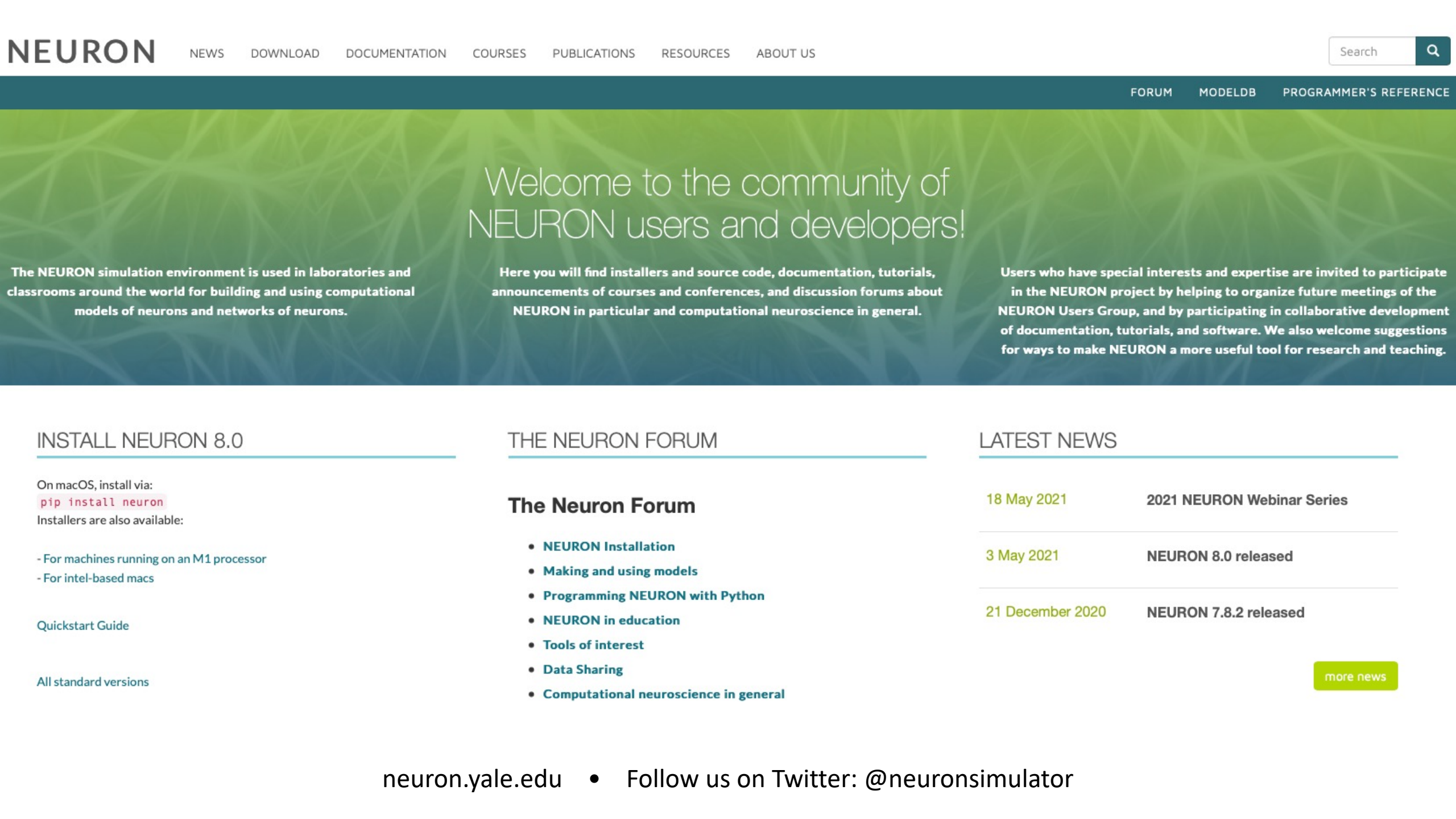
Outline of this session

- Overview of NEURON
- NEURON concepts and basic scripting
  - Slides
  - Exercises
- Reaction-Diffusion
  - Slides
  - Exercises



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NEURON Main Menu

Iconify

File Build Tools Graph Vector Window Help

Close Hide

File

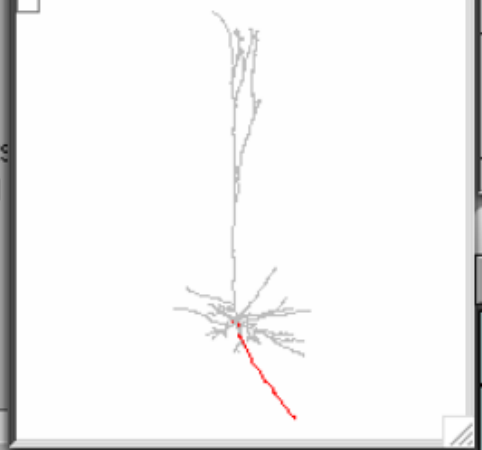
79 sections; 150 segments

* 1 real cells
  * root soma
    79 sections; 150 segments
    * 7 distinct values of nseg
    * 6 inserted mechanisms
      Ra = 100
      cm = 1
      * pas
      ena = 50
      ek = -77
      * hh
        gnabar_hh = 0.12
        gkbar_hh = 0.036
        gl_hh = 0.0003
        el_hh = -54.3
    * 3 subsets with constant parameters
    * 2 Point Processes
0 artificial cells
0 NetCon objects
0 LinearMechanism objects

ModelView[0]...

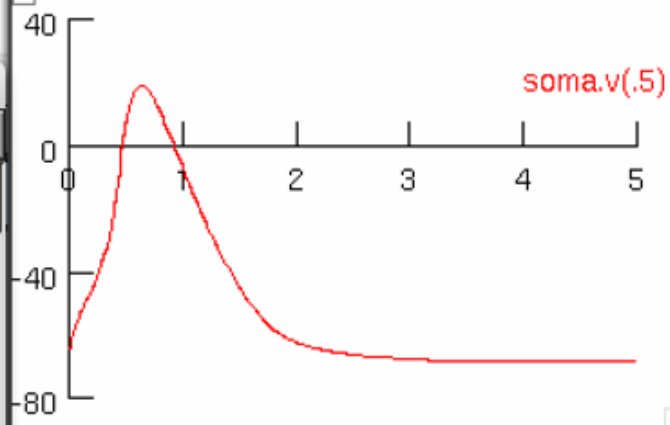
Close Hide

LengthScale



Graph[0] x -0.5 : 5.5 y -92 : 52

Close Hide



Absolute Tolerance Scale Factors

Close Hide

Analysis Run | Rescale | Original

*10 | /10 | Hints

v	10	76	0.011
m_hh	1	0.99	0.00035
h_hh	0.1	0.6	1.2e-05
n_hh	0.1	0.77	4.4e-06

Temperature

Close Hide

celsius (degC) 15

LogAvsX[0]

Close Hide

Redraw | Shape Select Action | Plot | Extras

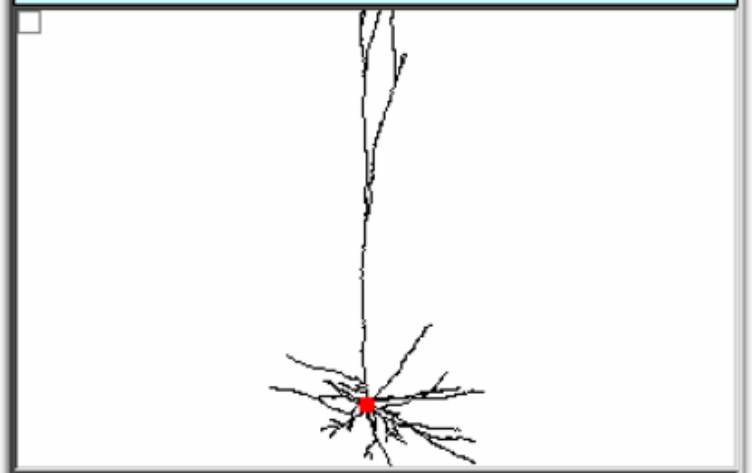
include dstate/dt contribution

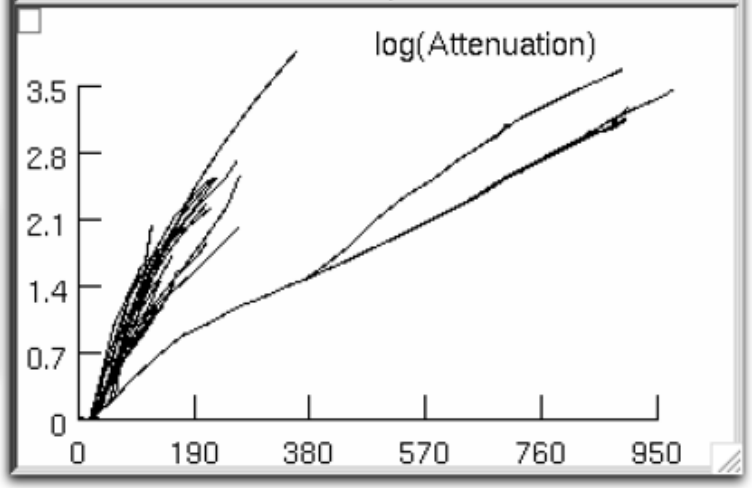
frequency (Hz) 0

Vin

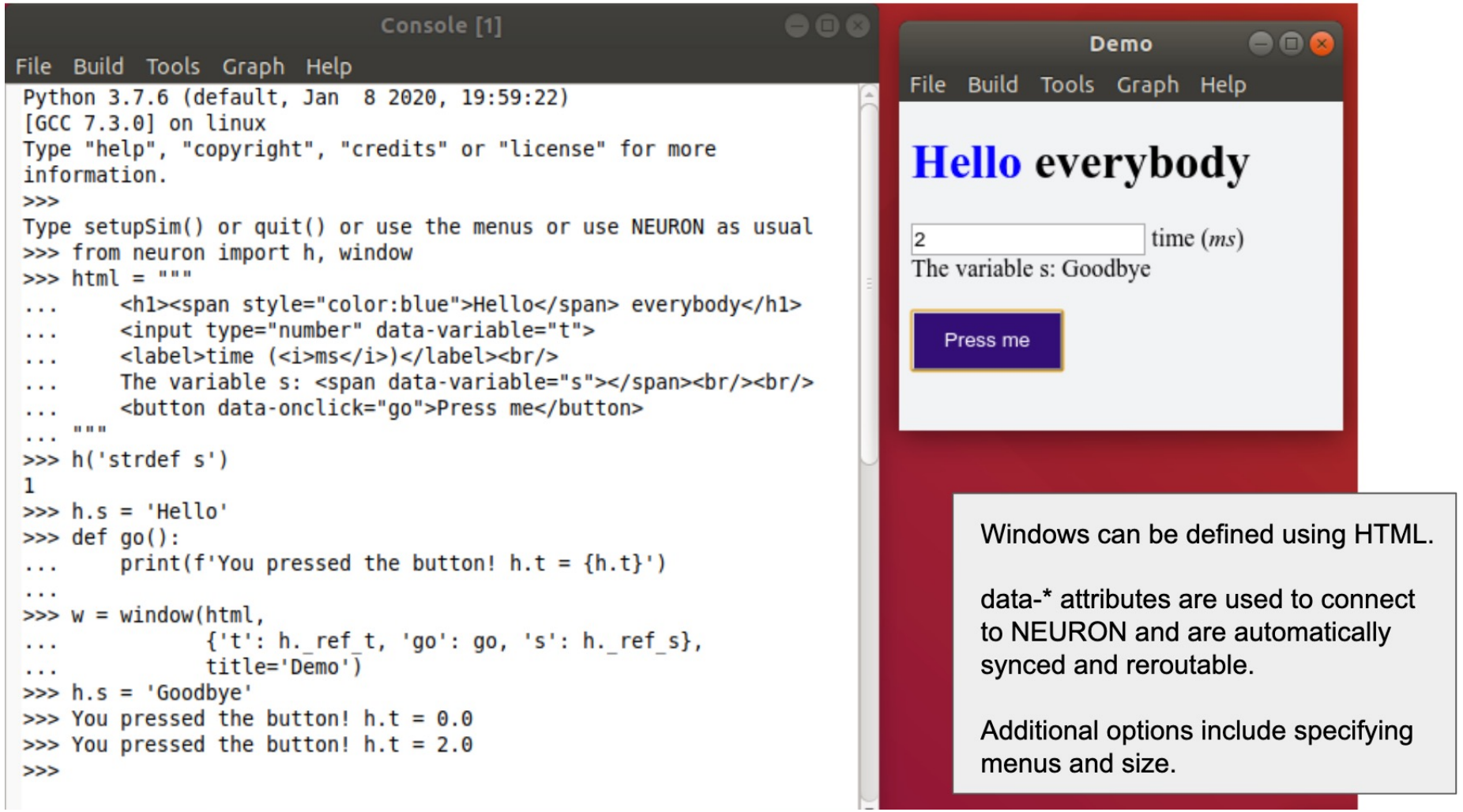
Vout

Measure (red) soma(0.5)



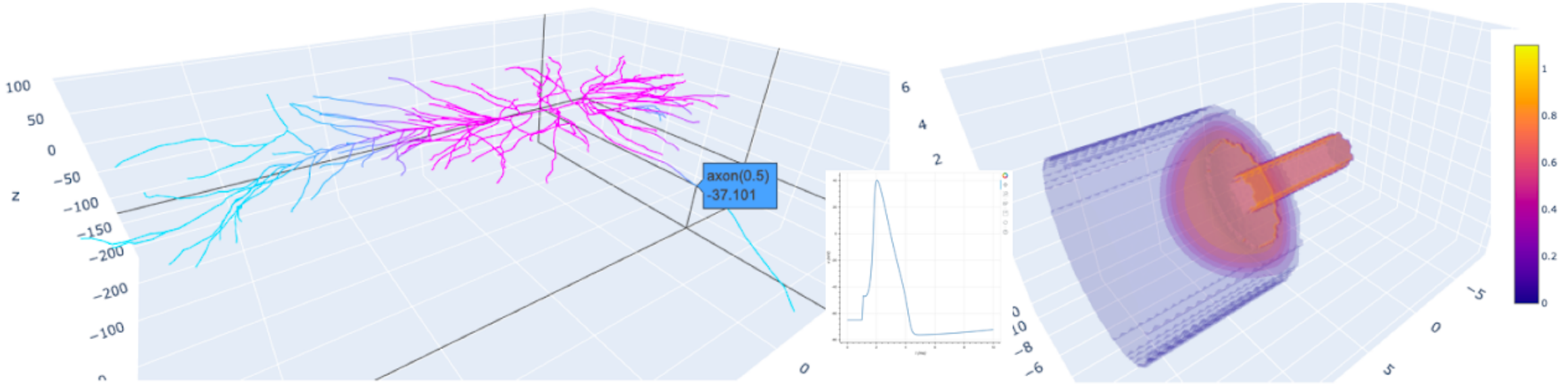


github.com/mcdougallab/neurongui2



NEURON Developer's meetings

- Third Friday of the month, 10am EDT; 16:00 CEST on zoom.
- Agenda is on the NEURON GitHub wiki: https://github.com/neuronsimulator/nrn/wiki




```
from neuron import h
from neuron.units import mV, ms
from matplotlib import cm
import plotly
h.load_file('stdrun.hoc')

h.load_file('c91662.ses')
```

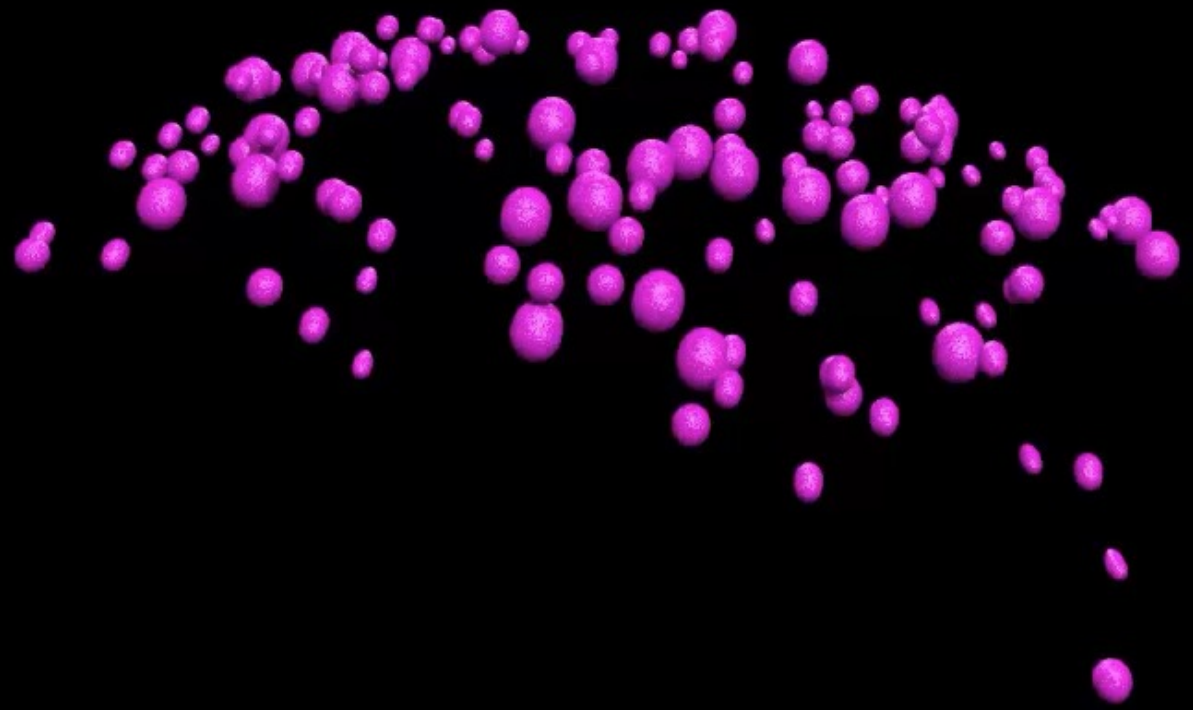
```
h.hh.insert(h.allsec())

ic = h.IClamp(h.soma(0.5))
ic.delay = 1 * ms
ic.dur = 1 * ms
ic.amp = 10
```

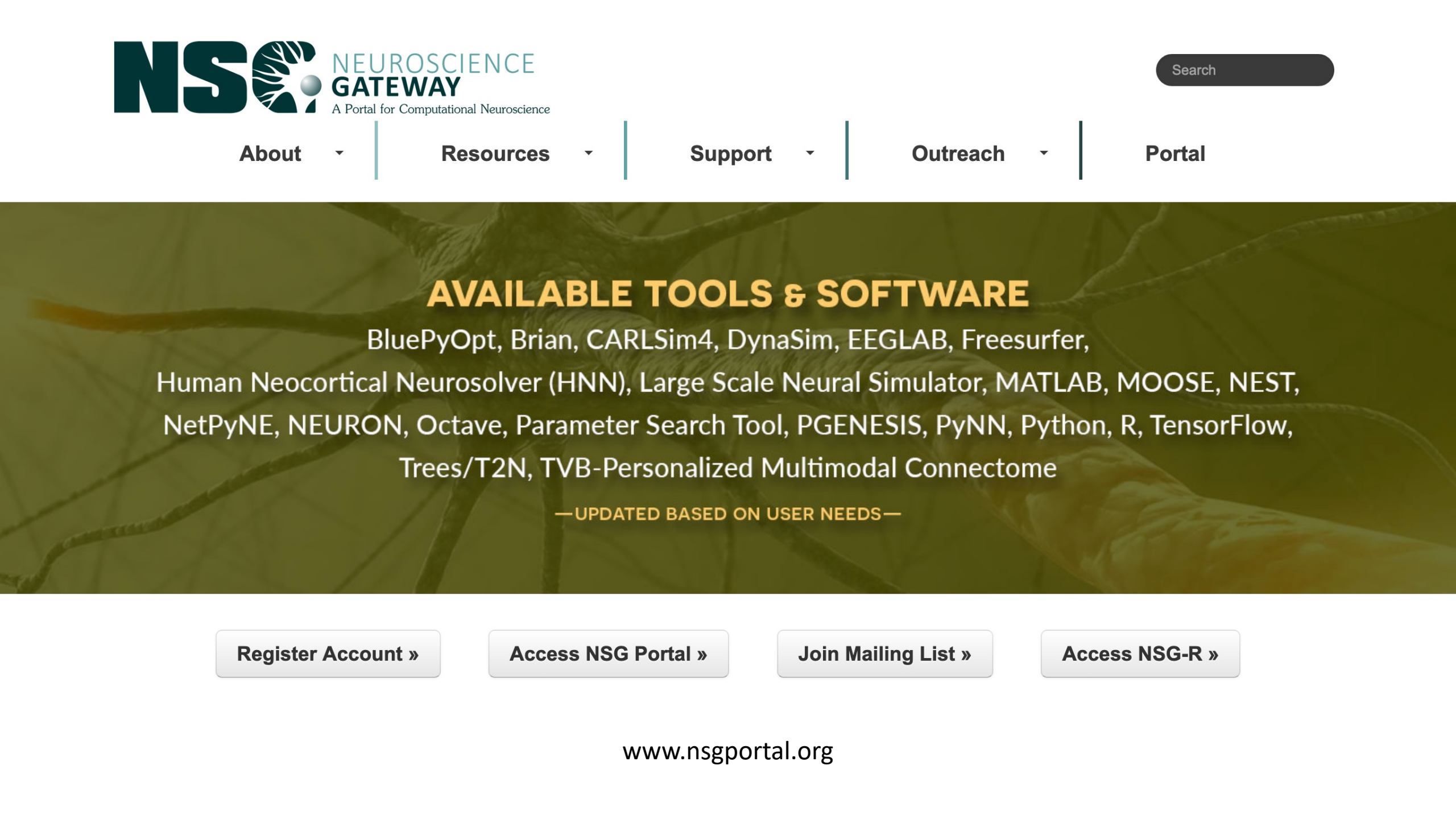
```
h.finitialize(-65 * mV)
h.continuerun(2 * ms)

ps = h.PlotShape(False)
ps.variable('v')
ps.plot(plotly, cmap=cm.cool).show()
```

Migliore et al., 2014

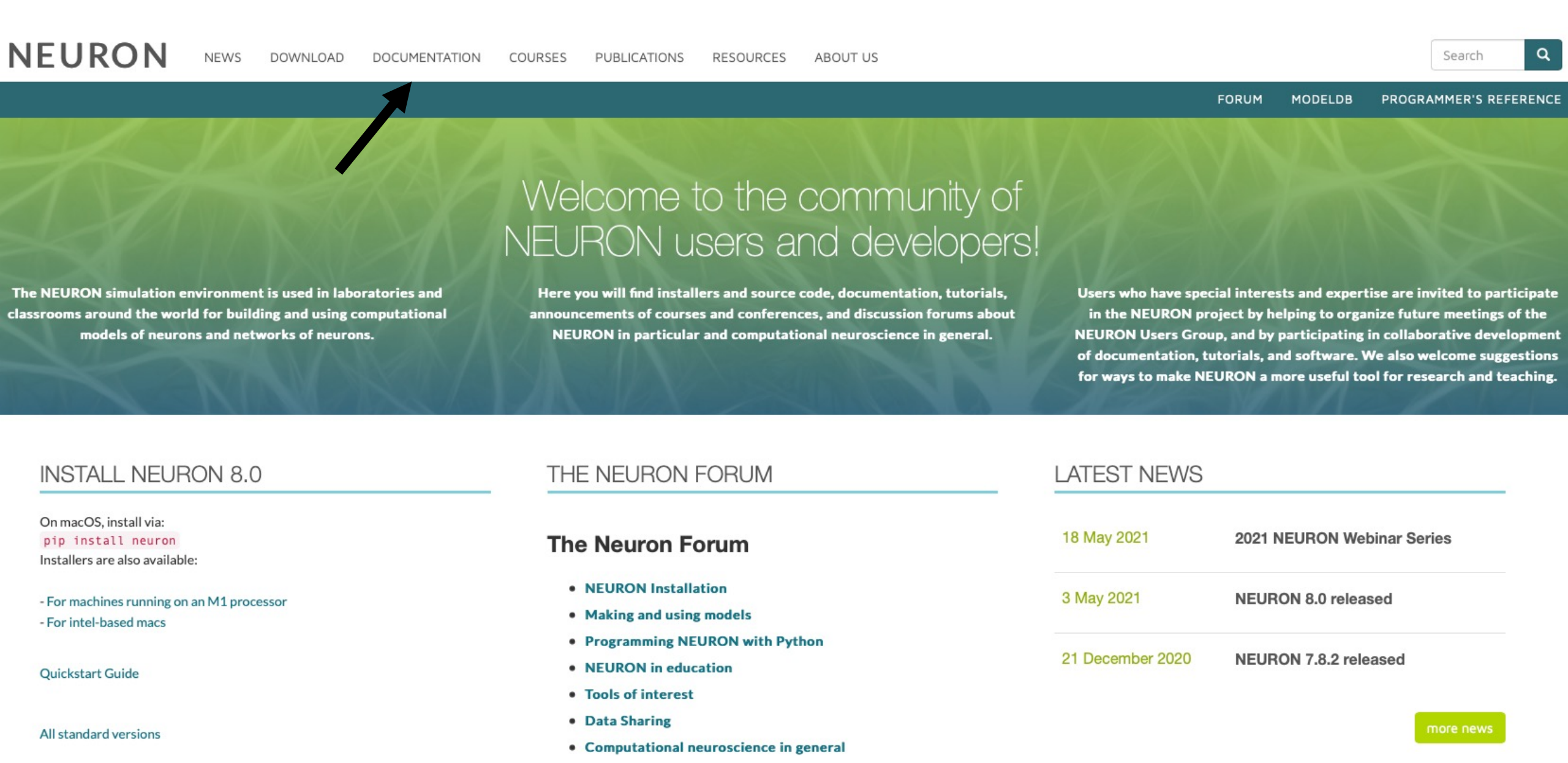
doi: 10.3389/fncom.2014.00050

modeldb.yale.edu/151681





www.nsgportal.org



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NEURON

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Search

FORUM MODELDB PROGRAMMER'S REFERENCE

Welcome to the community of NEURON users and developers!

The NEURON simulation environment is used in laboratories and classrooms around the world for building and using computational models of neurons and networks of neurons.

Here you will find installers and source code, documentation, tutorials, announcements of courses and conferences, and discussion forums about NEURON in particular and computational neuroscience in general.

Users who have special interests and expertise are invited to participate in the NEURON project by helping to organize future meetings of the NEURON Users Group, and by participating in collaborative development of documentation, tutorials, and software. We also welcome suggestions for ways to make NEURON a more useful tool for research and teaching.

INSTALL NEURON 8.0

On macOS, install via:
`pip install neuron`
Installers are also available:

- For machines running on an M1 processor
- For intel-based macs

Quickstart Guide

All standard versions

THE NEURON FORUM

The Neuron Forum

- **NEURON Installation**
- **Making and using models**
- **Programming NEURON with Python**
- **NEURON in education**
- **Tools of interest**
- **Data Sharing**
- **Computational neuroscience in general**

LATEST NEWS

18 May 2021	**2021 NEURON Webinar Series**
3 May 2021	**NEURON 8.0 released**
21 December 2020	**NEURON 7.8.2 released**

more news

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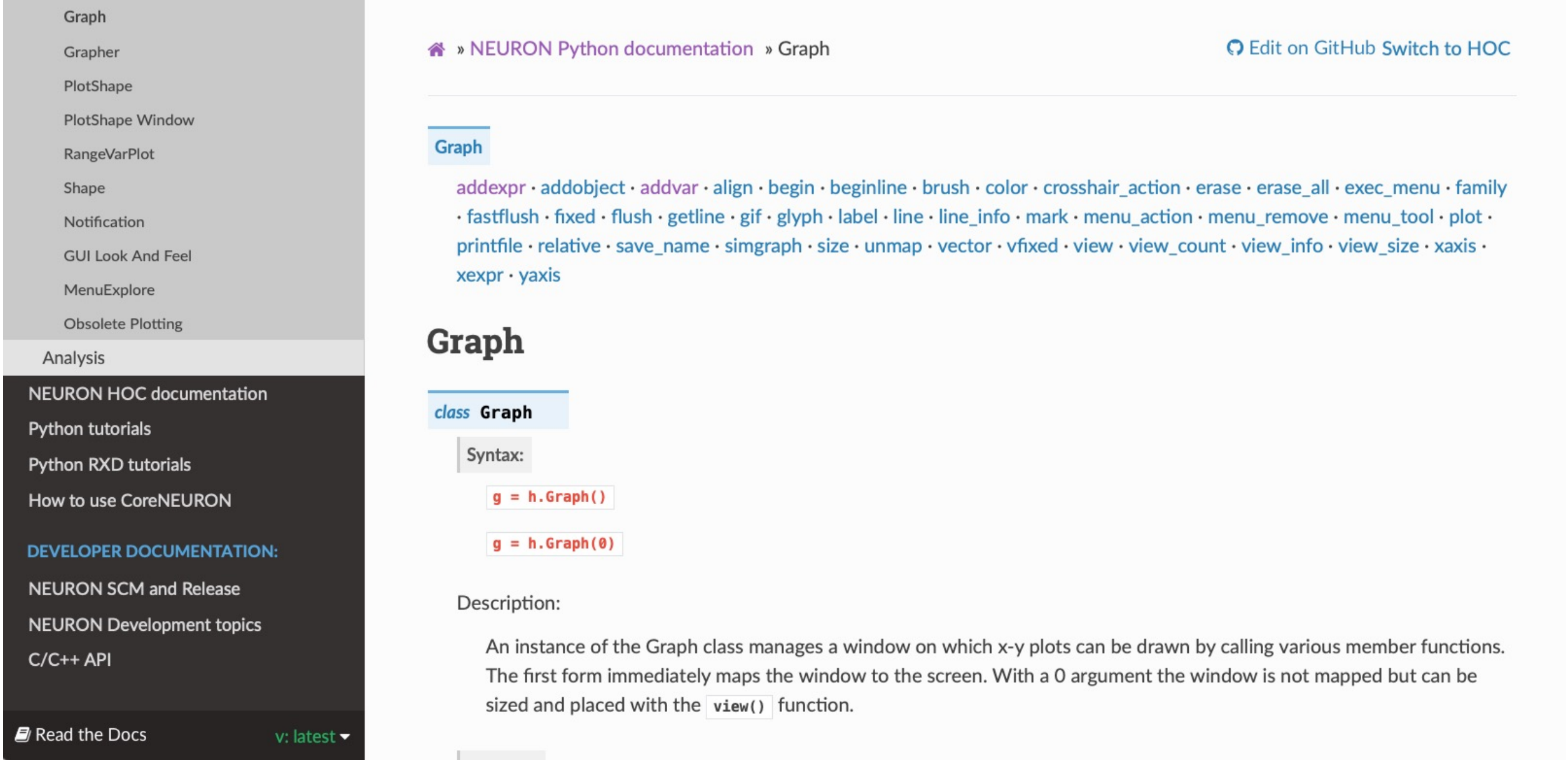
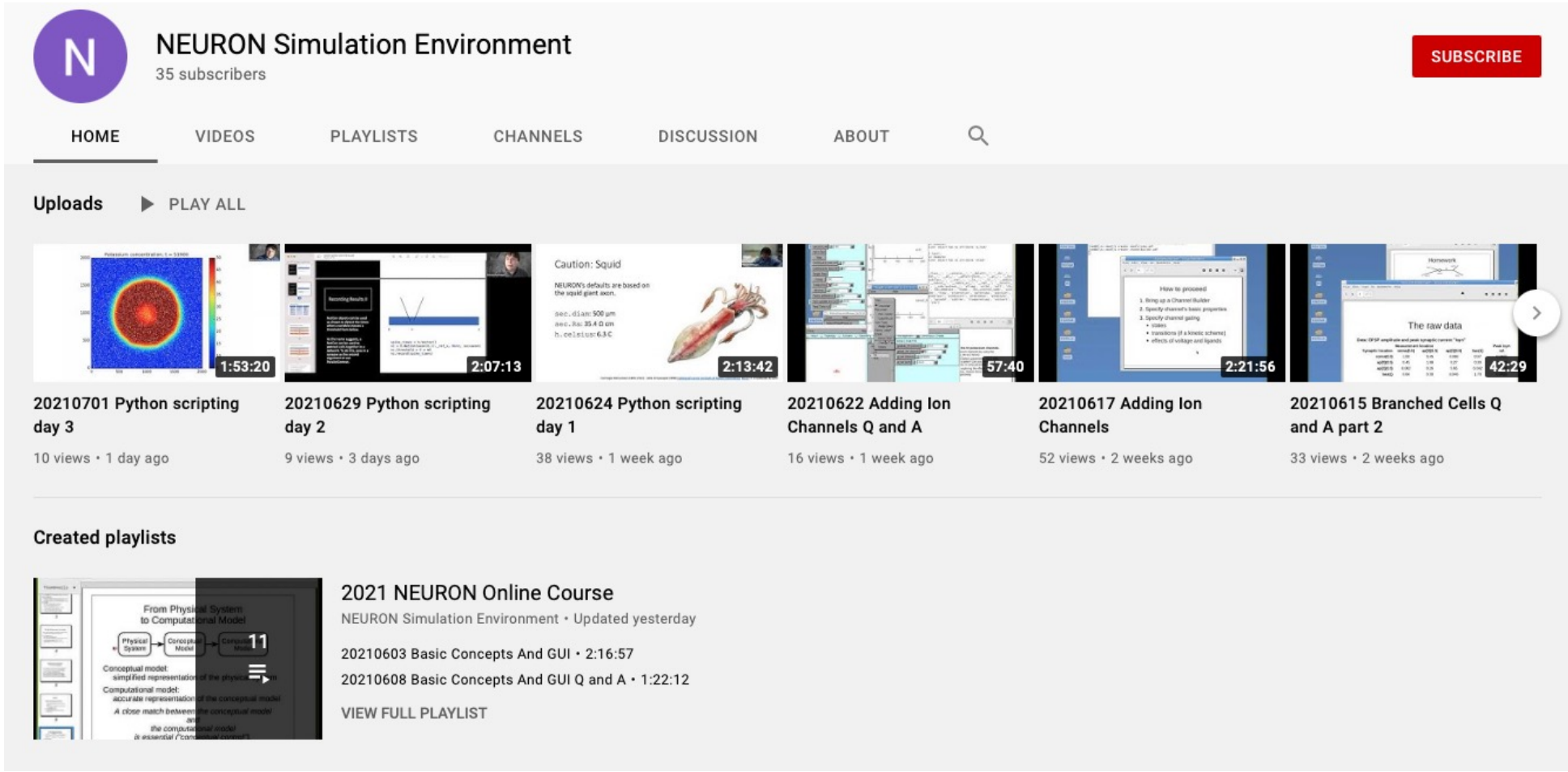


Direct documentation link: nrn.readthedocs.io

Use the “Switch to HOC” link in the upper-right corner of every page if you need documentation for HOC, NEURON’s original programming language. HOC may be used in combination with Python: use h.load_file to load a HOC library; the functions and classes are then available with an h. prefix.



For more...

tinyurl.com/neuron-videos

Installation

- macOS or Linux:

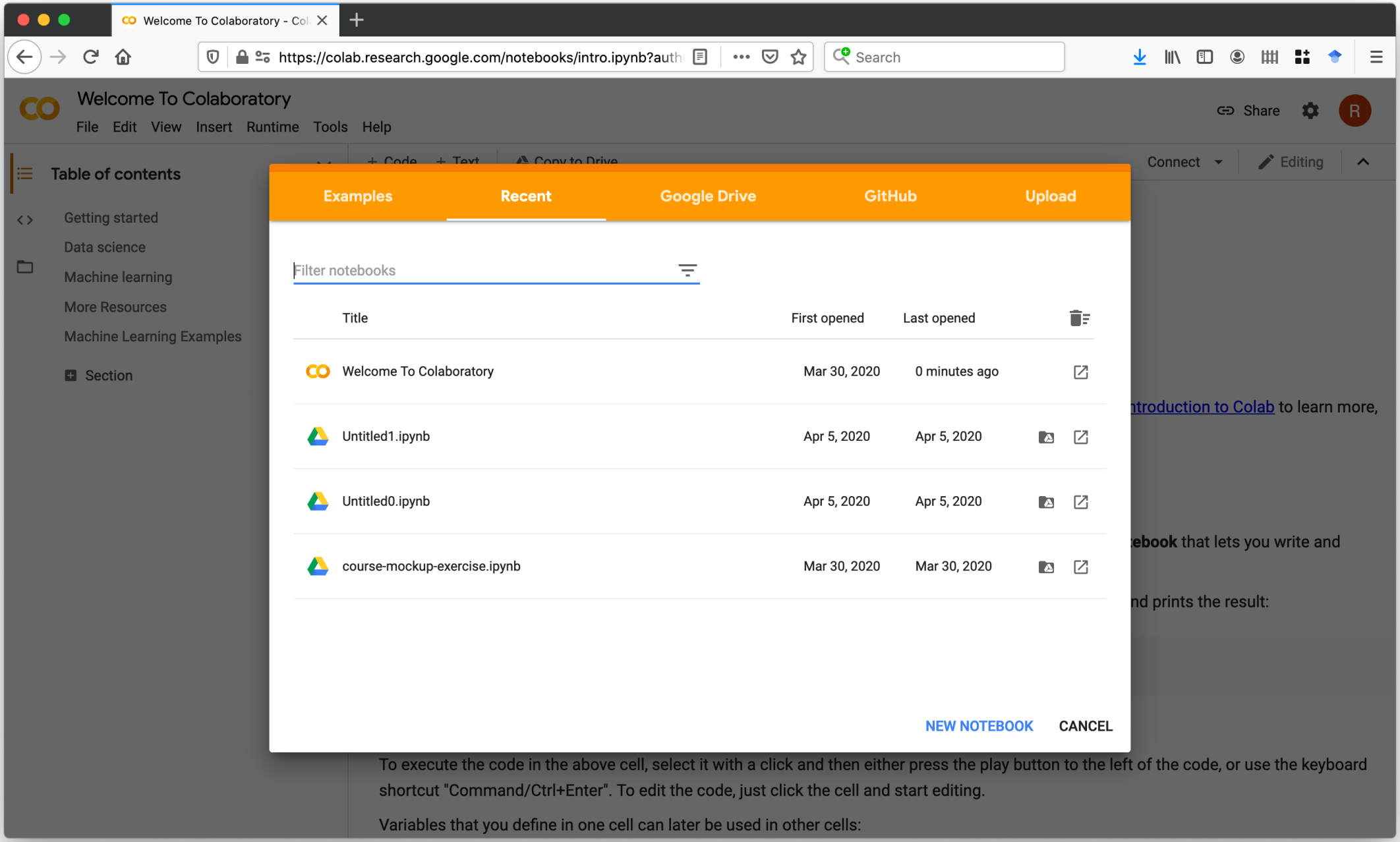
```
pip install neuron
```

or

```
pip install neuron-nightly
```

- Windows:

+ Python (e.g. Anaconda)

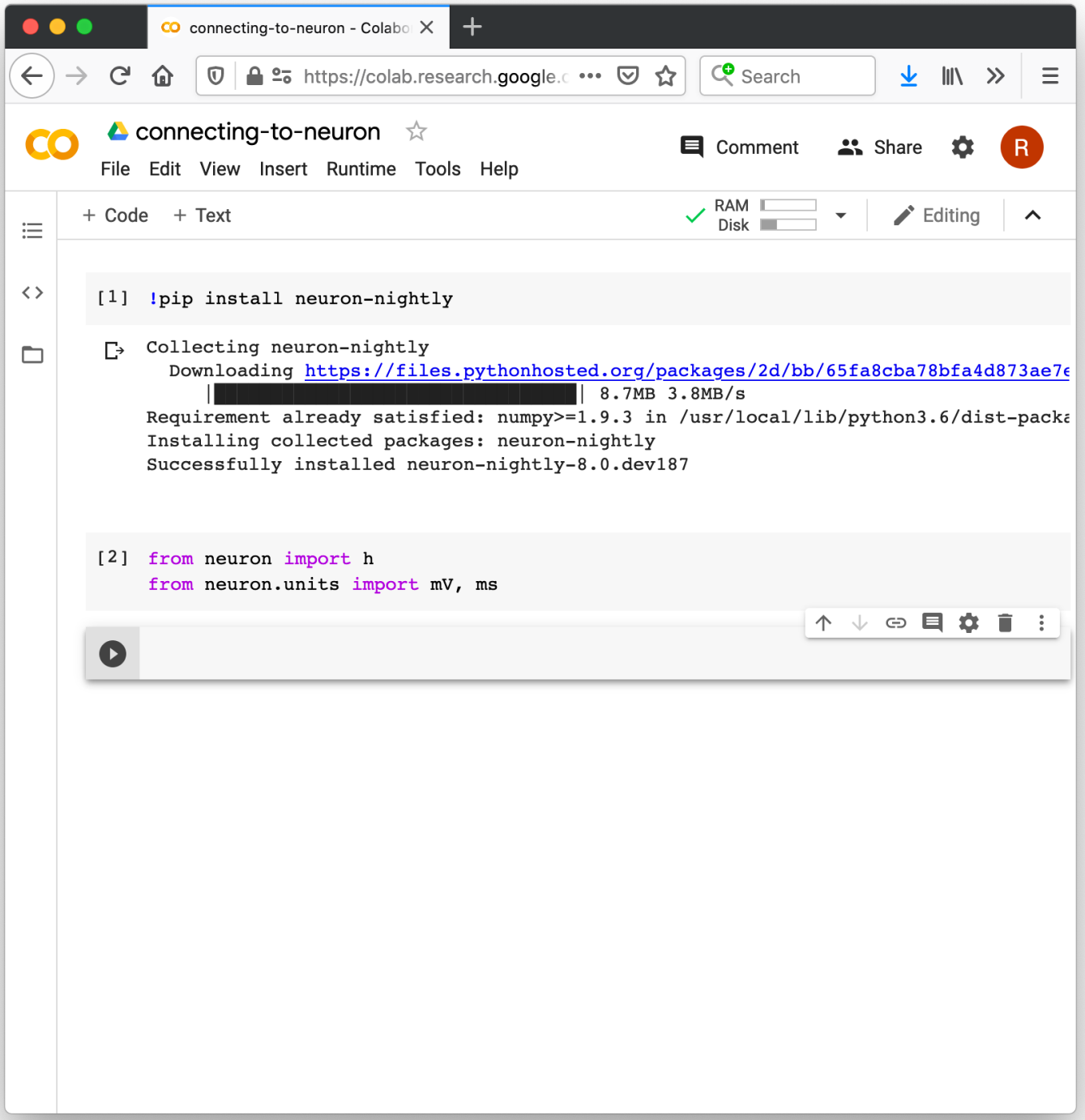


colab.research.google.com

Connecting to NEURON

- For today's tutorial, we will use Google Colab, but any way you like to use Python is a good way.

- The main NEURON submodule is called h, but there are also: units, rxd, and gui.



Basic unit: `h.Section`

```
soma = h.Section(name='soma')
```

Length: `soma.L`

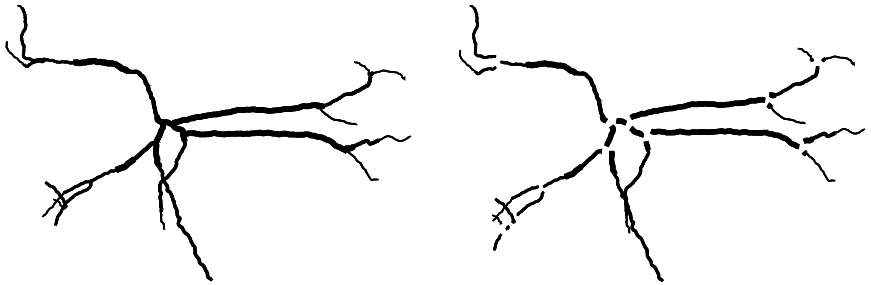
Diameter: `soma.diam`

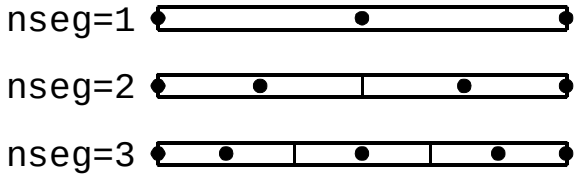
Discretization: `soma.nseg`

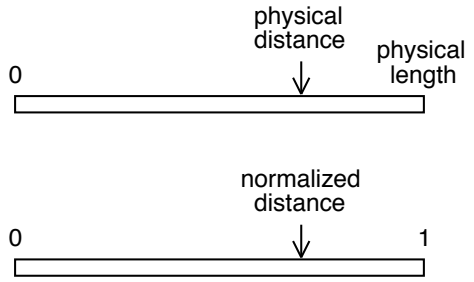
Inside a cell class, specify the cell argument as well:

```
soma = h.Section(
           name='soma',
           cell=self)
```

The `connect` method joins Section objects to define arbitrary morphologies.







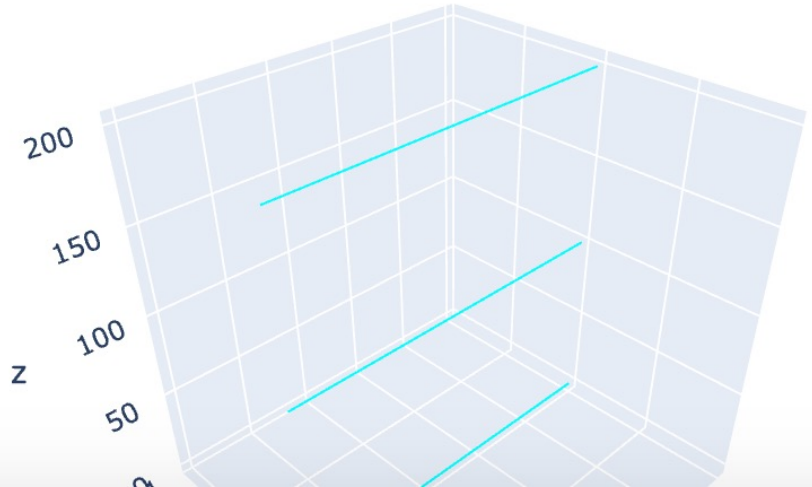
Anatomical data from A.I. Gulyas .
Images from Ted Carnevale.

```
[2] from neuron import h
    from neuron.units import mV, ms
    import plotly
```

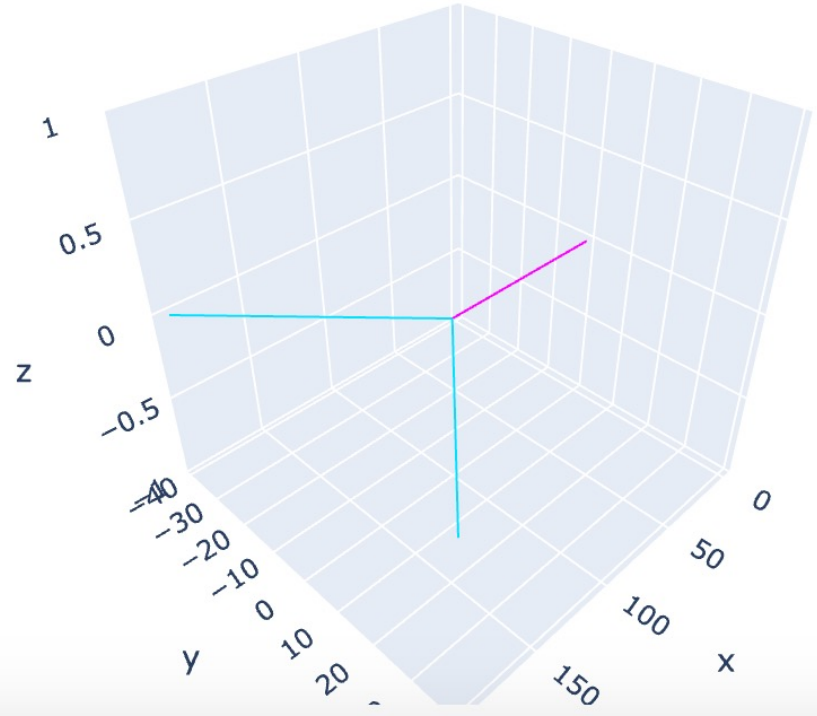
```
[3] main = h.Section(name='main')
    branch1 = h.Section(name='branch1')
    branch2 = h.Section(name='branch2')
    h.define_shape()
```

```
1.0
```

```
[4] h.PlotShape(False).plot(plotly).show()
```




```
[6] branch1.connect(main)
    branch2.connect(main)
    for sec in h.allsec():
      sec.pt3dclear()
    h.define_shape()
    ps = h.PlotShape(False)
    ps.variable('v')
    ps.plot(plotly).show()
```



Viewing voltage, sodium, etc…

Variable	Value	Pointer (e.g. for recording)	With PlotShape or RangeVarPlot
Voltage	seg.v	seg._ref_v	"v"
Na^+ (inside membrane)	seg.nai	seg._ref_nai	"nai"
Na^+ (outside membrane)	seg.nao	seg._ref_nao	"nao"
Na^+ (current)	seg.ina	seg._ref_ina	"ina"
Na^+ (reversal potential)	seg.ena	seg._ref_ena	"ena"
d(sodium current)/dv	seg.dina_dv_	seg._ref_dina_dv_	"dina_dv_"

Potassium is the same as for sodium, except with “k” replacing “na”; Chloride is the same except with “cl”; Calcium is the same except with “ca”, etc… ions may only be accessed when a mechanism using them is present or when they are explicitly inserted via sec.insert or rxd.

Ion Channels

- Specify using `insert` method.
- Built-in: Hodgkin-Huxley (`h.hh`), passive (`h.pas`)
- Hundreds more on ModelDB (`.mod` files)
- Compile mod files via: `nrnivmodl`

Model

Hodgkin-Huxley cable equations

$$\frac{D}{4R_a}\frac{\partial^2 V}{\partial x^2} = C_m\frac{\partial V}{\partial t}$$

$$+ \bar{g}m^3h\cdot(V-E_{na}) + \bar{g}_k n^4\cdot(V-E_k) + g_l\cdot(V-E_l)$$

$$\frac{dm}{dt} = -\alpha_m m + \beta_m(1-m) \quad \alpha_m = \frac{0.1(V+40)}{1-e^{-0.1(V+40)}} \quad \beta_m = 4e^{-(V+65)/18}$$

$$\frac{dh}{dt} = -\alpha_h h + \beta_h(1-h) \quad \alpha_h = 0.07e^{-0.05(V+65)} \quad \beta_h = \frac{1}{1+e^{-0.1(V+35)}}$$

$$\frac{dn}{dt} = -\alpha_n n + \beta_n(1-n) \quad \alpha_n = \frac{0.01(V+55)}{1-e^{-0.1(V+55)}} \quad \beta_n = 0.125e^{-(V+65)/80}$$

Simulation

Representation

```
axon = h.Section(name = 'axon')
axon.L = 2e4 * um
axon.diam = 100
axon.nseg = 43
h.hh.insert(axon)
```

Illustration adapted from one by Ted Carnevale.

```
TITLE hh.mod   squid sodium, potassium, and leak channels

COMMENT
 This is the original Hodgkin-Huxley treatment for the set of sodium,
  potassium, and leakage channels found in the squid giant axon membrane.
  ("A quantitative description of membrane current and its application
  conduction and excitation in nerve" J.Physiol. (Lond.) 117:500-544 (1952).)
 Membrane voltage is in absolute mV and has been reversed in polarity
  from the original HH convention and shifted to reflect a resting potential
  of -65 mV.
 Remember to set celsius=6.3 (or whatever) in your HOC file.
 See squid.hoc for an example of a simulation using this model.
 SW Jaslove  6 March, 1992
ENDCOMMENT

UNITS {
        (mA) = (milliamp)
        (mV) = (millivolt)
        (S) = (siemens)
}

? interface
NEURON {
        SUFFIX hh
        REPRESENTS NCIT:C17145   : sodium channel
        REPRESENTS NCIT:C17008   : potassium channel
        USEION na READ ena WRITE ina REPRESENTS CHEBI:29101
```

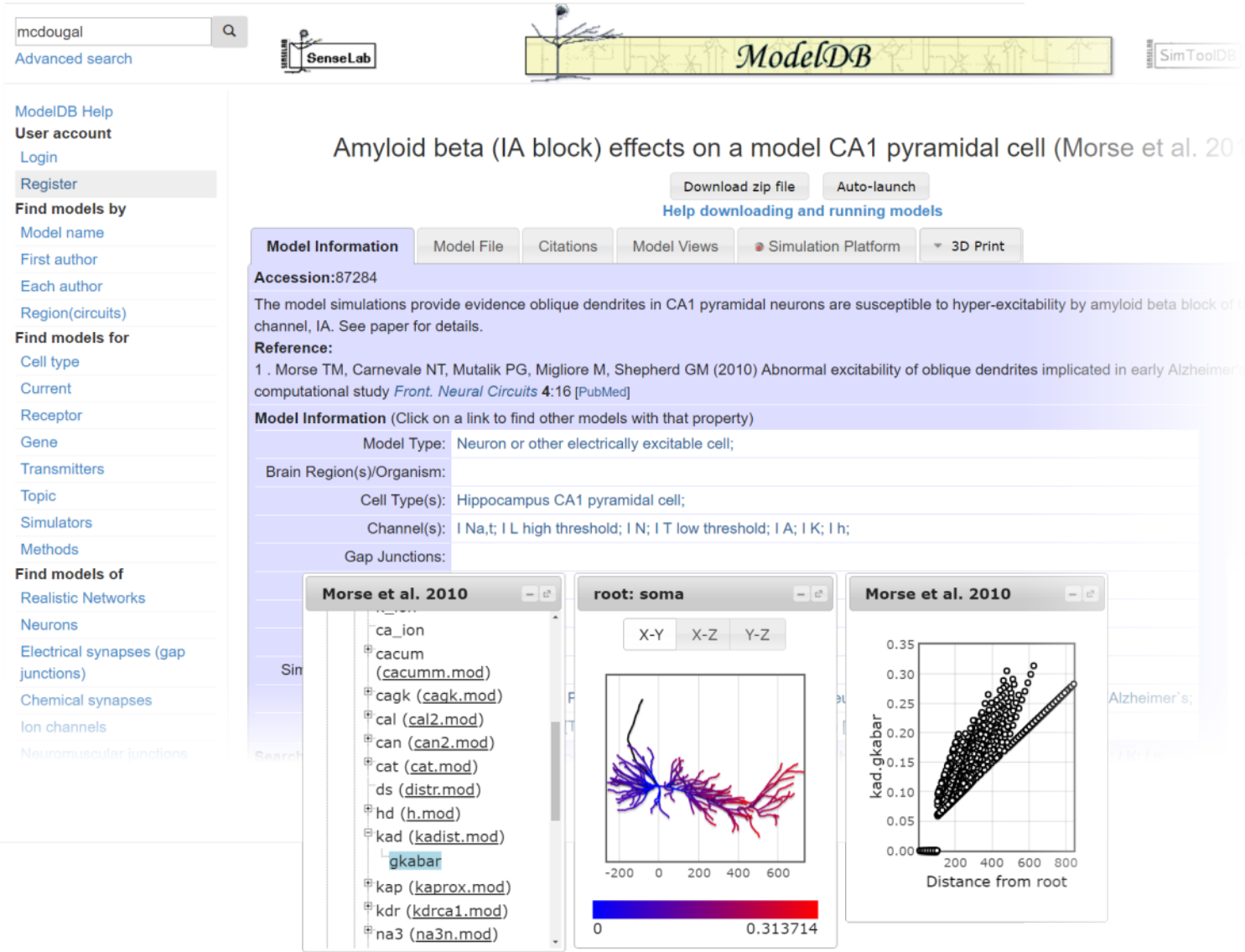
tinyurl.com/nmodl-preprint

Defining ion channels and synapses

tinyurl.com/hhmodfile

tinyurl.com/expsyn

Compile mod files on colab using:
`!nrnivmodl`




```
from neuron import h, rxd
import neuron.rxd.node as node
from matplotlib import pyplot
import time


h.load_file('stdrun.hoc')

soma = h.Section()
soma.L = 10
soma.diam = 10
soma.nseg = 11
dend = h.Section()
dend.connect(soma)
dend.L = 50
dend.diam = 2
dend.nseg = 51

def print_nodes():
    print ', '.join(str(v) for v in node._states)

print 'defining rxd'
region = rxd.Region(h.allsec(), nrn_region='i')
ca = rxd.Species(region, name='ca', d=1, charge=2, initial
reaction = rxd.Rate(ca, -ca * (1 - ca) * (0.3 - ca))

print 'initializing'
```

Morse TM, Carnevale NT, Mutalik PG, Migliore M, Shepherd GM (2010) Abnormal excitability of oblique dendrites implicated in early Alzheimer's: a computational study *Front. Neural Circuits* **4**:16[PubMed]

References and models cited by this paper

Acker CD, White JA (2007) Roles of I(A) and morphology in action potential propagation in CA1 pyramidal cell dendrites. *J Comput Neurosci* **23(2)**:201-16 [Journal] [PubMed]

- **Roles of I(A) and morphology in AP prop. in CA1 pyramidal cell dendrites (Acker and White 2007) [Model]**

Anderton BH, Callahan L, Coleman P, Davies P, Flood D, Jicha GA, Ohm T, Weaver C (1998) Dendritic changes in Alzheimer's disease and factors that may underlie these changes. *Prog Neurobiol* **55**:595-609 [PubMed]

Andrasfalvy BK, Makara JK, Johnston D, Magee JC (2008) Altered synaptic and non-synaptic properties of

References and models that cite this paper

Culmone V, Migliore M (2012) Progressive effect of beta amyloid peptides accumulation on CA1 pyramidal neurons: a model study suggesting possible treatments *Front Comput Neurosci* **6**:52 [Journal] [PubMed]

- **CA1 pyramidal neurons: effects of Alzheimer (Culmone and Migliore 2012) [Model]**

McDougal RA, Morse TM, Hines ML, Shepherd GM (2015) ModelView for ModelDB: online presentation of model structure *Neuroinformatics* **13(4)**:459-70 [Journal] [PubMed]

- **ModelView: online structural analysis of computational models (McDougal et al. 2015) [Model]**

modeldb.yale.edu • @senselabproject

McDougal, R. A., Morse, T. M., Carnevale, T., Marenco, L., Wang, R., Migliore, M., ... & Hines, M. L. (2017). Twenty years of ModelDB and beyond: building essential modeling tools for the future of neuroscience. *Journal of computational neuroscience*, *42*(1), 1-10. doi:10.1007/s10827-016-0623-7

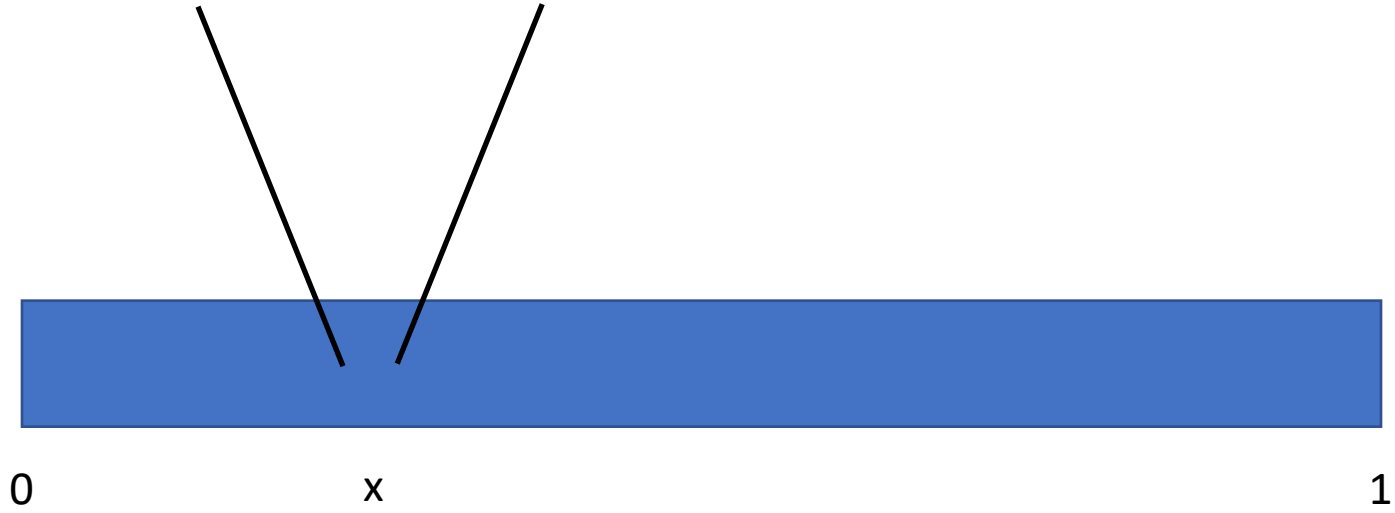
Stimulating a Model

We will inject current using an

`h.IClamp`

This object has several important properties:

- `delay`
- `amp`
- `dur`




```
iclamp = h.IClamp(axon(x))
```

Stimulating a Model II

Set potential

- soma(0.5).v = 10 * mV
- Voltage clamp
  - cl = h.SEClamp(soma(0.5))
  - cl.amp1 = -65 * mV
  - cl.dur1 = 10 * ms
  - Similarly for .amp2, .amp3, .dur2, .dur3
  - Could also: vec.play(cl._ref_amp2)
  - SEClamp – single electrode
  - VClamp – two electrode

Current Clamp

- ic = h.IClamp(soma(0.5))
- ic.delay = 5 * ms
- ic.dur = 0.1 * ms
- ic.amp = 1 # nA

Synaptic input

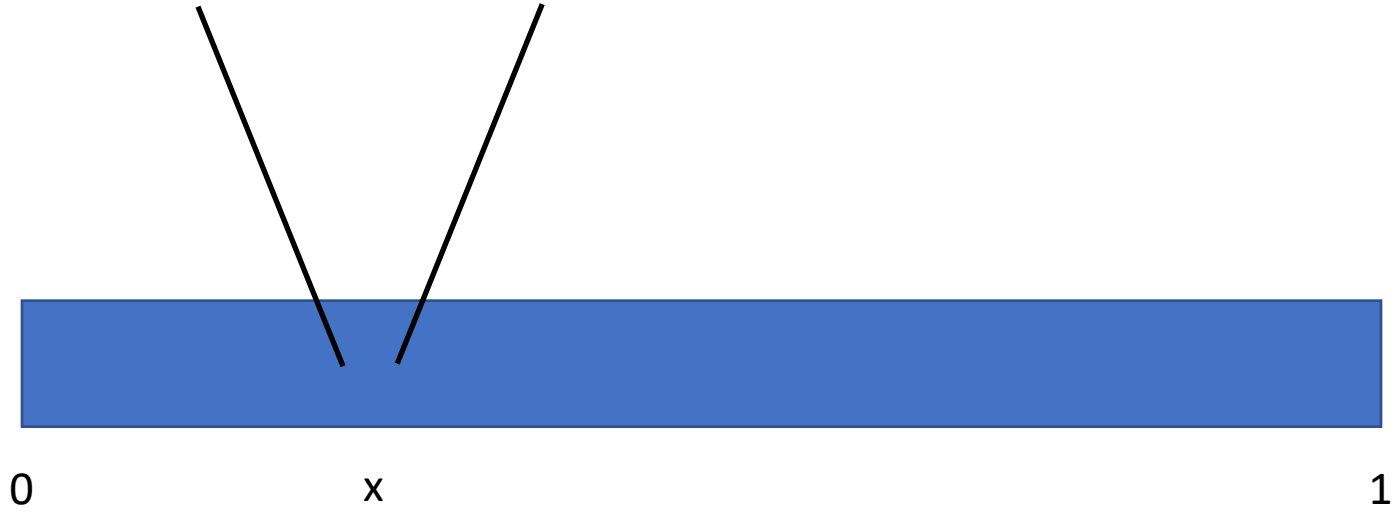
- ns = h.NetStim()
  - ns.number = 1
  - ns.start = 5 * ms
  - ns.noise = False
  - ns.interval = 20 * ms
    - Only matters for number > 1
- sy = h.ExpSyn(soma(0.5))
  - sy.tau = 5 * ms
  - sy.e = 0 * mV
- nc = h.NetCon(ns, sy)
  - nc.weight[0] = 1

Recording Results

We can read the instantaneous membrane potential at a location via, e.g.

```
axon(0.5).v
```

To record this value over time, we use an `h.Vector` and pass in the pointer (prefixed with `_ref_`) to the record method.



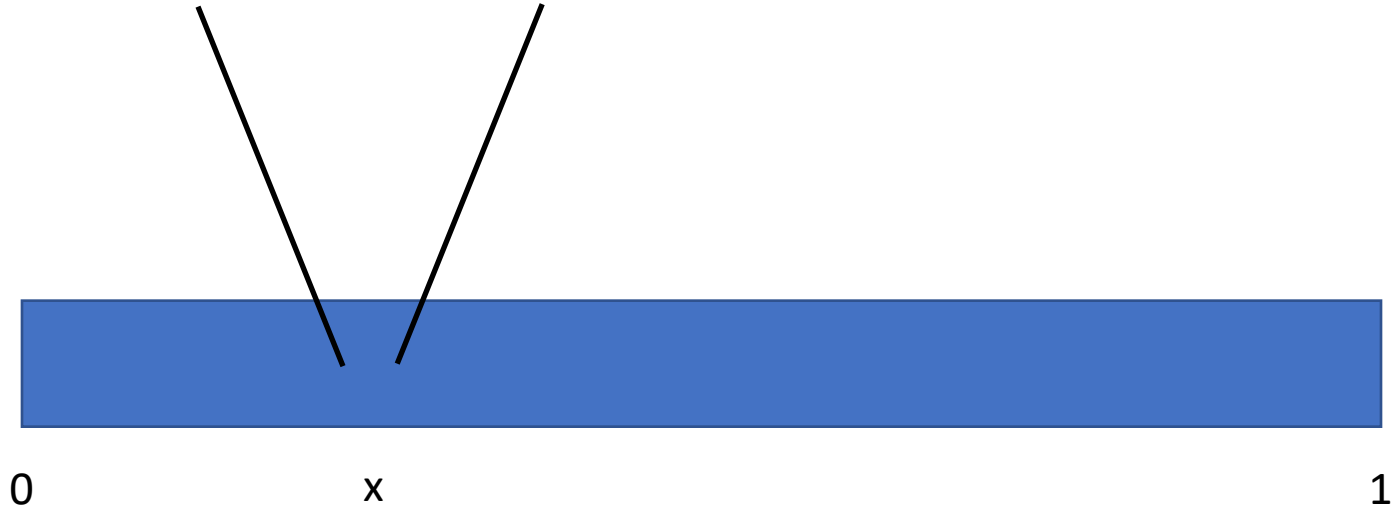

```
v = h.Vector().record(axon(x)._ref_v)
t = h.Vector().record(h._ref_t)
```

eFEL from the Blue Brain Project (pip install efel) can be used to identify electrophysiological features (action potential height, half width, etc) from the recorded timeseries.

Recording Results II

NetCon objects can be used as shown to detect the times when a variable crosses a threshold from below.

As the name suggests, a NetCon can be used to ***con***nect cells together in a ***net***work. To do this, pass in a synapse as the second argument or use ParallelContext.




```
spike_times = h.Vector()
nc = h.NetCon(axon(0.1)._ref_v, None, sec=axon)
nc.threshold = 0 * mV
nc.record(spike_times)
```

Running the Simulation

For convenience, we use a high-level simulation control functions defined in the `stdrun.hoc` library. Load this via:

```
h.load_file('stdrun.hoc')
```

Initialize to -65 mV:

```
h.finitialize(-65 * mV)
```

Run until time 10 ms:

```
h.continuerun(10 * ms)
```

Caution: Squid

NEURON's defaults are based on the squid giant axon.

`sec.diam`: 500 µm

`sec.Ra`: 35.4 Ω cm

`h.celsius`: 6.3 C

Comingio Merculiano (1845–1915) - Jatta di Guiseppe (1896) *Cefalopodi viventi nel Golfo di Napoli (sistematica)*, Berlin: R. Friedländer & Sohn.

Colab time

```
[1] !pip install neuron-nightly
```

```
Requirement already satisfied: neuron-nightly in /usr/local/lib/python3.6/dist-
Requirement already satisfied: numpy>=1.9.3 in /usr/local/lib/python3.6/dist-pa
```

```
[2] import plotly.graph_objects as go
    from neuron import h
    from neuron.units import mV, ms
    h.load_file('stdrun.hoc')
```

```
1.0
```

```
[3] soma = h.Section(name='soma')
    h.hh.insert(soma)
```

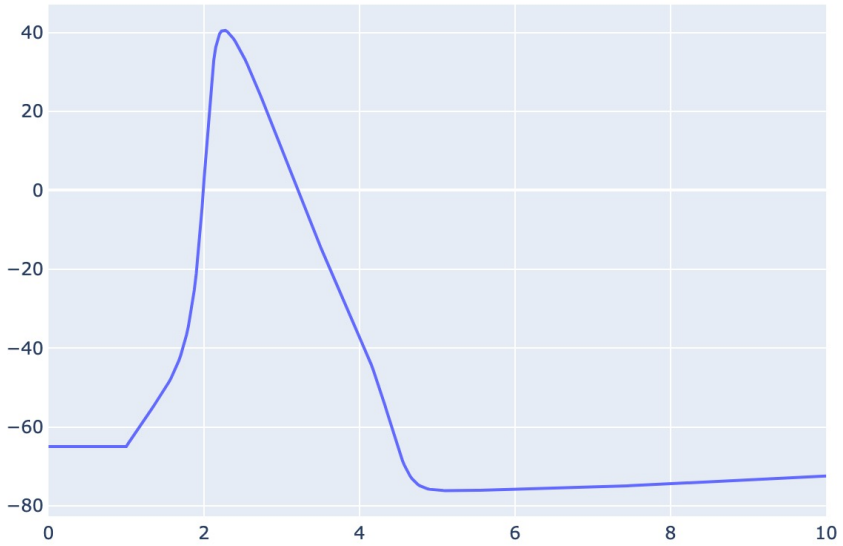
```
[4] ic = h.IClamp(soma(0.5))
    ic.delay = 1
    ic.amp = 50
    ic.dur = 1
```

```
[5] t = h.Vector().record(h._ref_t)
    v = h.Vector().record(soma(0.5)._ref_v)
```

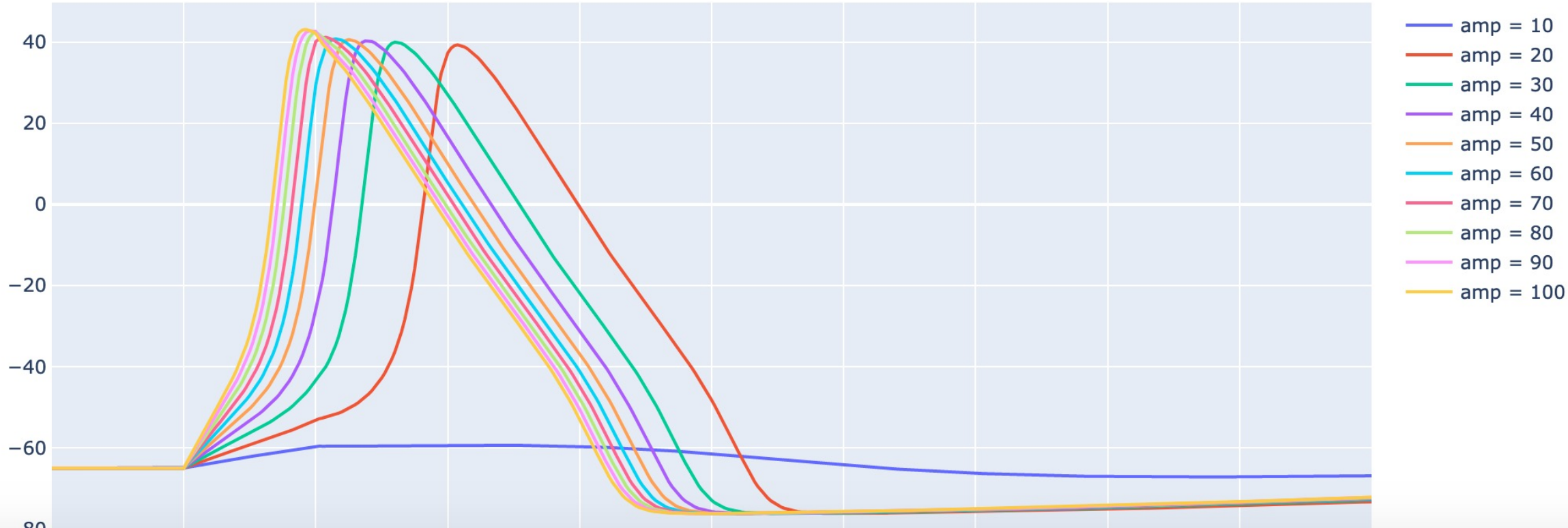
```
[6] h.finitialize(-65 * mV)
    h.continuerun(10 * ms)
```

```
0.0
```

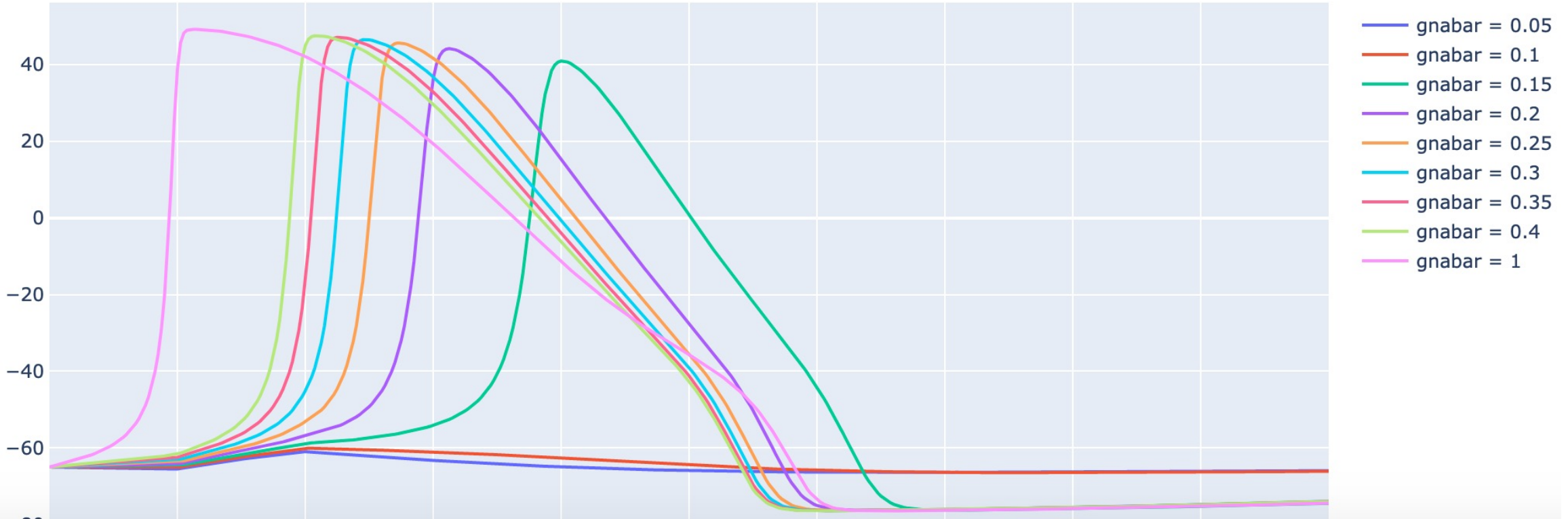
```
[7] go.Figure(data=go.Scatter(x=t, y=v))
```



```
[17] fig = go.Figure()

     for amp in [10, 20, 30, 40, 50, 60, 70, 80, 90, 100]:
       ic.amp = amp
       h.finitialize(-65 * mV)
       h.continuerun(10 * ms)
       fig.add_trace(go.Scatter(x=t, y=v, name=f'amp = {amp}'))

     fig.show()
```



```
[24] ic.amp = 10
     fig = go.Figure()
     for gnabar in [0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 1]:
       soma(0.5).hh.gnabar = gnabar
       h.finitialize(-65 * mV)
       h.continuerun(10 * ms)
       fig.add_trace(go.Scatter(x=t, y=v, name=f'gnabar = {gnabar}'))

     fig.show()
```



Increasing accuracy

Increase time resolution (by reducing time steps) via, e.g.

```
h.dt = 0.01
```

Enable variable step (allows error control):

```
h.CVode().active(True)
```

Set the absolute tolerance to e.g. 10−5:

```
h.CVode().atol(1e-5)
```

Increase spatial resolution by e.g. a factor of 3 everywhere:

```
for sec in h.allsec(): sec.nseg *= 3
```

NeuroMorpho.Org

Version 8.1.13 - Released: 2021-07-02 - Content: 150307 neurons

Total number of downloads: 30296545 Total site hits since August 1, 2006: 3173903

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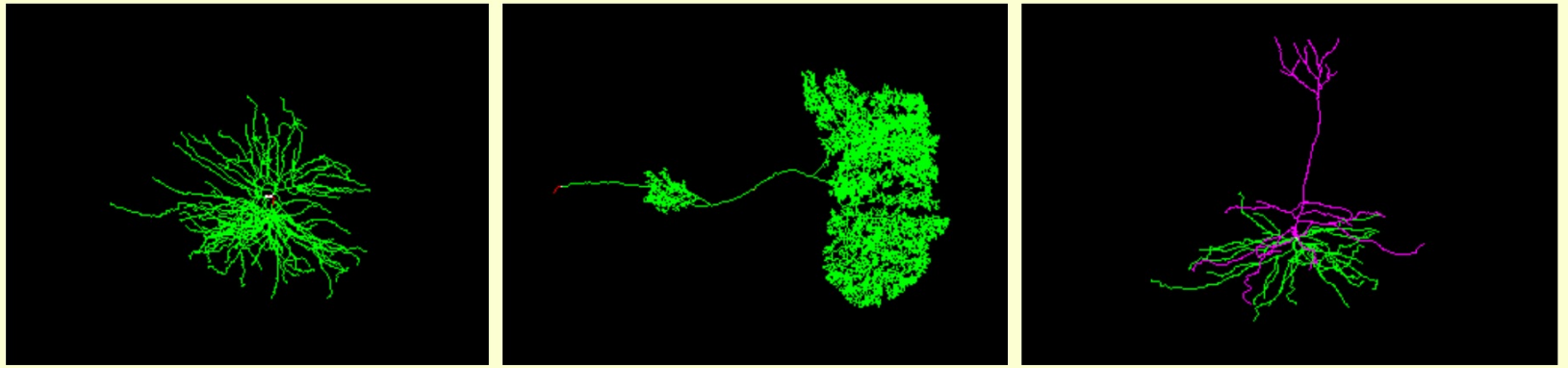
Home > Homepage

Contributions from 785 laboratories **Reconstructions from 953 celltypes**



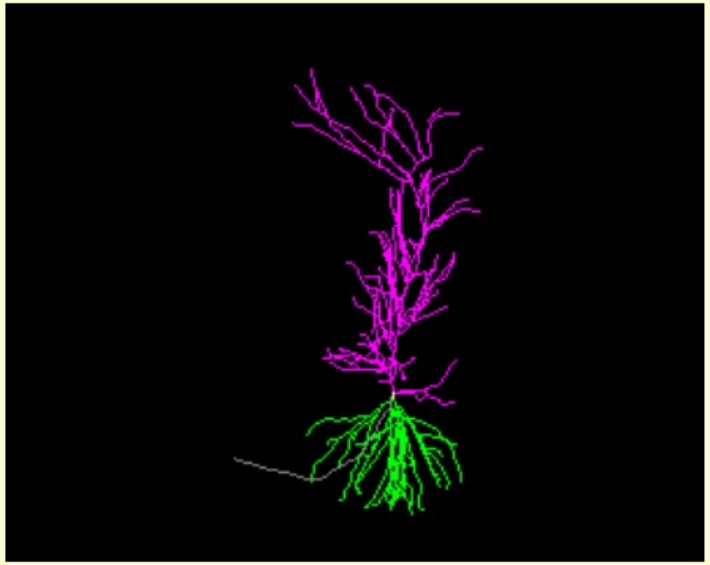
NeuroMorpho.Org is a centrally curated inventory of **digitally reconstructed**

150,307 reconstructions · 953 cell types · 384 brain regions

NeuroMorpho.Org

Version 8.1.13 - Released: 2021-07-02 - Content: 150307 neurons

HOME BROWSE SEARCH LITERATURE COVERAGE TERMS OF USE HELP 0



Morphology File (Standardized)
Morphology File (Original)
Log File (Standardized)
Log File (Original)

Get above files zipped

3D Neuron Viewer - Java, legacy
3D Neuron Viewer - WebGL, novel
Animation

Details about selected neuron	
NeuroMorpho.Org ID :	NMO_00227
Neuron Name :	c91662
Archive Name :	Amaral
Species Name :	rat
Strain :	Sprague-Dawley

Standardized:
Always SWC

Original format:
Could be anything

Ascoli, G. A., Donohue, D. E., & Halavi, M. (2007). NeuroMorpho. Org: a central resource for neuronal morphologies. *Journal of Neuroscience*, *27*(35), 9247-9251.

Metadata

NeuroMorpho.Org ID : NMO_00082
Neuron Name : n401
Archive Name : Turner
Species Name : rat
Strain : Fischer 344
Structural Domains : Dendrites, Soma, No Axon
Physical Integrity : Dendrites Complete
Morphological Attributes : Diameter, 3D, Angles
Min Age : 2.0 months
Max Age : 8.0 months
Gender : Male/Female
Min Weight : 200 grams
Max Weight : 350 grams
Development : young
Primary Brain Region : hippocampus
Secondary Brain Region : CA1
Tertiary Brain Region : Not reported
Primary Cell Class : principal cell
Secondary Cell Class : pyramidal
Tertiary Cell Class : Not reported
Original Format : CVAPP.swc
Experiment Protocol : in vivo
Experimental Condition : Control
Staining Method : biocytin
Slicing Direction : coronal
Slice Thickness : 80.00 µm
Tissue Shrinkage : Reported 25% in xy, 75% in z Corrected 133% in xy, 400% in z
Objective Type : oil
Magnification : 100x
Reconstruction Method : Neurolucida
Date of Deposition : 2005-12-31
Date of Upload : 2006-08-01

Soma Surface : 903.25 µm2
Number of Stems : 7
Number of Bifurcations : 113
Number of Branches : 233
Overall Width : 363.7 µm
Overall Height : 717.18 µm
Overall Depth : 364.21 µm
Average Diameter : 1.16 µm
Total Length : 22216.3 µm
Total Surface : 84796.1 µm2
Total Volume : 30674.3 µm3
Max Euclidean Distance : 668.56 µm
Max Path Distance : 1893.37 µm
Max Branch Order : 25
Average Contraction : 0.7
Total Fragmentation : 5460
Partition Asymmetry : 0.56
Average Rall's Ratio : 1.78
Average Bifurcation Angle Local : 89.59°
Average Bifurcation Angle Remote : 75.23°
Fractal Dimension : 1.07

THE JOURNAL OF COMPARATIVE NEUROLOGY 391:335–352 (1998)

Dendritic Properties of Hippocampal CA1 Pyramidal Neurons in the Rat: Intracellular Staining In Vivo and In Vitro

G.K. PYAPALI,[1,2] A. SIK,[3] M. PENTTONEN,[3] G. BUZSAKI,[3] AND D.A. TURNER[1,2,4*]
[1]Department of Neurosurgery, Duke University, Durham, North Carolina 27710
[2]Durham Veterans Affairs Medical Center, Durham, North Carolina 27710
[3]Center for Molecular and Behavioral Neuroscience, Rutgers,
The State University of New Jersey, Newark, New Jersey 07102
[4]Department of Neurobiology, Duke University, Durham, North Carolina 27710

Not everything was made for you

Not every morphology was reconstructed with the intent of being in a simulation.

Potential factors affecting the quality of the data:

- histology
  - staining, amputation, shrinkage
- physics
  - diameter
- spines

Before using a morphology found online, always read the associated paper(s) to make sure you understand any limitations of the reconstruction.

For example, why did they make this? Were they studying a disease (e.g. Alzheimer's) that alters morphology?

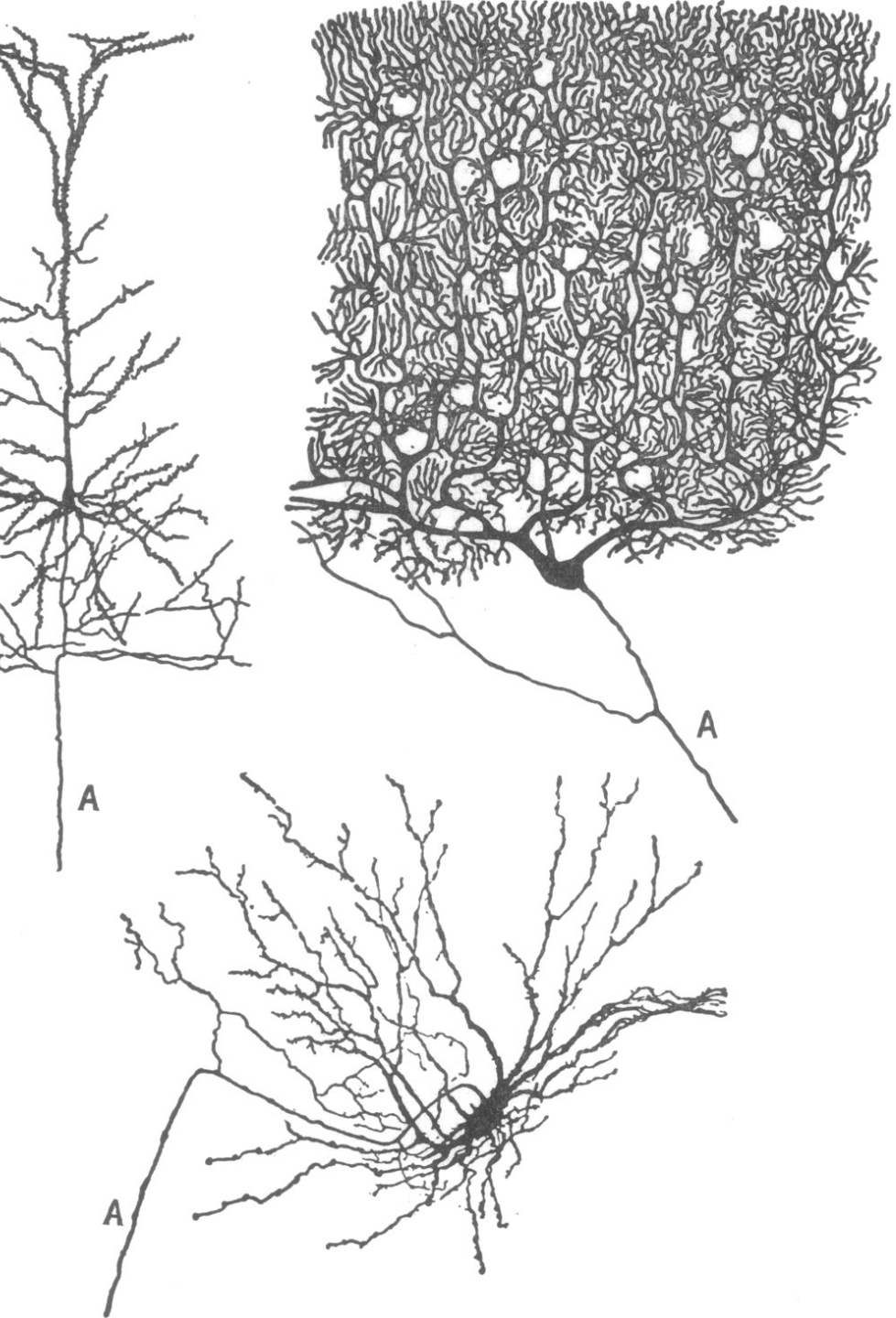
Qualitative tests

Look for orphan sections and bottlenecks.

Insert pas, set Ra and g_pas = pas.g low. Inject large depolarizing current at soma. Examine a PlotShape of v.

Look for z-axis drift and backlash.
Rotate the cell on a PlotShape and look for abrupt jumps.

Are diameters constant or varying? Are they reasonable?

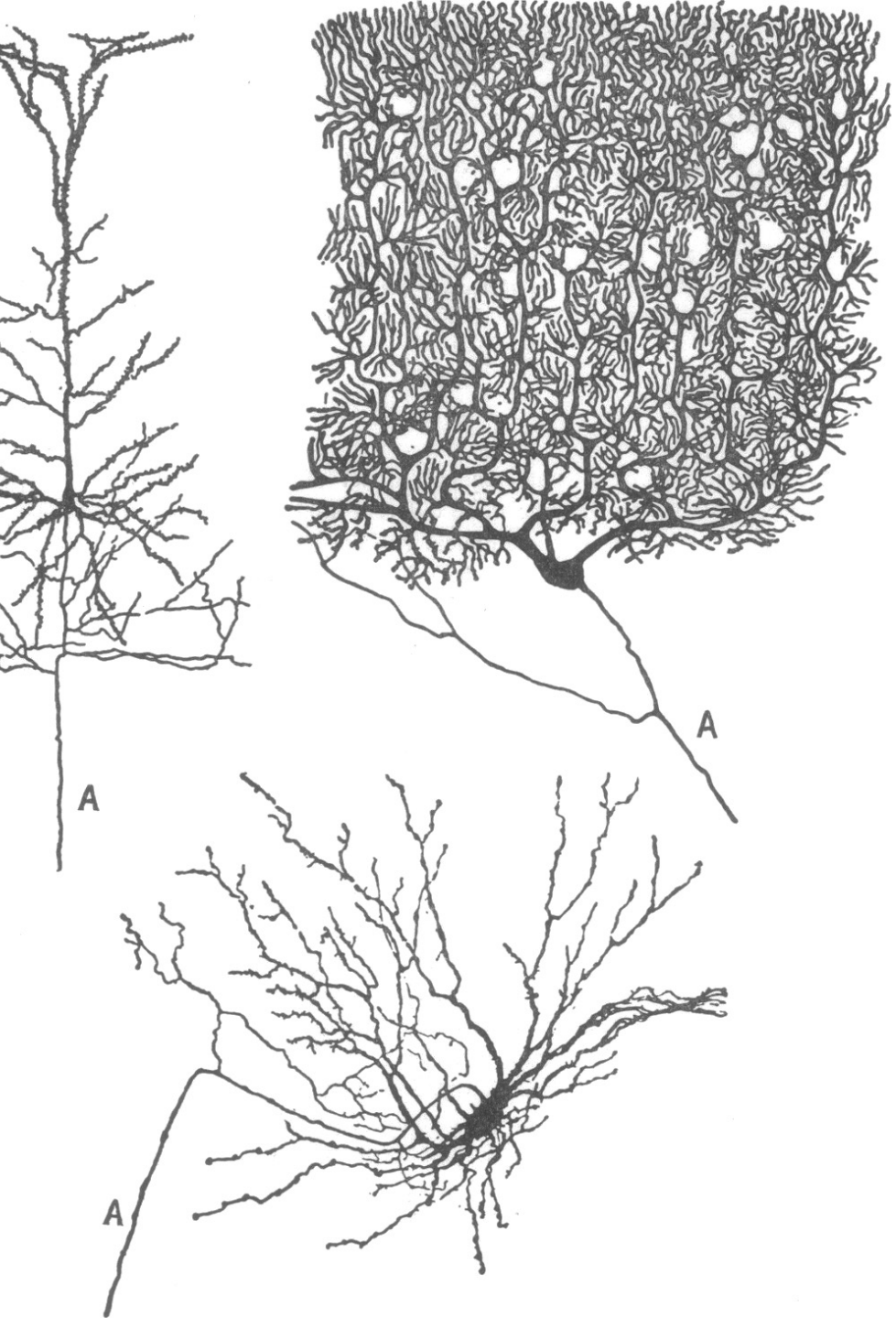


Loading Morphologies

```
from neuron import h
h.load_file('import3d.hoc')

cell = h.Import3d_SWC_read()
cell.input('filename.swc')
i3d = h.Import3d_GUI(cell, False)
i3d.instantiate(None) # or i3d.instantiate(self)
```

Morphology images from Cajal 1909 as reproduced in Rall 1962.



Plotting Morphologies

```
import plotly

ps = h.PlotShape(False)
ps.scale(-80, 40)
ps.variable('v')
ps.plot(plotly).show()
```

Morphology images from Cajal 1909 as reproduced in Rall 1962.

Does shape or position matter?

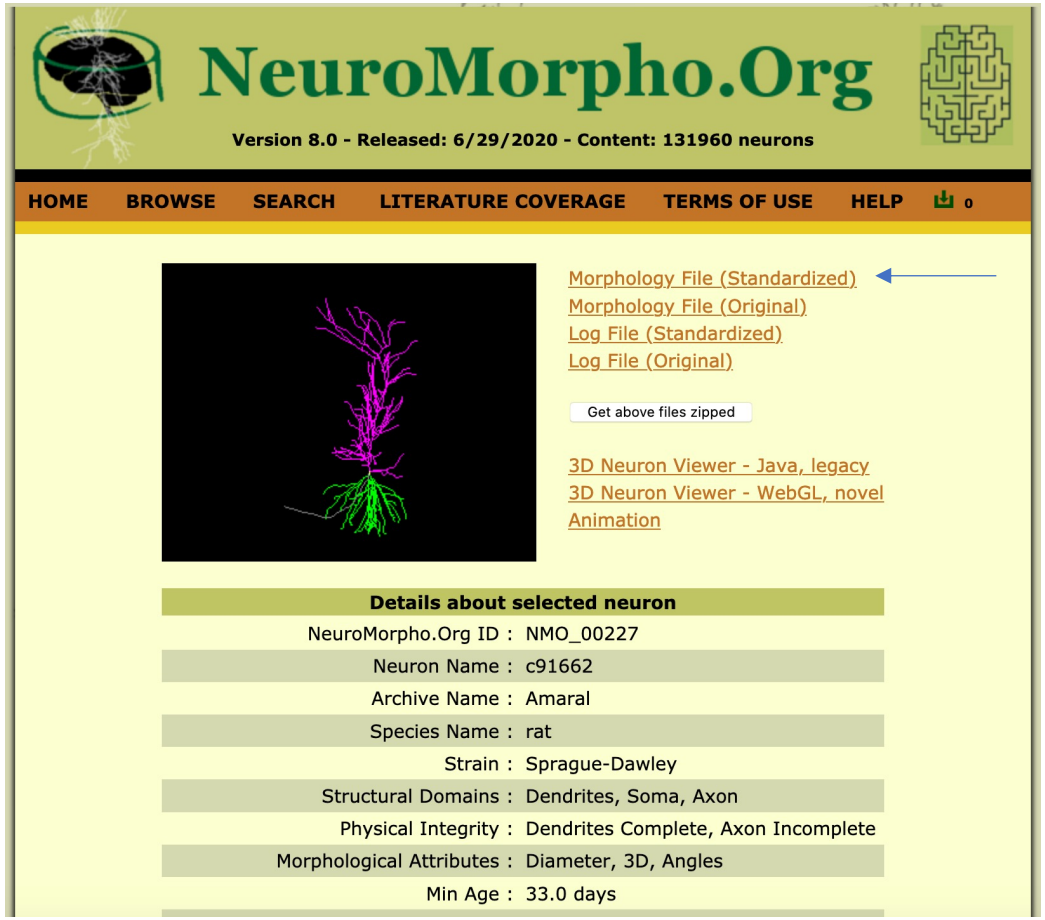
Sometimes.

They matter with:

- Connections based on proximity of axon to dendrite.
- Connections based on cell-to-cell proximity.
- Communicating about your model to other humans.
- Local field potentials.
- Extracellular stimulation.
- Extracellular diffusion.
- 3D intracellular chemical dynamics.

Ishizuka, N., Cowan, W. M., & Amaral, D. G. (1995). A quantitative analysis of the dendritic organization of pyramidal cells in the rat hippocampus. *Journal of Comparative Neurology*, *362*(1), 17-45.

Example




```
# Original file c91662.swc edited using StdSwc version 1.31 on 11/10/13.
# Irregularities and fixes documented in c91662.swc.std.  See StdSwc1.31.doc for more information.
#
# Neurolucida to SWC conversion from L-Measure. Sridevi Polavaram: spolavar@gmu.edu
# Original fileName:C:\Users\praveen\Desktop\Uzma\ErrorArchives\ToBeProcessed\Amaral\asc\c91662.asc
#The original file has a single soma contour that is averaged into 3 soma points
# NEUROMANTIC V1.6.3 (10/18/2013 6:55:13 PM): Saved to c91662-T1.swc
1 1 0.0 0.0 0.0 8.8677 -1
2 1 1.13 8.71 1.2 8.8677 1
3 1 -1.13 -8.71 -1.2 8.8677 1
4 4 -1.86 11.06 -0.47 1.85 1
5 4 -1.94 19.75 -0.65 1.6 4
6 4 -2.52 31.1 -1.23 1.35 5
7 4 -2.94 39.91 -2.02 1.35 6
8 4 -2.55 49.45 -1.47 1.1 7
9 4 -2.61 56.49 -0.77 1.1 8
10 4 -1.17 70.15 -1.59 1.1 9
11 4 2.04 83.45 -1.43 1.1 10
12 4 1.89 91.65 -1.68 1.1 11
13 4 4.35 106.58 -1.57 1.1 12
14 4 5.09 115.06 -1.02 1.1 13
15 4 7.16 126.11 -1.93 1.1 14
16 4 7.13 129.63 -1.58 1.1 15
17 4 9.19 135.02 -2.02 1.1 16
18 4 11.82 145.77 -1.23 1.1 17
19 4 13.47 151.73 -1.73 0.9 18
20 4 14.65 157.05 -0.86 0.9 19
21 4 15.6 164.42 0.15 0.9 20
22 4 17.22 166.37 -0.76 0.9 21
23 4 17.27 175.11 -1.42 0.8 22
24 4 17.43 180.1 -0.87 0.8 23
25 4 18.41 192.2 -0.94 0.8 24
26 4 20.93 207.62 -0.75 0.8 25
27 4 22.64 214.07 -1.18 0.8 26
28 4 26.23 231.47 2.1 0.8 27
29 4 28.89 246.23 3.3 0.8 28
30 4 31.83 252.62 2.17 0.8 29
31 4 33.06 266.68 2.37 0.8 30
32 4 36.17 276.41 2.67 0.8 31
33 4 38.23 281.8 2.23 0.8 32
34 4 43.26 297.81 3.18 0.8 33
35 4 49.51 314.69 4.04 0.8 34
36 4 51.98 319.51 3.66 0.8 35
37 4 55.37 329.56 5.11 0.8 36
38 4 59.09 339.26 5.05 0.8 37
39 4 63.87 351.94 0.9 0.8 38
40 4 65.01 361.5 0.62 0.8 39
41 4 64.84 372.28 0.1 0.6 40
42 4 63.56 393.06 -1.8 0.6 41
43 4 63.28 401.93 -3.07 0.6 42
44 4 62.98 405.13 -3.87 0.6 43
45 4 61.56 411.24 -2.61 0.6 44
46 4 57.99 423.02 -3.47 0.6 45
```

http://tinyurl.com/neuromorpho-c91662

http://tinyurl.com/neuromorpho-c91662-swc

Colab time

- Load the cell from tinyurl.com/neuromorpho-c91662-swc, run a simulation, plot with PlotShape midway through a spike.
- Show a pseudo-line-scan path through it (use RangeVarPlot).
- Do the same thing showing a propagating wave at various time points.

tinyurl.com/neuron-morphology-example

```
[3] import plotly
```

```
[4] from neuron import h
    from neuron.units import mV, ms
    h.load_file('stdrun.hoc')
    h.load_file('import3d.hoc')
```

```
    1.0
```

```
[5] cell = h.Import3d_SWC_read()
    cell.input('neuromorpho-c91662-swc')
    i3d = h.Import3d_GUI(cell, False)
    i3d.instantiate(None)
```

```
    One point section Import3d_Section[2] ending at line 10 has been removed
    One point section Import3d_Section[1] ending at line 9 has been removed
    0.0
```

```
[6] h.hh.insert(h.allsec())
    for sec in h.allsec():
      sec.nseg = 1 + 2 * int(sec.L / 40)
```

```
[7] ic = h.IClamp(h.soma[0](0.5))
    ic.amp = 10
    ic.delay = 1
    ic.dur = 1
```

```
[8] h.finitialize(-65 * mV)
    h.continuerun(3 * ms)
```

```
[11] fig = rvp.plot(plotly, name='t=3')
     h.continuerun(4 * ms)
     fig = rvp.plot(fig, name='t=4')
     h.continuerun(5 * ms)
     fig = rvp.plot(fig, name='t=5')
     fig.update_layout(
         xaxis_title='distance from center of soma (μm)',
         yaxis_title='membrane potential (mV)'
     )
     fig.show()
```