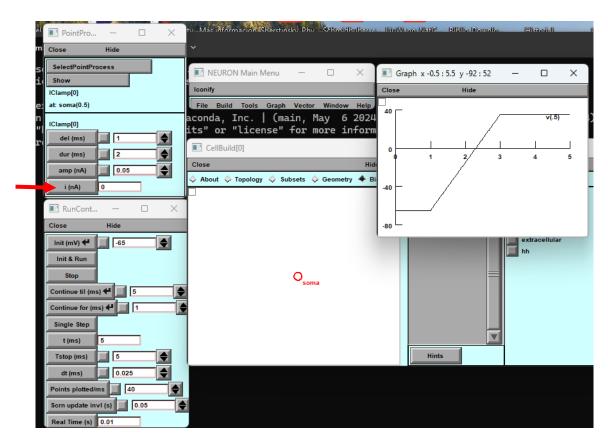


- -> Construyendo un modelo simple de compartimiento único (soma)
 - Establecer una simulación: Main menu -> Tools -> RunControl
 - Visualizar un resultado: Main menu -> Graph -> Voltage axis

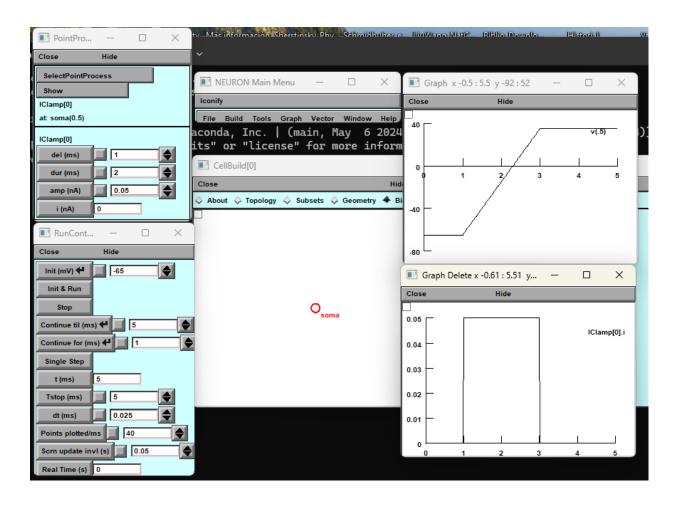


- -> Construyendo un modelo simple de compartimiento único (soma)
 - Estimular a la célula: Main menu -> Tools -> Point Processes -> Managers -> Point manager
 - Seleccionar "IClamp" en SelectPointProcess y establecer parámetros

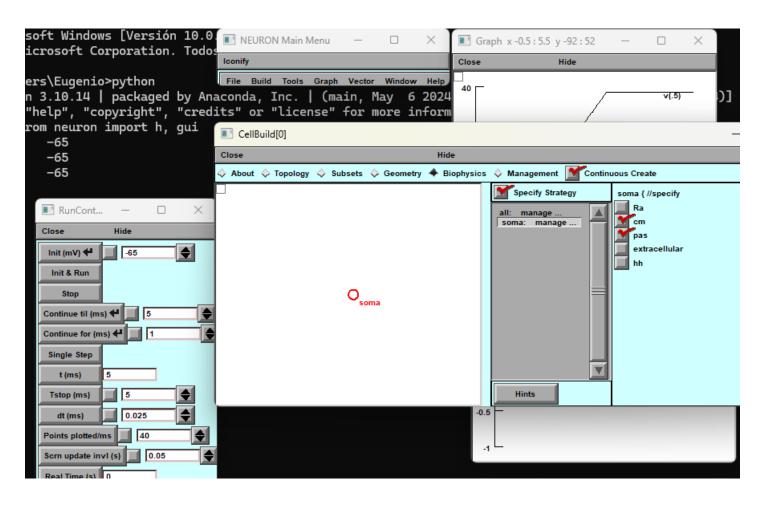
Nombre de la variable allocada por el objeto



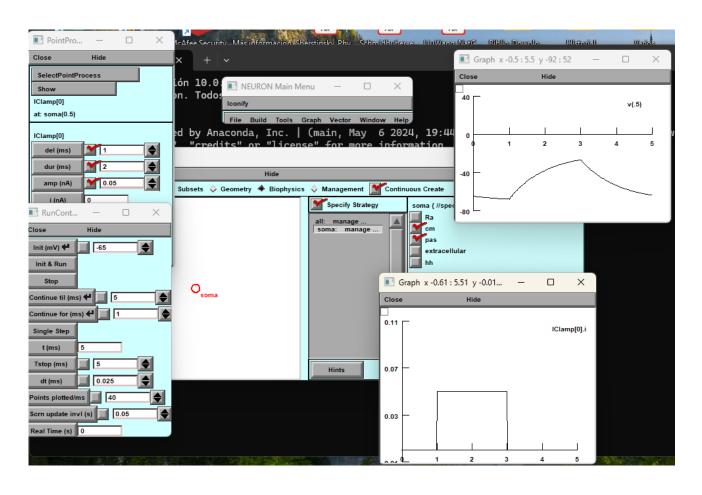
- -> Construyendo un modelo simple de compartimiento único (soma)
 - Visualizar la estimulación: Main menu -> Graph -> Current axis -> Plot what? -> Iclamp[0].i



- -> Construyendo un modelo simple de compartimiento único (soma)
 - Ponemos canales pasivos a la membrana: Main menu -> Tools -> CellBuilder -> Biophysics -> Cliquear "pas"



- -> Construyendo un modelo simple de compartimiento único (soma)
 - Ponemos canales pasivos a la membrana: Main menu -> Tools -> CellBuilder -> Biophysics -> Cliquear "pas"



- -> Construyendo un modelo con extensión espacial
 - Elemento central -> Sección (h.Section)

Conceptual Overview of Sections

Sections are unbranched lengths of continuous cable connected together to form a neuron. Sections can be connected to form any tree-shaped structure but loops are not permitted. (You may, however, develop membrane mechanisms, such as electrical gap junctions which do not have the loop restriction. But be aware that the electrical current flows through such connections are calculated by a modified euler method instead of the more numerically robust fully implicit/crank-nicholson methods)

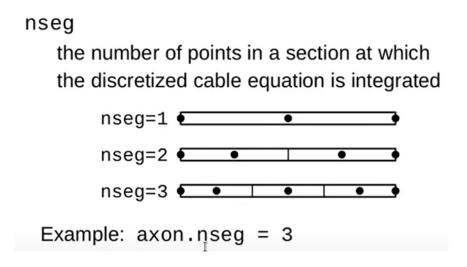
Do not confuse sections with segments. Sections are divided into segments of equal length for numerical simulation purposes (see section.nseg). NEURON uses segments to represent the electrical circuit shown below.

Such segments are similar to compartments in compartmental modeling programs.

Normalized distance (0-1) + Range variables (v, diam, cm, g_pas or pas.g, etc)
 -> variables y parámetros que pueden variar a lo largo de la distancia
 normalizada -> asociados a cada nodo

```
secname(range).rangevar
dend(0.5).v
```

- -> Construyendo un modelo con extensión espacial
 - Resolución espacial de la sección -> Se controla/define con una propiedad



-> Usar números impares (así el nodo central está representado)

- -> Construyendo un modelo con extensión espacial
 - Ejemplo

Conceptual Model

Hodgkin-Huxley cable equations

$$\begin{split} \frac{D}{4\,R_a} \frac{\partial^2 V}{\partial x^2} &= C_m \frac{\partial V}{\partial t} \\ &+ \bar{g} \, m^3 \, h \cdot (V - E_{na}) + \bar{g}_k n^4 \cdot (V - E_k) + g_l \cdot (V - E_l) \\ \frac{dm}{dt} &= -\alpha_m m + \beta_m (1 - m) \quad \alpha_m = \frac{0.1 (V + 40)}{1 - \mathrm{e}^{-0.1 (V + 40)}} \quad \beta_m = 4 \mathrm{e}^{-(V + 65)/18} \\ \frac{dh}{dt} &= -\alpha_h h + \beta_h (1 - h) \quad \alpha_h = 0.07 \mathrm{e}^{-0.05 (V + 65)} \quad \beta_h = \frac{1}{1 + \mathrm{e}^{-0.1 (V + 35)}} \\ \frac{dn}{dt} &= -\alpha_n n + \beta_n (1 - n) \quad \alpha_n = \frac{0.01 (V + 55)}{1 - \mathrm{e}^{-0.1 (V + 55)}} \quad \beta_n = 0.125 \mathrm{e}^{-(V + 65)/800} \end{split}$$

Computational implementation

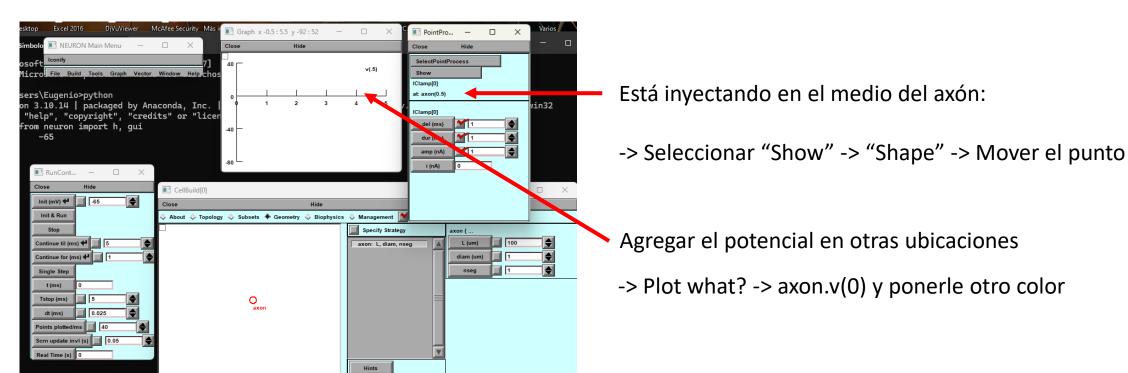
Python for NEURON

```
axion = h.Section(name = 'axon')
axon.L = 2.0e4
axon.diam = 100.0
axon.nseg = 43
axon.insert('hh')
```

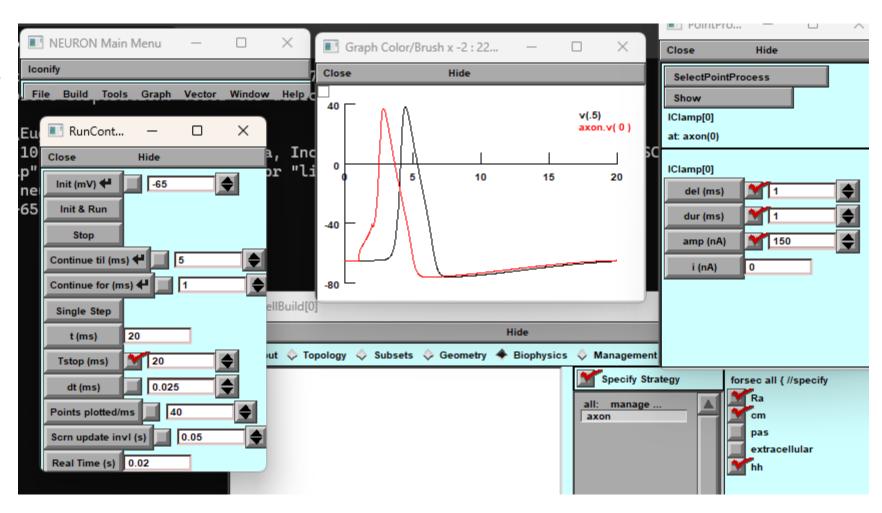
Implementa un trozo de membrana (capacitor)

- -> Construyendo un modelo con extensión espacial
 - En GUI: Main menu -> Build / CellBuilder
 - Topology -> Cambiar nombre a "axon" (Basename -> axon)
 - Geometry -> Cliquear "axon". Seleccionar "L", "diam", "nseg" y descliquer "Specify strategy"
 - Poner 20000, 100, 43.
 - Biophysics -> Cliquear "axon". Seleccionar "Ra", "cm", "hh" y descliquer "Specify strategy"
 - Dejar valores por defecto
 - "Continuous Create"

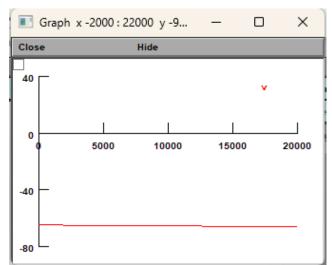
- -> Construyendo un modelo con extensión espacial
 - En GUI: Main menu -> Tools / RunControl
 - En GUI: Main menu -> Graph / Voltage axis
 - En GUI: Main menu -> Tools / Point Processes /Managers / Point Manager -> Set IClamp & specify (1, 1, 1)

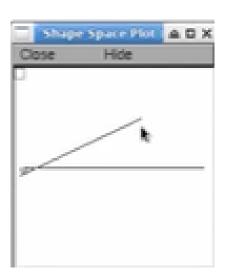


- -> Construyendo un modelo con extensión espacial
 - IClamp -> poner 150 nA
 - RunControl -> Tstop 50 ms

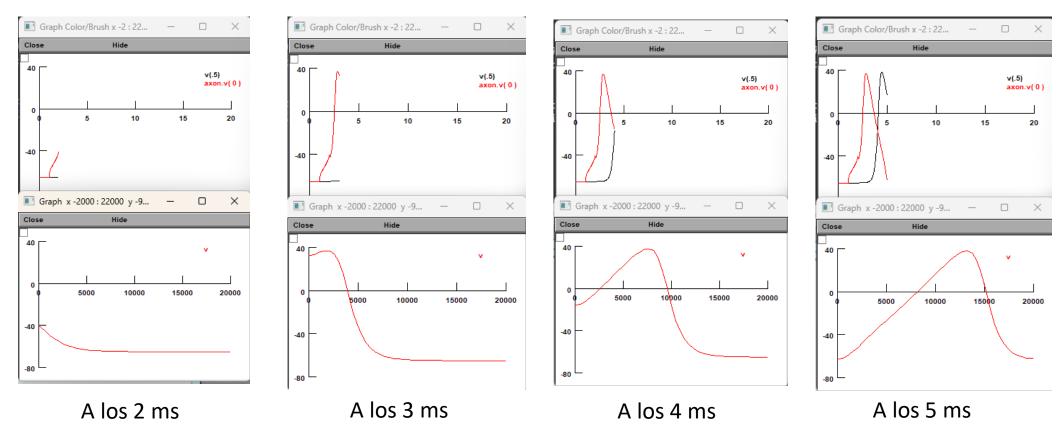


- -> Construyendo un modelo con extensión espacial
 - Crear un gráfico del potencial a lo largo de la sección
 - Main menu -> Graph -> Shape Plot
 - Menu del gráfico -> Especificar SpacePlot
 - Cliquear desde el extremo izquierdo hasta el derecho en la representación de la sección
 - Abre un gráfico donde el eje x es la distancia a lo largo de la sección



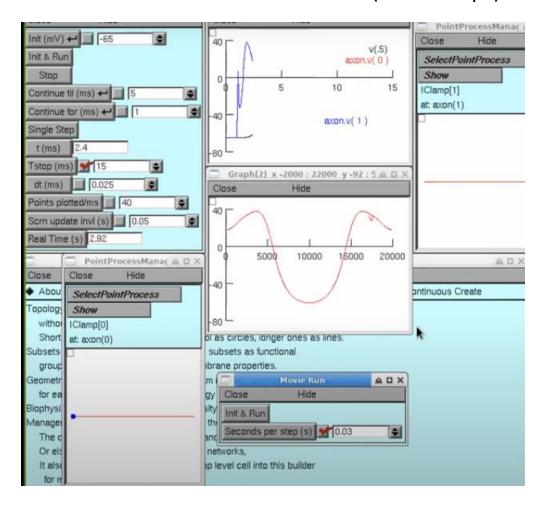


- -> Construyendo un modelo con extensión espacial
 - En Run Control, puedo ir cliqueando "Continue for 1ms" y el gráfico se va actualizando con la solución



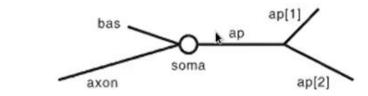
Tools -> Movie Run -> Genera una versión mas lenta de lo anterior

- -> Construyendo un modelo con extensión espacial
 - Hacer un modelo con estimulación en ambos extremos (dos Iclamps)



- -> Construyendo un modelo con extensión espacial
 - Modelo de varios compartimientos

Step 1: using the CellBuilder to make a stylized model



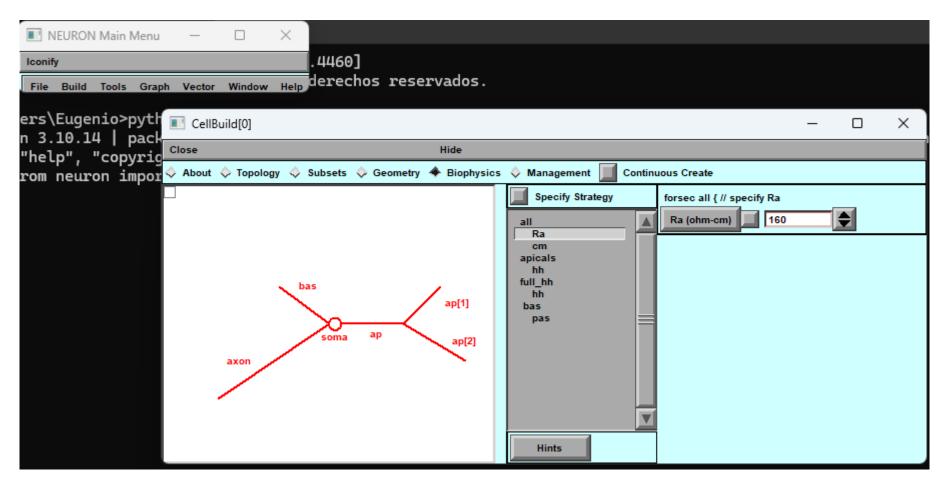
Section	L	diam	Biophysics
soma	20 μm	20 μm	hh
ap[0]	400	2	reduced hh *
ap[1]	300	1	reduced hh *
ap[2]	500	1	reduced hh *
bas	200	3	pas §
axon	800	1	hh

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

Throughout the cell Ra = 160 W cm, cm = 1 μ f / cm²

[§] e_pas = -65 mV

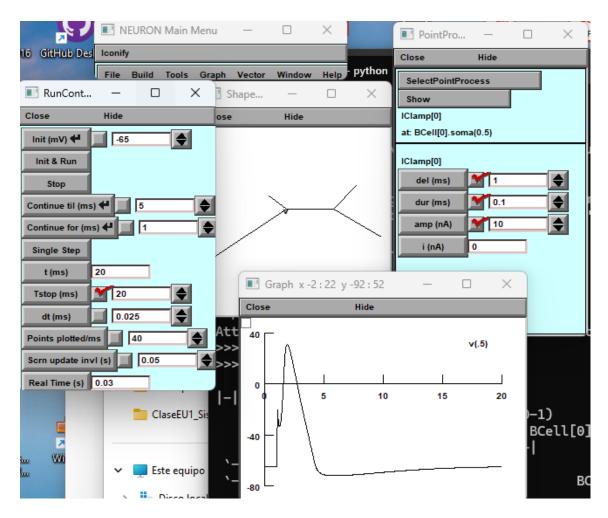
- -> Construyendo un modelo con extensión espacial
 - Modelo de varios compartimientos



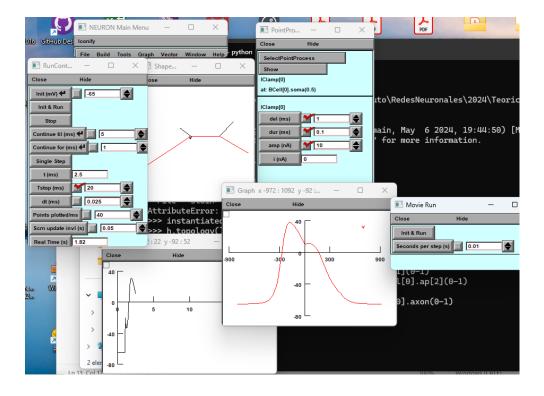
- -> Construyendo un modelo con extensión espacial
 - Exportar como .hoc (en CellBuilder -> Management: Nombrar Bcell a la Classname y "Save hoc code in file")
 - Luego en Python se puede hacer:

```
Python 3.10.14 | packaged by Anaconda, Inc. | (main, May 6 2024, 19:44:50) [MSC v.1916 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license" for more information.
>>> from neuron import h, qui
>>> h.load_file("Bcell.hoc")
1.0
>>> instantiated_cell = h.Bcell()
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
AttributeError: 'hoc.HocObject' object has no attribute 'Bcell'. Did you mean: 'BCell'?
>>> instantiated_cell = h.BCell()
>>> h.topology()
          BCell[0].soma(0-1)
                        BCell[0].ap[0](0-1)
                                        BCell[0].ap[1](0-1)
                                                BCell[0].ap[2](0-1)
                BCell[0].bas(0-1)
                                              BCell[0].axon(0-1)
1.0
>>>
```

- -> Construyendo un modelo con extensión espacial
 - Generemos un experimento:
 - Main menu: Tools -> RunControl
 - Main menu: Graph -> Voltage
 - Main menu: Tools -> Point Processes
 - > Managers
 - -> Point Manager
 - -> IClamp (1, 0.1, 10)



- -> Construyendo un modelo con extensión espacial
 - Hacemos un ShapePlot y creamos un SpacePlot a lo largo de una secuencia de secciones (del axón al ap[2])
 - Mirar la simulación con "Continue for" o con Tools -> MovieRun



Ver efecto en el axón (el disparo no se inicia en el soma, aún cuando se inyecta ahí)

- -> Construyendo un modelo con extensión espacial
 - Agregando canales y biofísica: nmodl
 - Canales iónicos
 - Dinámica de acumulación (ligando / ion)
 - Difusión
 - Transporte
 - Reacciones gobernadas por ODEs, esquemas cinéticos
 - Mecanismos sinápticos, incluyendo plasticidad

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 = 0.036 (S/cm2) <0, 1e9> . . . }
STATE { n . . . }
ASSIGNED { ik (mA/cm2) . . . }

Default initial values for states

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

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

```
(and specify how states are integrated)
BREAKPOINT {
    SOLVE_I deriv METHOD cnexp
    ik = gbar * n^4 * (v - ek)
}
```

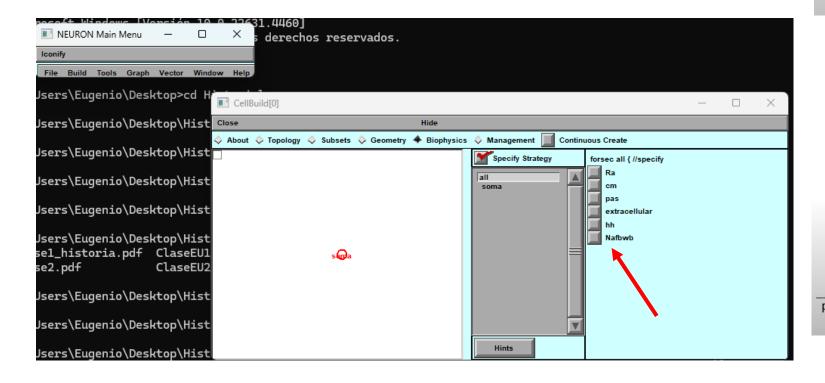
State equations

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

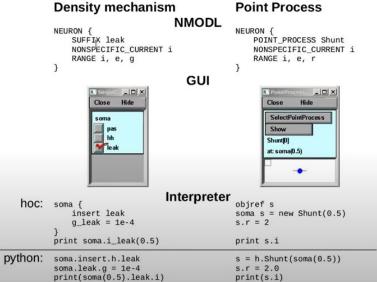
Functions and procedures

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

- -> Construyendo un modelo con extensión espacial
 - Una vez que está compilado (nrnivmodl), el mecanismo está presente para incorporarse en una sección (distribuído) o en una locación (point process)



Density mechanism Point Process NEURON { NEURON { SUFFIX leak POINT_PROCESS Shunt NONSPECIFIC_CURRENT i NONSPECIFIC_CURRENT i RANGE i, e, g RANGE i, e, r PARAMETER { PARAMETER { g = 0.001 (mho/cm2) < 0, 1e9 >r = 1 (gigaohm) <1e-9,1e9>e = -65 (millivolt) e = 0 (millivolt) ASSIGNED ASSIGNED { i (milliamp/cm2) i (nanoamp) v (millivolt) v (millivolt) BREAKPOINT BREAKPOINT { $i = g^*(v - e)$ i = (0.001)*(v - e)/r



- -> Construyendo un modelo con extensión espacial
 - Channel Builder
 - Main manu -> Build -> Channel Builder -> Density
 - Properties -> Channel Name: myNa
 - Selective for ion ...

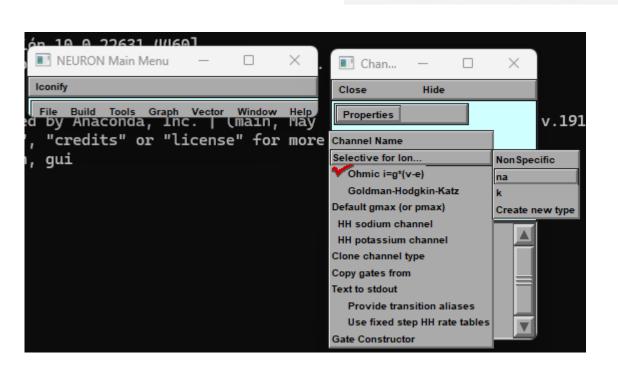
The Channel Builder

Voltage- and ligand-gated channels
Kinetic schemes, HH-style differential equations
Optional stochastic gating mode for point processes
Faster than equivalent NMODL mechanisms

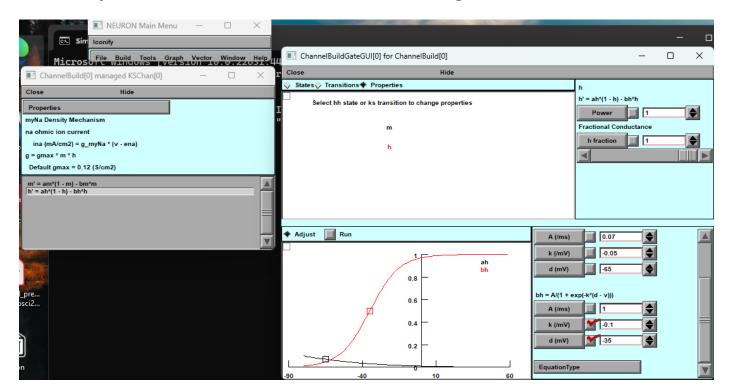
Much easier to use than writing NMODL code
Limited to channels

NMODL needed for pumps, buffers, diffusion, event-driven

synaptic mechanisms, artificial spiking cells



- -> Construyendo un modelo con extensión espacial
 - Channel Builder
 - Default gmax: Setear 0.12 S/cm2
 - Seleccionar debajo de todo "Select here to construct gates"



-> Modelando via python

```
from neuron import h
     from neuron.units import ms, mV, µm
     import matplotlib.pyplot as plt
     h.load_file("stdrun.hoc")
     soma = h.Section(name='soma')
     soma.L = soma.diam = 10 * \mu m
     soma.insert(h.hh)
 9
     ic = h.IClamp(soma(0.5))
10
     ic.delay = 2 * ms
11
     ic.dur = 0.1 * ms
12
13
     ic.amp = 1
14
     t = h.Vector().record(h._ref_t)
15
     v = h.Vector().record(soma(0.5)._ref_v)
16
17
     h.finitialize(-65 * mV)
18
     h.continuerun(10 * ms)
19
20
     plt.plot(t, v)
21
22
     plt.show()
```

-> Construyendo modelos de redes

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

- 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

-> Construyendo modelos de redes

Graded synaptic transmission

Physical system:

A presynaptic variable governs continuous transmitter release

Transmitter modulates a postsynaptic property



```
Link postsynaptic variable to the presynaptic variable
with a POINTER

NMODL specification of synaptic mechanism:

NEURON {
    POINT_PROCESS Syn
    POINTER vpre
    }

hoc usage
    objref syn
    dend syn = new Syn(0.5)
    setpointer syn.vpre, precell.axon.v(1)

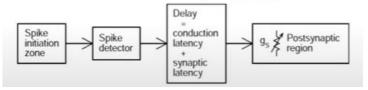
Python usage
    syn = h.Syn(dend(0.5))
    syn._ref_vpre = precell.axon(1)._ref_v
```

-> Construyendo modelos de redes

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

More efficient: "virtual spike propagation"



The NetCon class

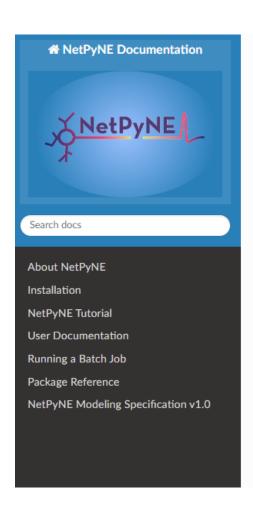
```
Python usage
    nc = h.NetCon(source, target)
    nc = h.NetCon(source_ref_v, target
        [, threshold, delay, weight,
        spc = section])

Defaults
    nc.threshold = 10
    nc.delay = 1 # must be >= 0
    nc.weight[0] = 0 # weight is an array

NMODL specification of synaptic mechanism
    NET_RECEIVE(weight(microsiemens)) {
        . . .
}
```

```
NEURON {
               POINT_PROCESS ExpSyn
               RANGE tau, e, i
               NONSPECIFIC CURRENT i
       UNITS {
               (nA) = (nanoamp)
               (mV) = (millivolt)
10
               (uS) = (microsiemens)
11
12
13
14
               tau = 0.1 (ms) <1e-9,1e9>
15
               e = 0 (mV)
16
17
18
       ASSIGNED {
19
               v (mV)
20
               i (nA)
21
22
23
       STATE {
24
               g (uS)
25
26
       INITIAL {
28
29
30
31
       BREAKPOINT {
32
               SOLVE state METHOD cnexp
33
               i = g*(v - e)
34
35
       DERIVATIVE state {
37
               g' = -g/tau
38
39
       NET_RECEIVE(weight (uS)) {
41
               g = g + weight
42
```

-> Overview de NetPyNE



Welcome to the NetPyNE homepage!

NetPyNE is an open-source Python package to facilitate the development, parallel simulation, analysis, and optimization of biological neuronal networks using the NEURON simulator. See our recent publication in eLife for more details.

To make NetPyNE more accessible, we have released a (beta version) graphical user interface (GUI). The GUI is freely available at gui.netpyne.org with documentation here.

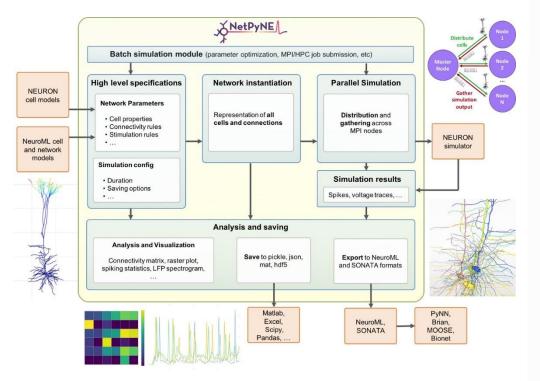
For a detailed overview of NetPyNE, including an interactive tutorial utilizing the GUI, please see our CNS*2020 tutorial: Building mechanistic multiscale models: from molecules to networks using NEURON and NetPyNE. The complete video is available here and slides are available here.

Check out our latest tutorial: Virtual Environments, Jupyter Notebooks, and NetPyNE basics. The video is available here and the notebook is available here.

Join our NetPyNE mailing list to receive updates on version releases and other major announcements. Get your questions answered and participate in the NetPyNE community at the NetPyNE forum or the NetPyNE section of the NEURON forum.

NetPyNE is available as a resource through Neuroscience Gateway Portal (NSG); Open Source Brain (OSB); Human Brain Project (HBP) EBRAINS; NIH SPARC initiative.

-> Overview de NetPyNE



Major Features

- · Converts a set of high-level specifications into a NEURON network model
- · Specifications are provided in a simple, standardized, declarative Python-based format
- · Can easily define:
 - Populations: cell type and model, number of neurons or density, spatial extent, ...
 - Cell properties: morphology, biophysics, implementation, ...
 - Synaptic mechanisms: time constants, reversal potential, implementation, ...
 - Stimulation: spike generators, current clamps, spatiotemporal properties, ...
 - Connectivity rules: conditions of pre- and post-synaptic cells, different functions, ...
 - Simulation configuration: duration, saving and analysis, graphical output, ...
 - Reaction-diffusion (RxD): species, regions, reactions, ...

· Cell properties highlights:

- Import existing HOC and Python defined cell models into NetPyNE format
- Readily change model implementation e.g., from Hodgkin-Huxley multicompartment to Izhikevich point neuron
- · Combine multiple cell models into hybrid networks for efficient large-scale networks

Connectivity rules highlights:

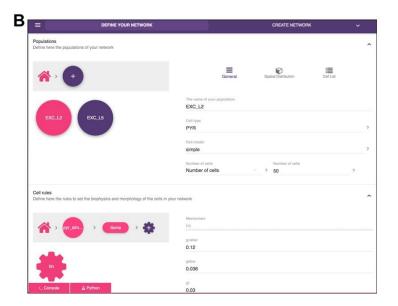
- Flexible connectivity rules based on pre- and post-synaptic cell properties (e.g., cell type or location)
- Connectivity functions available: all-to-all, probabilistic, convergent, divergent, and explicit list
- Can specify parameters (e.g., weight, probability or delay) as a function of pre/post-synaptic spatial properties, e.g.,
 delays or probability that depend on distance between cells or cortical depth
- Can specify subcellular distribution of synapses along the dendrites, and will be automatically adapted to the morphology of each model neuron.
- Can easily add learning mechanisms to synapses, including STDP and reinforcement learning

• Generates NEURON network instance ready for MPI parallel simulation

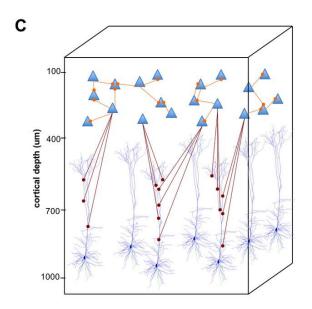
- Takes care of cell distribution
- Handles gathering of data

-> Overview de NetPyNE

```
popParams['EXC_L2'] = {
                                                      rxdParams['regions'] = {
                                                                                                       synMechParams['AMPA'] = {
     cellType': 'PYR',
                                                        'cyt': {'cells':
                                                                              'all',
                                                                                                         'mod': 'Exp2Syn',
     'cellModel': 'simple',
                                                                'secs':
                                                                              'soma',
                                                                                                         'tau1': 0.8,
     'yRange':
                 [100, 400],
                                                                'nrn_region': 'i'}}
                                                                                                         'tau2': 5.3,
     'numCells': 50}
                                                                                                         'e': 0}
                                                      rxdParams['species'] = {
                                                               {'regions': 'cyt',
    popParams['EXC_L5'] = {
                                                                  'charge': 2,
                                                                                                       connParams['L2->E2'] = {
     cellType': 'PYR',
                                                                                                         'preConds': {'y': [100, 400]},
                                                                  'initial': 1e-4},
     'cellModel': 'complex',
                                                        'buf': {'regions': 'cyt',
                                                                                                         'postConds': {'pop': 'EXC_L2'},
                 [700, 1000],
     'yRange':
                                                                  'initial': 1e-4},
                                                                                                         'probability': '1*exp(-dist_3D/200)',
                 80e3}
     'density':
                                                        'cabuf': {'regions': 'cyt',
                                                                                                                       0.4,
                                                                                                         'delay':
                                                                  'initial': 0}}
                                                                                                         'synMech':
                                                                                                                        'AMPA'}
    cellParams['PYR_simple'] = {
                                                       rxdParams['reactions'] = {
      conds': {'cellType': 'PYR',
                                                        'buffering': {'reactant': '2*ca+buf'
               'cellModel': 'simple'},
                                                                                                  Viii) connParams['E2->L5'] = {
                                                                      'product': 'cabuf',
     'secs': {'soma'
                                                                                                         'preConds': {'pop': 'EXC_L2'},
                                                                      'rate f': 1e6,
                'geom': {'diam': 18, 'L': 18},
                                                                      'rate_b': 1e-2}}
                                                                                                         'postConds': {'y': [700,1100],
                'mechs': {'hh':
                                                                                                                        'cellModel': 'complex'},
                          {'gnabar': 0.12,
                                                       rxdParams['rates'] = {
                                                                                                         'convergence': 25,
                           'gkbar': 0.036,
                                                        'degradation': {'species': 'buf',
                                                                                                         'weight':
                                                                                                                       '0.001 * post ynorm',
                           'gl': 0.003,
                                                                                                                       'dist_3D/propVelocity',
                                                                        'rate': '-1e-3*buf'}}
                                                                                                         'delay':
                                 -70}}}
                                                                                                                       'allDend',
                                                                                                         'sec':
                                                                                                         'synMech':
                                                                                                                       'AMPA',
                                                                                                         'synsPerConn': 3}
iV) importCellParams(
    label = 'PYR_complex',
    conds = {'cellType': 'PYR',
               'cellModel': 'complex'},
    fileName = 'L5 pyr full.hoc',
```



cellName = 'PYR L5')



-> Overview de NetPyNE

```
Model.py ×
   from netpyne import specs, sim
   Dt = 0.05
   Convert a string or number to a floating point number, if possible.
   netParams = specs.NetParams() # object of class NetParams to store the network parameters
   netParams.defaultThreshold = 0.0
   ## Cell types
   # Pyramidal cell
   PyrCell = {'secs':{}}, 'globals': {'ko0 k ion': 3.82, 'ki0 k ion': 160, 'cao0 ca ion': 2, 'cai0 c
   PyrCell['secs']['soma'] = {'geom': {}, 'mechs': {}}
   PyrCell['secs']['soma']['geom'] = {'diam': 23, 'L': 23, 'cm': 1.2, 'Ra': 150, 'nseg': 1}
   PyrCell['secs']['soma']['mechs'] = {
       'pas': {'a': 3.33e-5, 'e': -70},
       'kdyn': {},
       'Naf': {'qnafbar': 0.086},
       'Nap': {'anapbar': 0.0022},
       'Hva': {'ahvabar': 0.00034},
       'kdr': {'akdrbar': 0.0338},
       'IKs': {'gKsbar': 0.00014},
       'iC': {'akcbar': 0.0022},
       'cadyn': {'CAF': 385.948e-9, 'tca': 250}}
   # basal dendrite
   PyrCell['secs']['Bdend'] = {'geom': {}, 'mechs': {}}
   PyrCell['secs']['Bdend']['geom'] = {'diam': 16.0, 'L': 150.0, 'cm': 2.3, 'Ra': 150, 'nseg': 1}
   PyrCell['secs']['Bdend']['topol'] = {'parentSec': 'soma', 'parentX': 0, 'childX': 0}
   PyrCell['secs']['Bdend']['mechs'] = {
       'pas': {'a': 6.39e-5, 'e': -70},
```