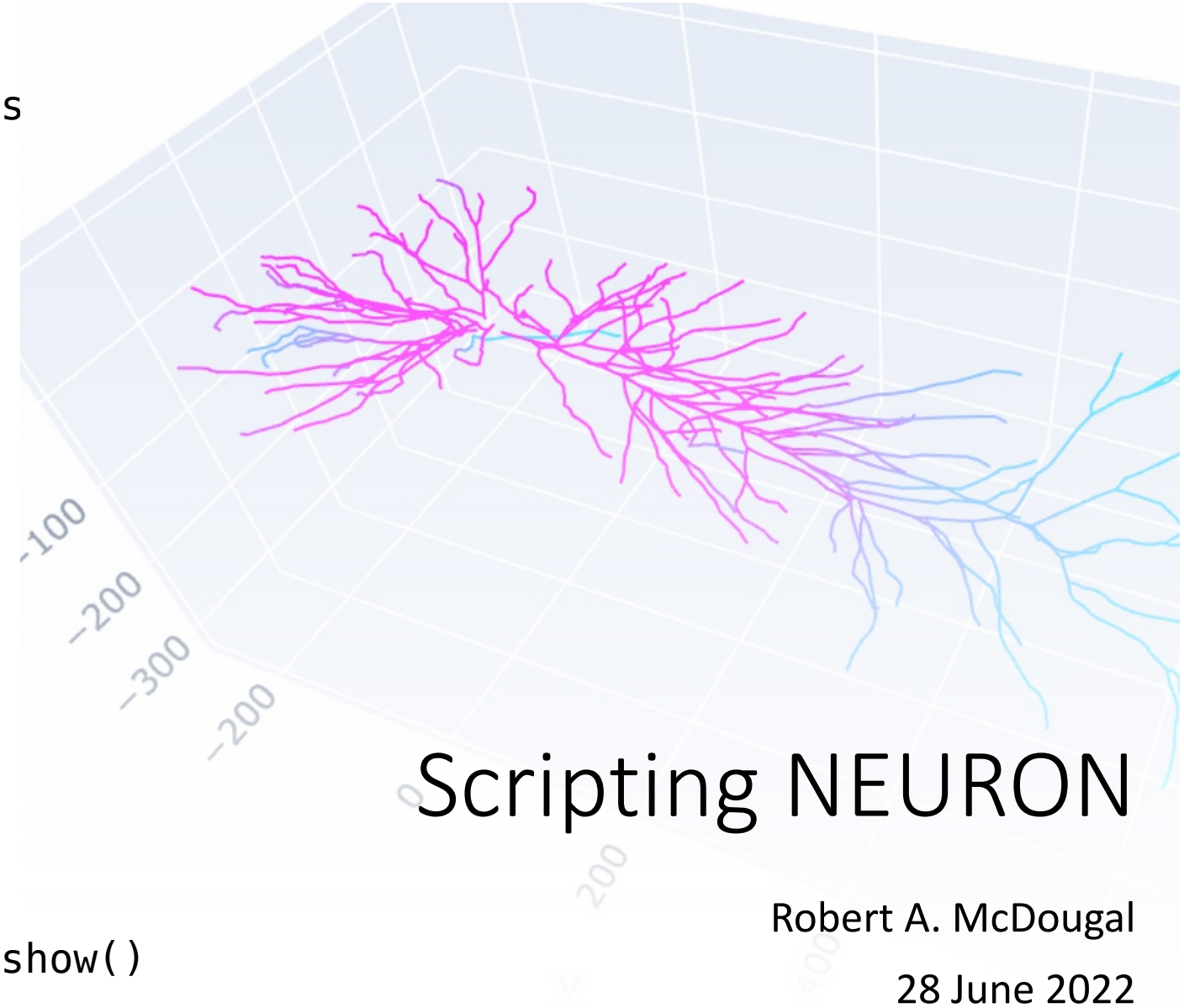
```
from neuron import h
from neuron.units import mV, ms
from matplotlib import cm
import plotly
h.load_file('stdrun.hoc')

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()
```



Scripting NEURON

Robert A. McDougal

28 June 2022

NEURON Main Menu

Iconify

File Build Tools Graph Vector Window Help

Close Hide

File

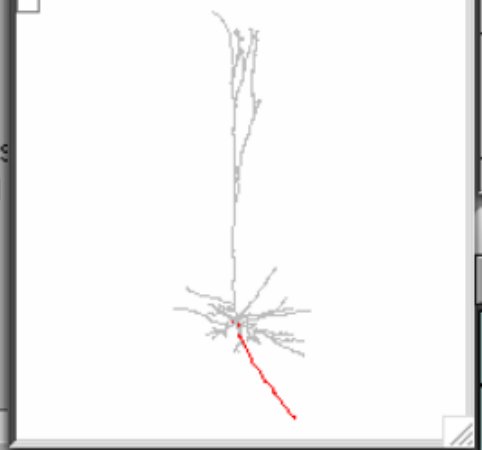
79 sections; 150 segments

* 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]...

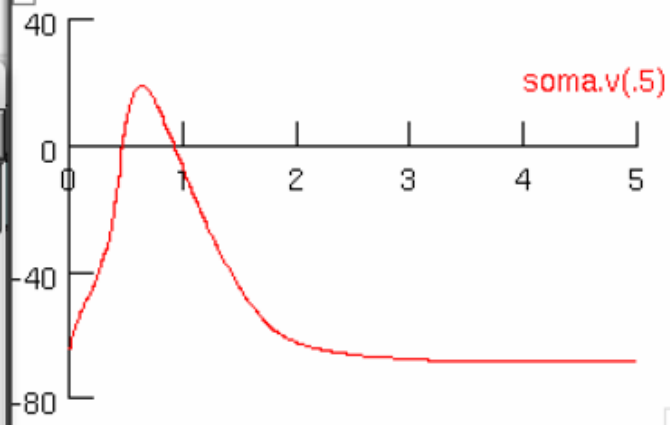
Close Hide

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

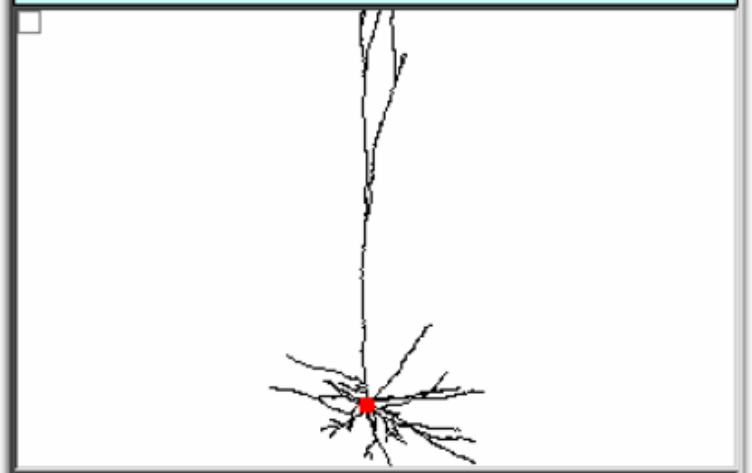
include dstate/dt contribution

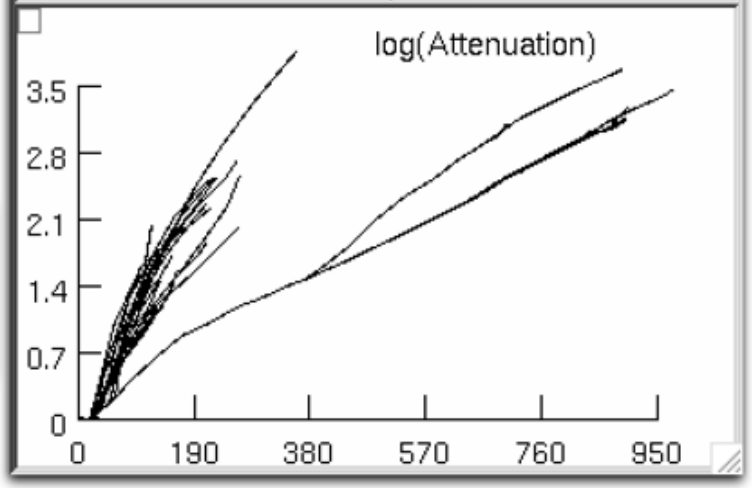
frequency (Hz) 0

Vin

Vout

Measure (red) soma(0.5)





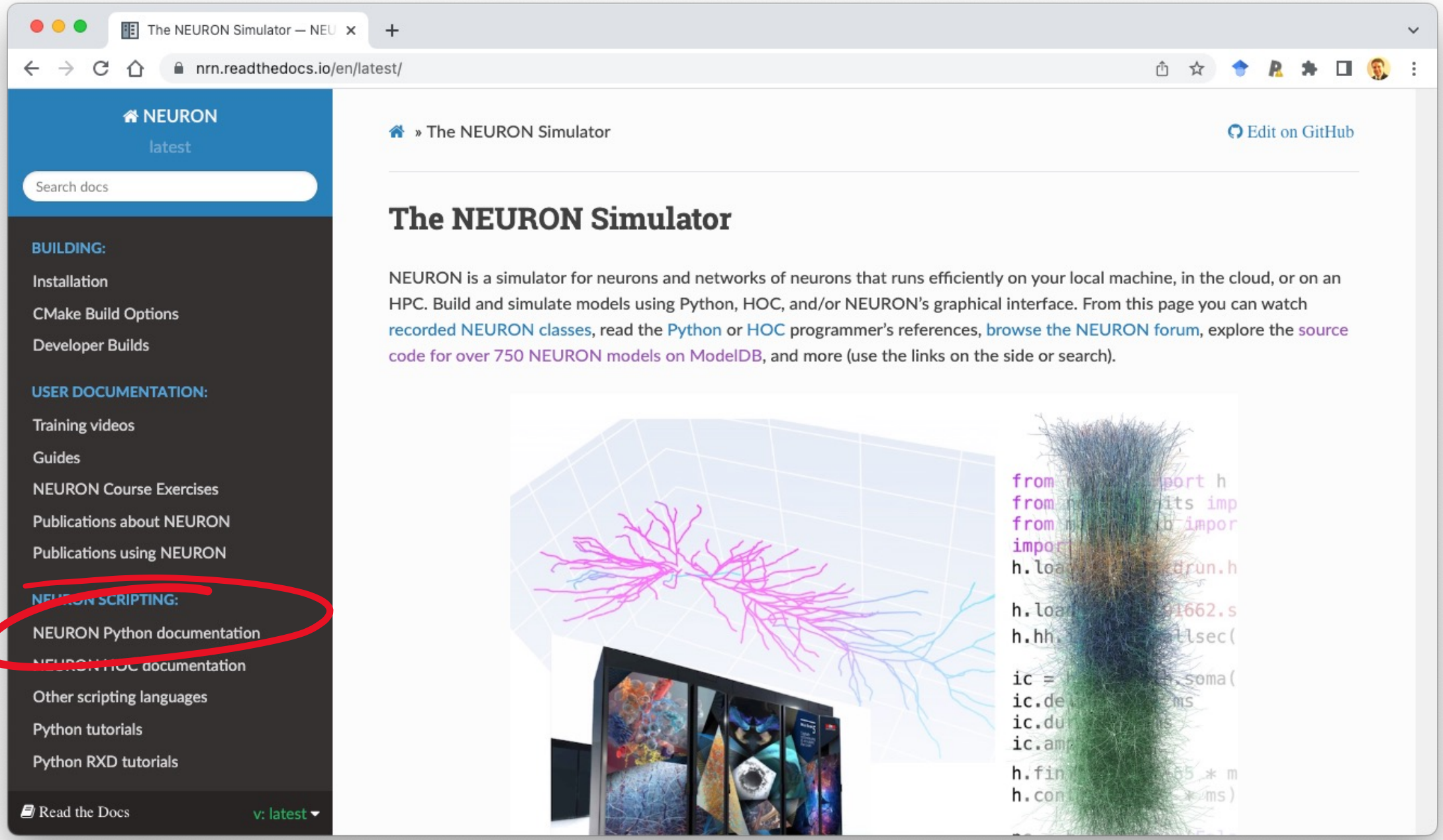
What is a script?

- A **script** is a file with computer-readable instructions for performing a task.

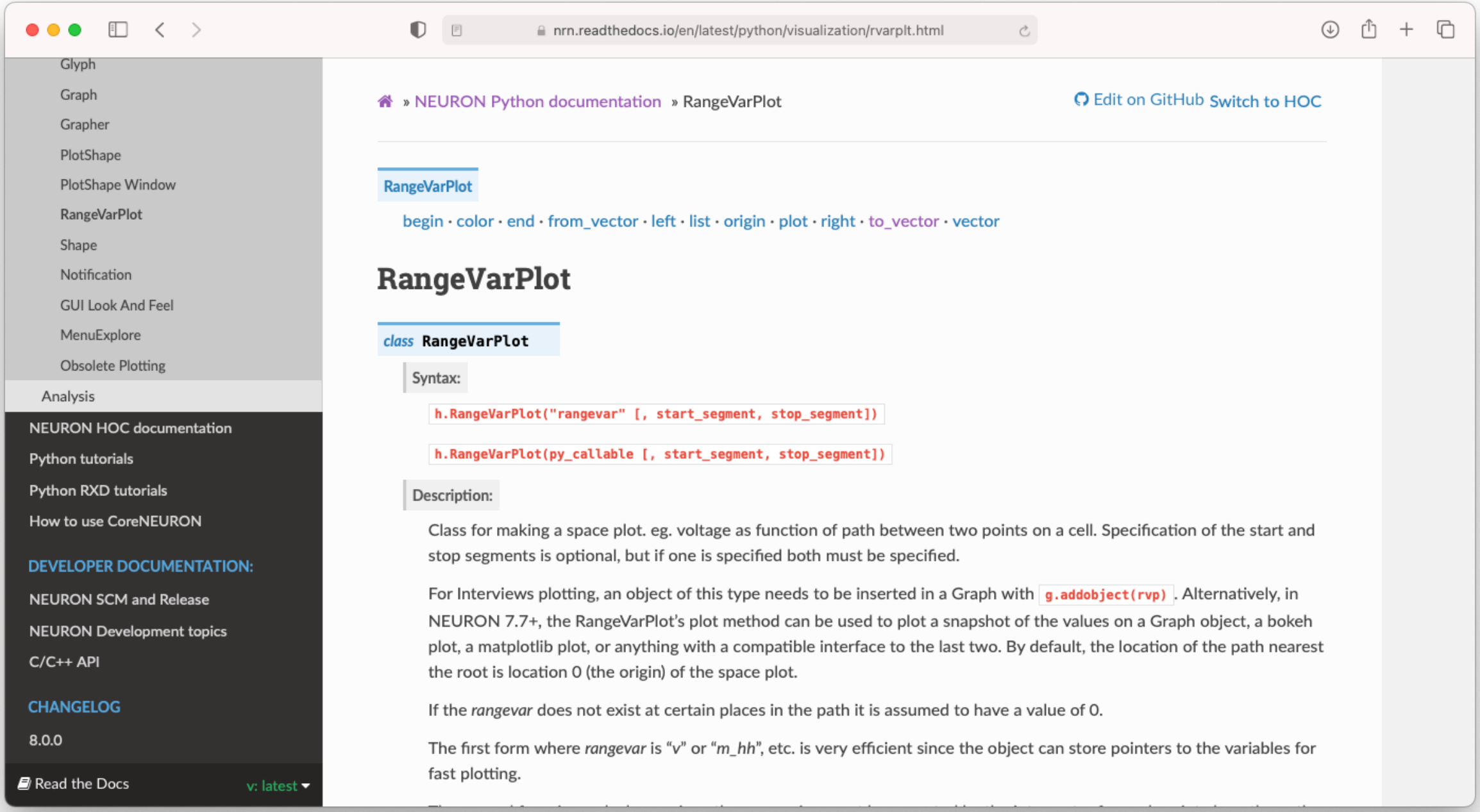
- In NEURON, scripts can:
  - set-up a module
  - define and perform an experimental protocol
  - record data
  - save and load data
  - and more …

Why write scripts for NEURON?

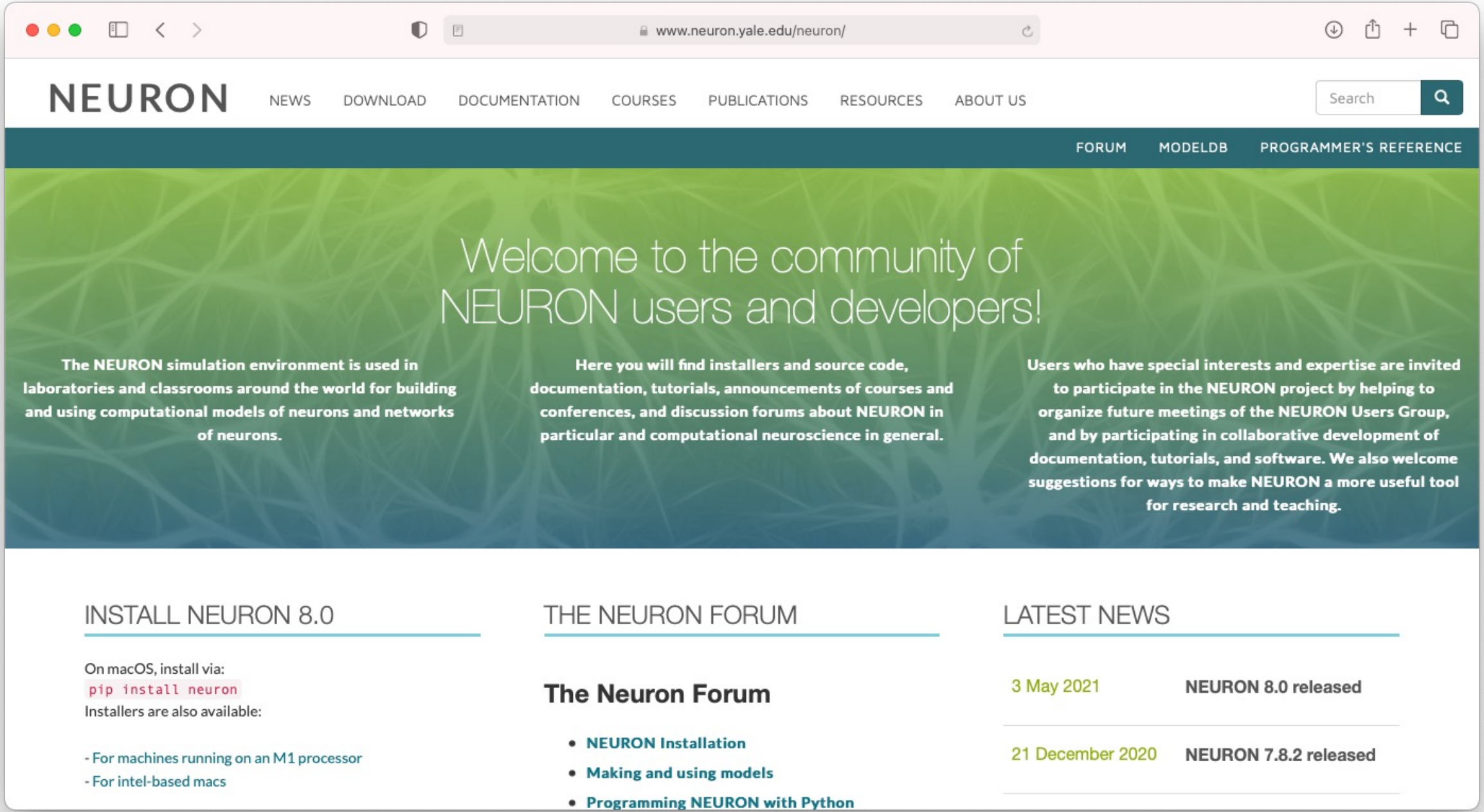
- Automation ensures **consistency** and reduces manual effort.
- Facilitates **comparing the suitability** of different models.
- Facilitates **repeated experiments** on the same model with different parameters (e.g. drug dosages).
- Facilitates **re-collecting data** after change in experimental protocol.
- Provides a complete, **reproducible** version of the experimental protocol.



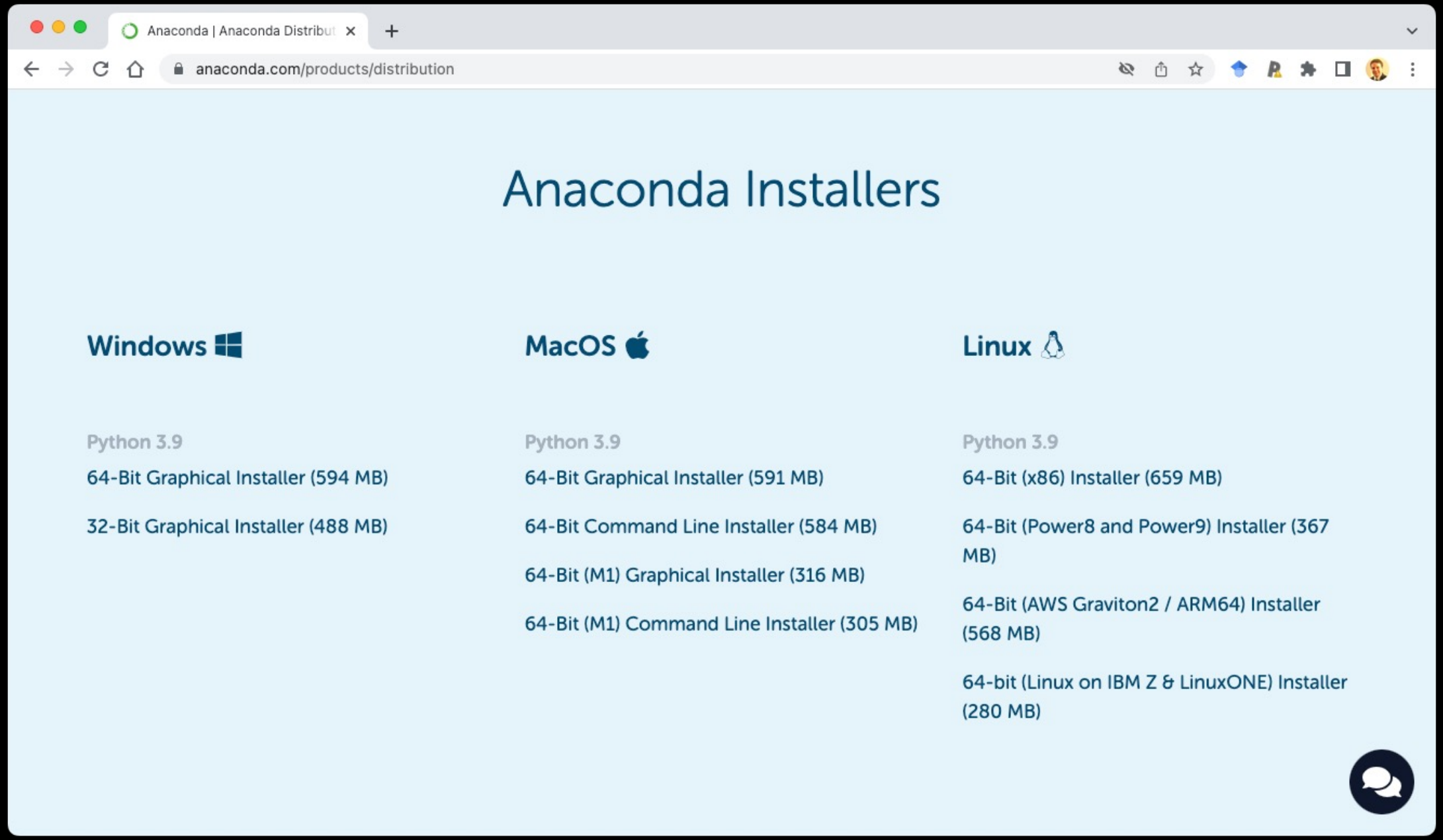
nrn.readthedocs.io



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.



neuron.yale.edu



There are many Python distributions. Any should work, but many people prefer Anaconda as it comes with a large set of useful libraries.

spike-demo.py

spike-demo.py

sers > ramcdougal > Dropbox > notebook > 20201122 > spike-demo.py > ...

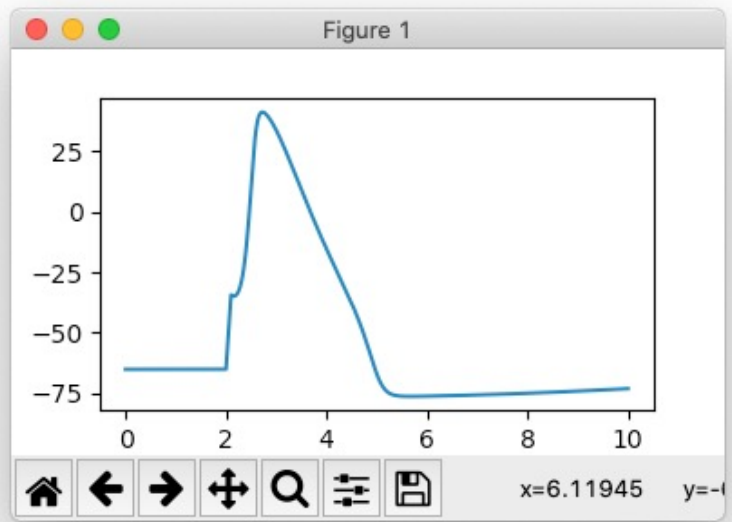
```
1   from neuron import h
2   from neuron.units import ms, mV, µm
3   import matplotlib.pyplot as plt
4   h.load_file("stdrun.hoc")
5
6   soma = h.Section(name='soma')
7   soma.L = soma.diam = 10 * µm
8   soma.insert(h.hh)
9
10  ic = h.IClamp(soma(0.5))
11  ic.delay = 2 * ms
12  ic.dur = 0.1 * ms
13  ic.amp = 1
14
15  t = h.Vector().record(h._ref_t)
16  v = h.Vector().record(soma(0.5)._ref_v)
17
18  h.finitialize(-65 * mV)
19  h.continuerun(10 * ms)
20
21  plt.plot(t, v)
22  plt.show()
```

master* Python 3.8.3 64-bit ('base': conda) ⊗ 1 ⚠ 0

20201122 — python spike-demo.py — 69×30

~/Dropbox/notebook/20201122 — python spike-demo.py

```
Last login: Sun Nov 22 20:44:33 on ttys004
(base) ramcdougal@Roberts-MacBook-Pro 20201122 % python
Python 3.8.3 (default, Jul  2 2020, 11:26:31)
[Clang 10.0.0 ] :: Anaconda, Inc. on darwin
Type "help", "copyright", "credits" or "license" for more information
.
>>> from neuron import h
>>> h.celsius
6.3
>>> exit()
(base) ramcdougal@Roberts-MacBook-Pro 20201122 % python spike-demo.py
```



localhost:8888/notebooks/spike-demo.ipynb

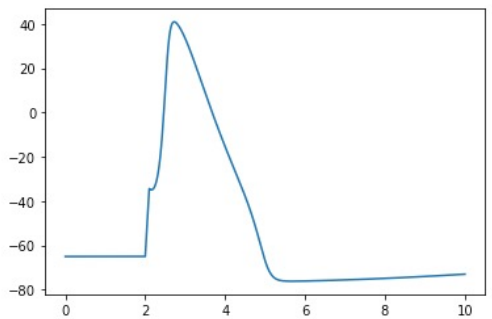
jupyter spike-demo (autosaved)

Logout

File Edit View Insert Cell Kernel Widgets Help Trusted Python 3

Run Code

In [1]:
```
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 * µm
soma.insert(h.hh)

ic = h.IClamp(soma(0.5))
ic.delay = 2 * ms
ic.dur = 0.1 * ms
ic.amp = 1

t = h.Vector().record(h._ref_t)
v = h.Vector().record(soma(0.5)._ref_v)

h.finitialize(-65 * mV)
h.continuerun(10 * ms)

plt.plot(t, v)
plt.show()
```



In [ ]:

colab.research.google.com/drive/1t91Ebz3oy

spike-demo.ipynb

File Edit View Insert Runtime Tools Help All chang...

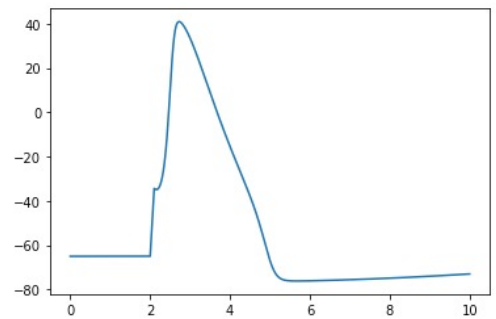
Comment Share

+ Code + Text RAM Disk Editing

[11] `!pip install neuron`

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

```
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 * µm
soma.insert(h.hh)

ic = h.IClamp(soma(0.5))
ic.delay = 2 * ms
ic.dur = 0.1 * ms
ic.amp = 1

t = h.Vector().record(h._ref_t)
v = h.Vector().record(soma(0.5)._ref_v)

h.finitialize(-65 * mV)
h.continuerun(10 * ms)

plt.plot(t, v)
plt.show()
```



Introduction to Python

tinyurl.com/neuron2022-python-intro

Displaying results: the print function

```
[1]  print("NEURON is a great tool for simulation.")
```

```
NEURON is a great tool for simulation.
```

```
[2]  print(5 * (3 + 2))
```

```
25
```

```
[6]  print(soma.diam)
```

```
10.0
```

Variables

- Give things a name to access them later:

```
diameter = 4
print("The diameter is", diameter)
print("The square of the diameter is", diameter ** 2)
```

```
The diameter is 4
The square of the diameter is 16
```

Lists and for loops

- To do the same thing to several items, put the items in a list and use a `for` loop:

```
cell_parts = ["soma", "apical", "basal", "axon"]
for part in cell_parts:
    print(part)
```

- Items in a list can be accessed directly using the [] notation.
  Note: lists start at position 0.

```
print(cell_parts[2])
```

```
basal
```

- To check if an item is in a list, use `in`:

```
print("brain" in cell_parts)
```

```
False
```

Dictionaries

- If there is no natural order, specify your own key-value pairs:

```
diameters = {"soma": 10, "axon": 2, "apical": 5}
print(diameters["apical"])
```

```
5
```

- Loop over keys and values using `.items()`:

```
for name, diam in diameters.items():
    print("The diameter of", name, "is", diam, "microns")
```

```
The diameter of soma is 10 microns
The diameter of axon is 2 microns
The diameter of apical is 5 microns
```

Functions

- If a calculation is used more than once, give it a name via `def` and refer to it by the name.
- If there is a complicated self-contained calculation, give it a name.
- Return the result of the calculation with the `return` keyword.

```
def volume_of_cylinder(diameter, length):
    return (3.14 / 4) * diameter ** 2 * length
```

```
vol1 = volume_of_cylinder(5, 20)
apical_vol = volume_of_cylinder(apical.diam, apical.L)
```

Libraries (aka “modules”)

- Python modules provide functions, classes, and values that your scripts can use.
- To load a module, use import:

```
import math
```

- Use dot notation to access a function or value from the module:

```
print(math.cos(math.pi / 3))
```

```
0.5000000000000001
```

- One can also load specific items from a module or give a short-hand name for the module:

```
from neuron import h, gui
```

```
import pandas as pd
```

Other useful Python modules

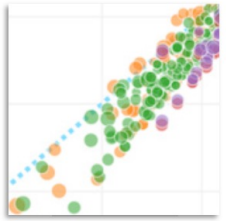
- `math`
  - Basic math functions
- `numpy`
  - Advanced math functions
- `pandas`
  - Basic data science and database access
- `sklearn`
  - Machine learning
- `plotly`, `plotnine`, `matplotlib`
  - Plotting

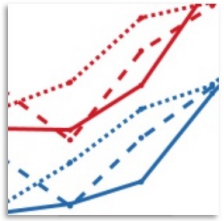
plotly

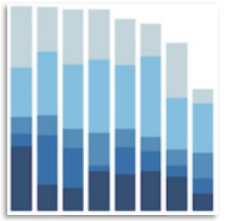
Free (MIT licensed), full-featured graphics library

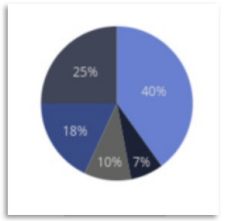
Graphs are interactive and can be saved.

Supports both Python and JavaScript.

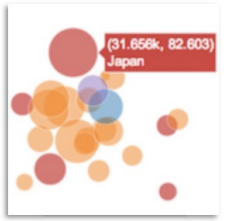

Scatter Plots


Line Charts

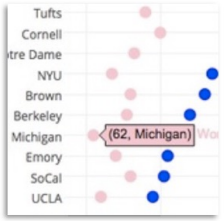

Bar Charts



Pie Charts

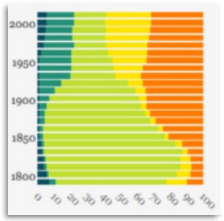


Bubble Charts

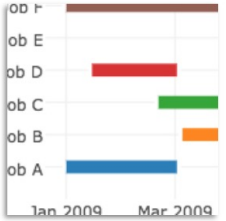


Dot Plots

Filled Area Plots

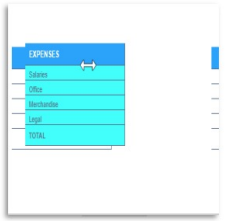


Horizontal Bar Charts

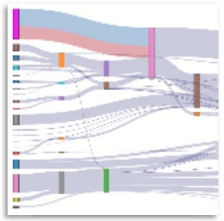


Gantt Charts

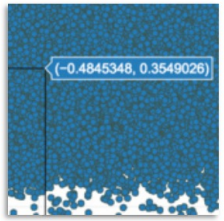

Sunburst Charts



Tables


Sankey Diagram

Treemap Charts



WebGL vs SVG

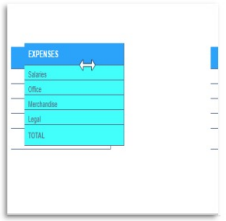
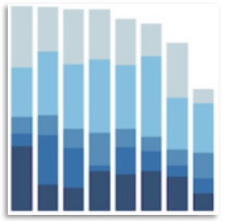


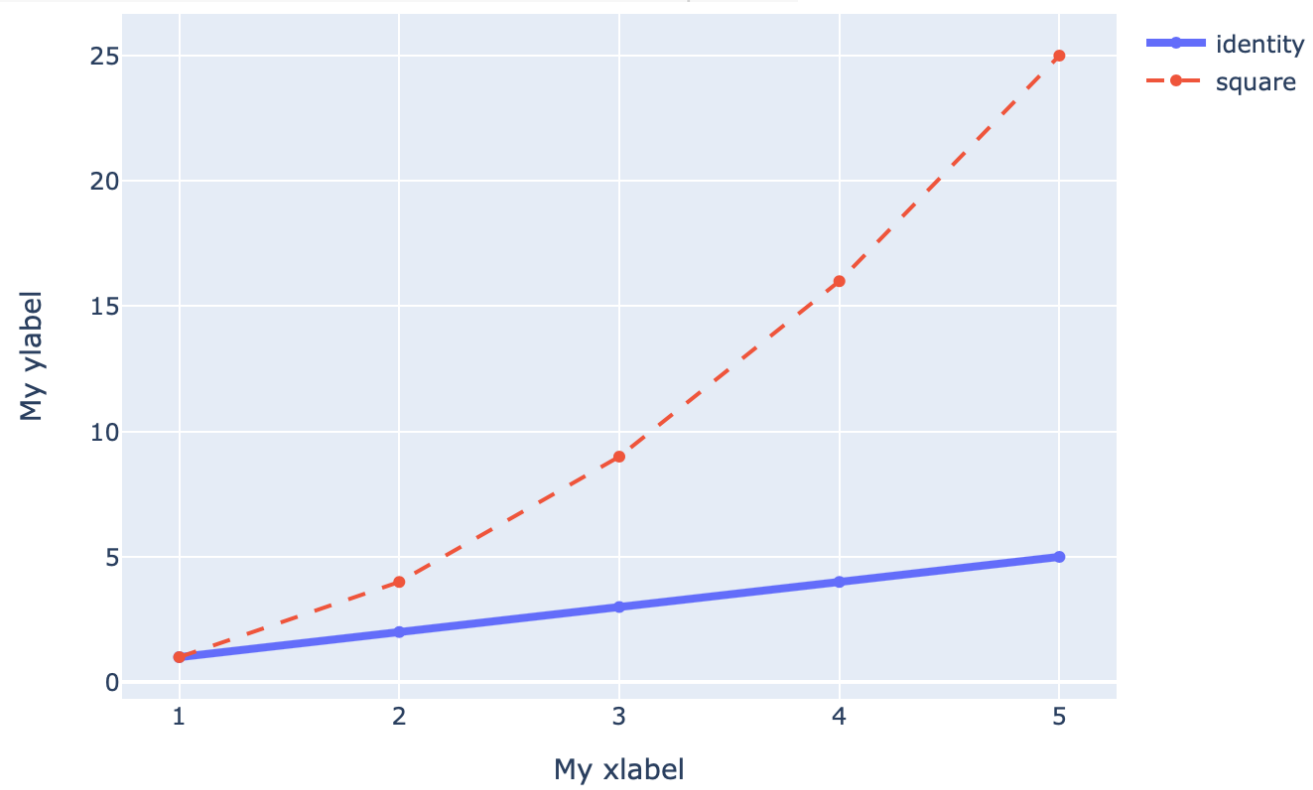
Figure Factory Tables


Categorical Axes

https://plotly.com/python/basic-charts/

```
import plotly.graph_objects as go
```

```
fig = go.Figure()
fig.add_trace(
    go.Scatter(x=[1,2,3,4,5], y=[1,2,3,4,5], name="identity", line={"width": 4})
)
fig.add_trace(
    go.Scatter(x=[1,2,3,4,5], y=[1,4,9,16,25], name="square", line={"dash": "dash"})
)
fig.update_layout({
    "xaxis_title": "My xlabel",
    "yaxis_title": "My ylabel"
})
fig.show()
```



For NEURON built-in graphs, we'll just use:

```
import plotly
```

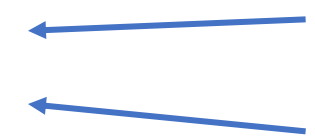
String formatting

- We'll often want to insert variables into text
  - labeling time points in graphs, storing parameters in data filenames, …
- In Python, this is done using an f-string:

```
tstop = 10
my_string = f"We should stop at t = {tstop} ms"
```

- Formatting can be specified e.g. to round to a certain number of digits.

```
f"pi is approximately {pi:.5}"
f"pi is approximately {pi:.7}"
```



pi is approximately 3.1416

pi is approximately 3.141593

Getting help

- To get a list of functions, etc. in a module (or class) use dir:

```
from neuron import h
print(dir(h))
```

```
['APCount', 'AlphaSynapse', 'AtolTool', 'AtolToolItem', 'BBSaveState',
'CVode', 'DEG', 'Deck', 'E', 'ExecCommand', 'Exp2Syn', 'ExpSyn', 'FARAD
AY', 'FInitializeHandler', 'Family', 'File', 'GAMMA', 'GUIMath', 'Glyph
', 'Graph', 'HBox', 'IClamp', 'Impedance', 'Inserter', 'IntFire1', 'Int
Fire2', 'IntFire4', 'KSChan', 'KSGate', 'KSState', 'KSTrans', 'L', 'Lin
earMechanism', 'List', 'Matrix', 'MechanismStandard', 'MechanismType',
```

Getting help

- To see help information for a specific function, use help:

```
help(h.IClamp)
```

```
NEURON+Python Online Help System
================================

Syntax:
    ``stimobj = h.IClamp(section(x))``
```

Getting help

Python is widely used, and there are many online resources available, including:

- docs.python.org – the official documentation
- Stack Overflow – a general-purpose programming forum
- The NEURON programmer's reference – NEURON documentation
- The NEURON forum – for NEURON-related programming questions

Basic NEURON Scripting

Loading NEURON

- Core NEURON functionality

```
from neuron import h
```

- Unit definitions

```
from neuron.units import mV, ms, um
```

You will almost always need these.

- Chemical dynamics

```
from neuron import rxd
```

NEURON run control library

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

stdrun.hoc loads NEURON's "standard run" system, which provides the h.continuerun function for running a simulation until a specific time.

Creating and naming sections

- A Section in NEURON is an unbranched stretch of e.g. dendrite.
- To create a Section, use h.Section and assign the result to a variable:

```
apical = h.Section(name="apical")
```

- A single Section can have multiple references to it.

```
a = apical
print(a == apical)
```

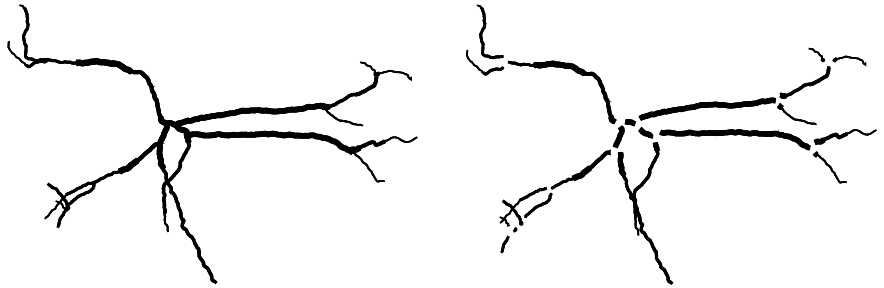
```
True
```

- Printing a Section displays its name. Use str(section) to get the name as a string:

```
s = str(apical)
print(apical)
```

```
apical
```

Basic unit: `h.Section`

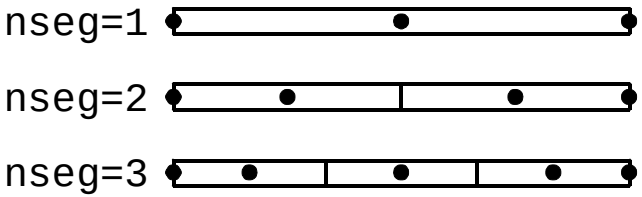


```
soma = h.Section(name='soma')
```

Length: `soma.L`

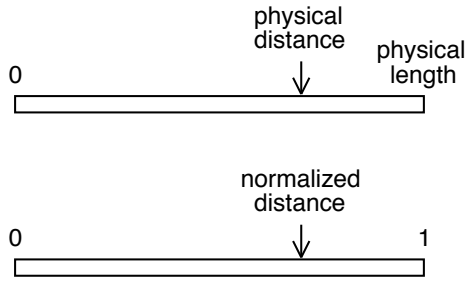
Diameter: `soma.diam`

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.

Looping over a Section gives the Segments

```
dend = h.Section(name="dend")
dend.L = 3
dend.diam = 2
dend.nseg = 3

for seg in dend:
  print(seg, seg.area())
```

```
dend(0.166667) 6.283185307179586
dend(0.5) 6.283185307179586
dend(0.833333) 6.283185307179586
```

Getting x and Section

```
seg = dend(0.5)
print(seg.x, seg.sec == dend)
```

```
0.5 True
```

Select specific Segments; they can have different properties

```
dend(0.5).diam = 4

for seg in dend:
  print(seg, seg.area())
```

```
dend(0.166667) 6.283185307179586
dend(0.5) 12.566370614359172
dend(0.833333) 6.283185307179586
```

Not limited to cylinders

```
dend.nseg = 1
dend.pt3dclear()
dend.pt3dadd(0, 0, 0, 1)
dend.pt3dadd(10, 0, 0, 5)
dend(0.5).volume()
```

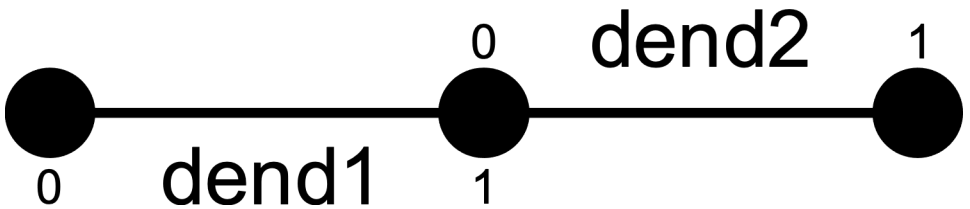
```
81.15781021773631
```

Connecting sections

To construct a neuron's full branching structure, individual sections must be connected using .connect:

```
dend2.connect(dend1(1))
```

Each section is oriented and has a 0- and a 1-end. In NEURON, traditionally the 0-end of a section is attached to the 1-end of a section closer to the soma. In the example above, `dend2`'s 0-end is attached to `dend1`'s 1-end.



To print the topology of cells in the model, use `h.topology()`.

If no position is specified, the 0-end will be connected to the 1-end as in the example.

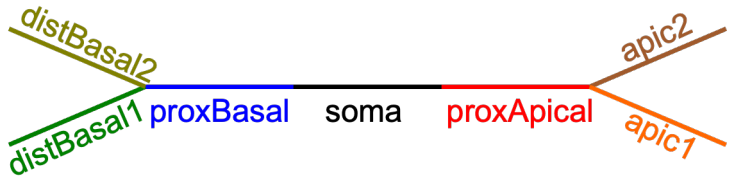
Example

```
from neuron import h

# define sections
soma = h.Section(name="soma")
papic = h.Section(name="proxApical")
apic1 = h.Section(name="apic1")
apic2 = h.Section(name="apic2")
pb = h.Section(name="proxBasal")
db1 = h.Section(name="distBasal1")
db2 = h.Section(name="distBasal2")

# connect them
papic.connect(soma)
pb.connect(soma(0))
apic1.connect(papic)
apic2.connect(papic)
db1.connect(pb)
db2.connect(pb)

# list topology
h.topology()
```

Output:

```
|-| soma(0-1)
   `| proxApical(0-1)
     `| apic1(0-1)
     `| apic2(0-1)
 `| proxBasal(0-1)
   `| distBasal1(0-1)
   `| distBasal2(0-1)
```

Morphology:



Length, diameter, and position

Set a Section's length with .L and diameter with .diam:

```
sec.L = 20 * um
sec.diam = 2 * um
```

diameter may also be specified per segment

If no units are specified, NEURON assumes µm.

To specify the $(x, y, z; d)$ points a section `sec` passes through, use e.g. `sec.pt3dadd(x, y, z, d)`. The section `sec` has `sec.n3d()` 3D points; their i^{th} x-coordinate is `sec.x3d(i)`. The methods `.y3d`, `.z3d`, and `.diam3d` work similarly.

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.

Tip: define classes of cells not individual cells

- Consider the code

```
class Pyramidal:
    def __init__(self):
        self.soma = h.Section(name="soma", cell=self)
        self.soma.L = self.soma.diam = 10
```

- The `__init__` method is run whenever a new `Pyramidal` cell is created; e.g. via

```
pyr1 = Pyramidal()
```

- The soma can be accessed using dot notation:

```
print(pyr1.soma.diam)
```

```
10.0
```

Tip: define classes of cells not individual cells

- By defining a cell in a class, once we are happy with it, we can a copy of the cell in a single line of code:

```
pyr2 = Pyramidal()
```

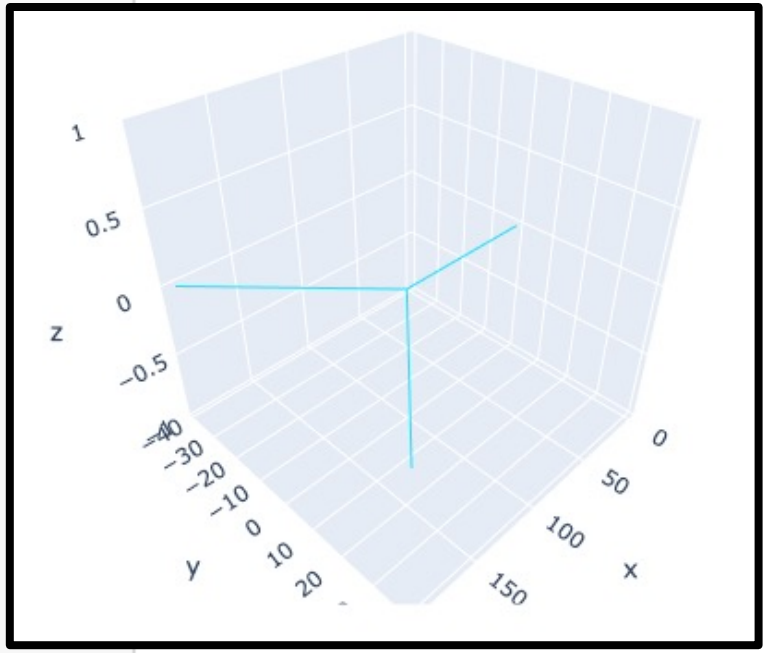
- Or even many copies:

```
pyrs = [Pyramidal() for i in range(1000)]
```

- For network models, helpful to associate a number (a gid) with each cell.

Viewing the morphology with h.PlotShape

```
from neuron import h
from neuron.units import um
import plotly

class Cell:
    def __init__(self):
        main = h.Section(name="main", cell=self)
        dend1 = h.Section(name="dend1", cell=self)
        dend2 = h.Section(name="dend2", cell=self)

        dend1.connect(main)
        dend2.connect(main)

        main.diam = 10 * um
        dend1.diam = 2 * um
        dend2.diam = 2 * um

        # important: store the sections
        self.main = main; self.dend1 = dend1; self.dend2 = dend2
        self.all = main.wholetree()

my_cell = Cell()
ps = h.PlotShape(False)
ps.plot(plotly).show()
```



Passing `True` instead of `False` will plot in an InterViews window instead.

The InterViews windows can be saved as postscript using e.g.

```
ps.printfile("filename.eps")
```

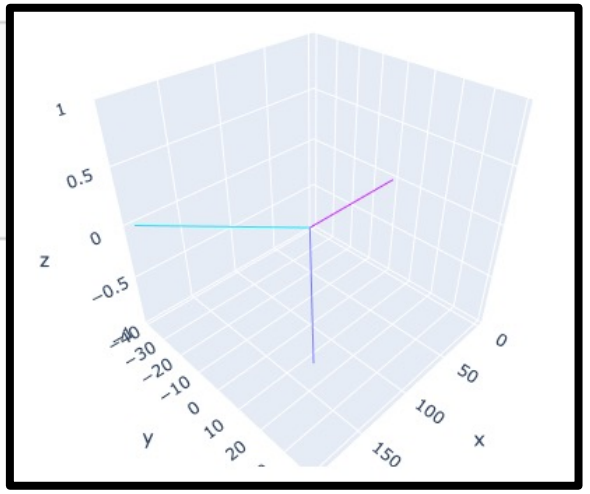
Viewing voltage, sodium, etc…

- Suppose we make the voltage (‘v’) nonuniform which we can do via:

```
my_cell.main.v = 50
my_cell.dend1.v = 0
my_cell.dend2.v = -65
```

- We can create a PlotShape that color-codes the sections by voltage:

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



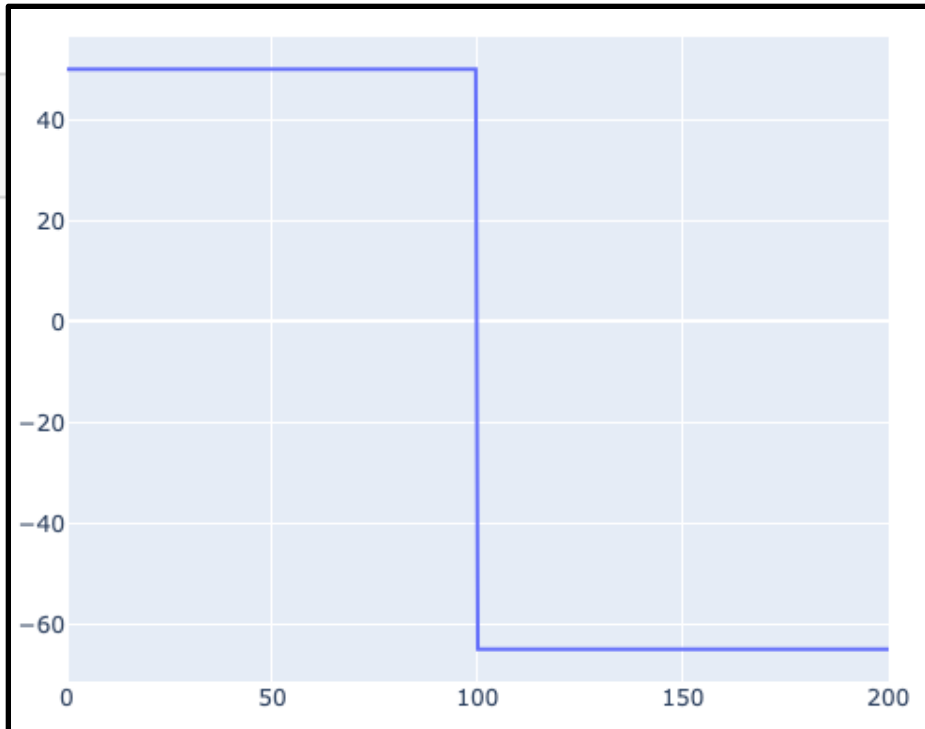
Viewing voltage, sodium, etc…

- After increasing the spatial resolution:

```
for sec in my_cell.all: sec.nseg = 101
```

- We can plot the voltage as a function of distance from `main(0)` to `dend2(1)`:

```
rvp = h.RangeVarPlot('v', my_cell.main(0), my_cell.dend2(1))
rvp.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.

Distributed mechanisms

- Insert a distributed mechanism (e.g. from a mod file) into a section or list of sections with `.insert`:

```
h.hh.insert(apical)
```

```
h.hh.insert([apical, soma, basal])
```

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

- Mechanisms may also be inserted one-at-a-time into a single section via e.g.

```
apical.insert(h.hh)
```

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`

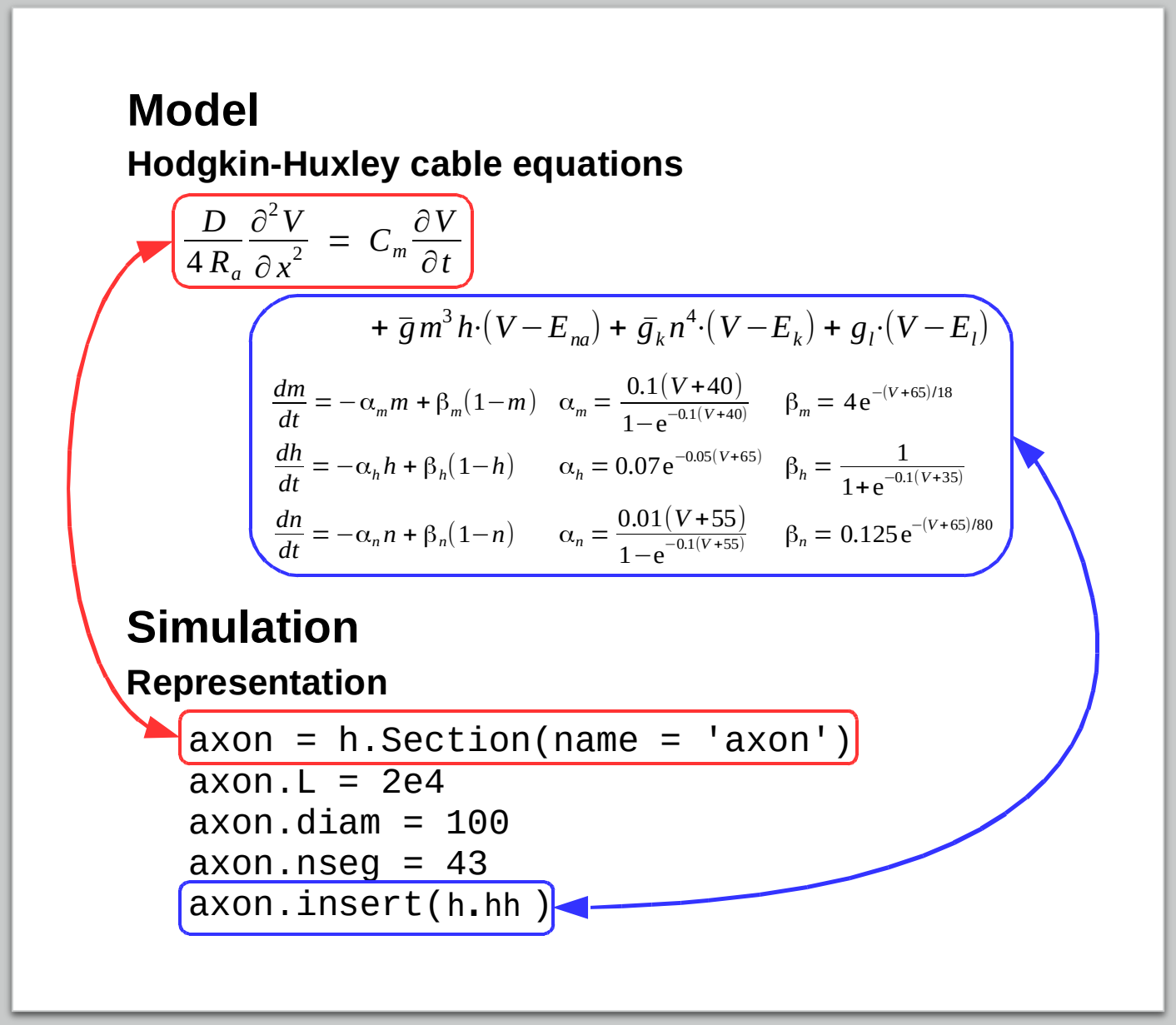


Illustration adapted from one by Ted Carnevale.

Defining ion channels, synapses, etc

tinyurl.com/hhmodfile

tinyurl.com/expsyn

```
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
```

Compile mod files on your local machine using:
`nrnivmodl`

Hundreds of mod files from published work are available at modeldb.yale.edu

Point processes

- To insert a point process, specify the segment when creating it, and *save the return value*. e.g.

```
pp = h.IClamp(soma(0.5))
```

- To find the segment containing a point process `pp`, use

```
seg = pp.get_segment()
```

- The section is then `seg.sec` and the normalized position is `seg.x`.

- *The point process is removed when no variables refer to it.*

Setting and reading parameters

- In NEURON, each section has normalized coordinates from 0 to 1.
- To read the value of a parameter defined by a range variable at a given normalized position, use: `sec(x).MECHANISM.VARNAME` e.g.

```
gkbar = apical(0.2).hh.gkbar
```

- Setting variables works the same way:

```
apical(0.2).hh.gkbar = 0.037
```

Setting and reading parameters

- To specify how many evenly-sized pieces (segments) a section should be broken into (each potentially with their own value for range variables), use `section.nseg`:

```
apical.nseg = 11
```

- To specify the temperature, use `h.celsius`:

```
h.celsius = 37
```

Setting and reading parameters

- Often you will want to read or write values on all segments in a section. To do this, use a `for` loop over the Section:

```
for seg in apical:
    seg.hh.gkbar = 0.037
```

- The above is equivalent to `apical.gkbar_hh = 0.037`, however the first version allows setting values nonuniformly, e.g.

```
for sec in h.allsec():
    for seg in sec:
        seg.hh.gkbar = some_function(h.distance(seg, soma(0.5)))
```

h.allsec() is an iterable of all sections

- A list comprehension can be used to create a Python list of all the values of a given property in a segment:

```
apical_gkbars = [segment.hh.gkbar for segment in apical]
```

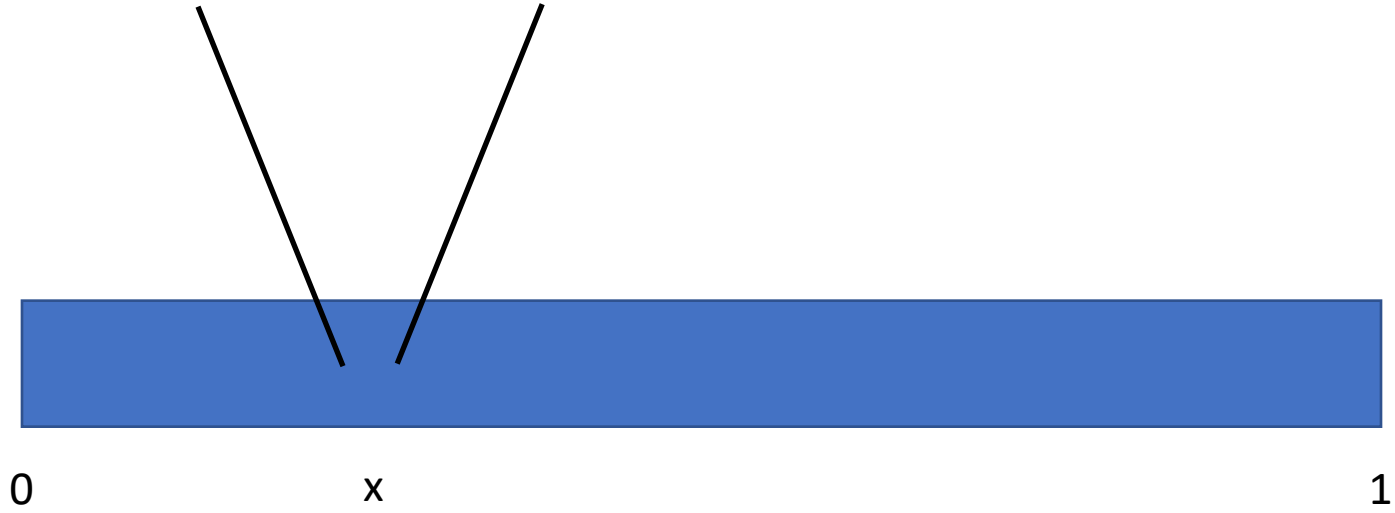
Note: looping over a Section only returns true Segments. If you want to include the voltage-only nodes at 0 and 1, iterate over, e.g. apical.allseg() instead. HOC's for (x,0) and for (x) are equivalent to looping over a section and looping over allseg, respectively.

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.

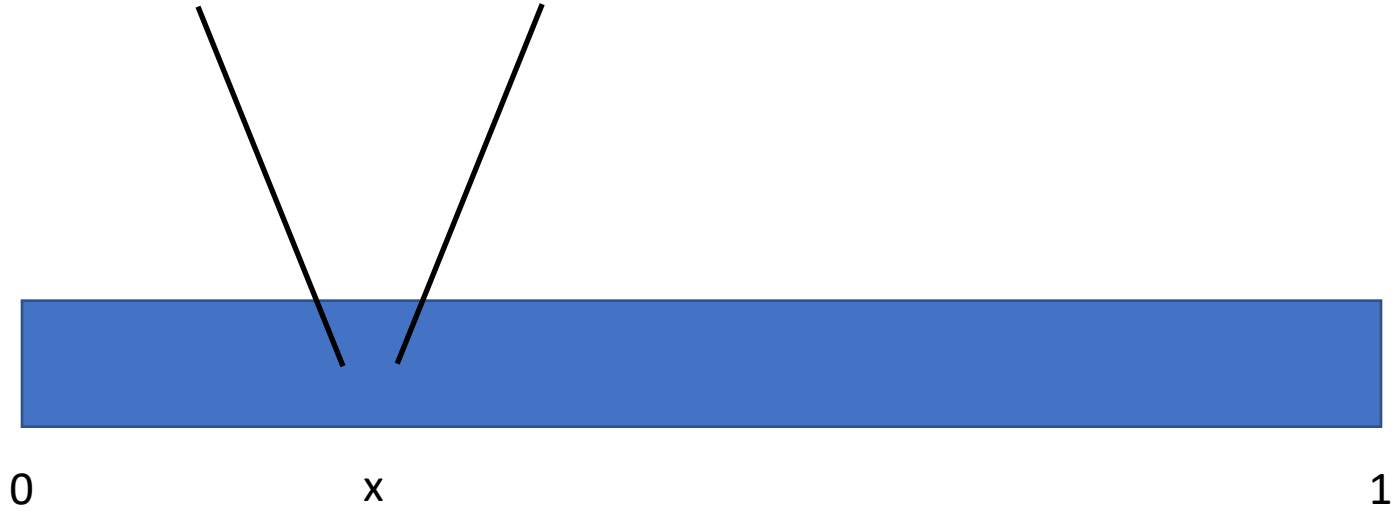



```
v = h.Vector().record(axon(x)._ref_v)
t = h.Vector().record(h._ref_t)
```

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)
```

Stimulating a model

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

Running simulations: the basics

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)
```

Running simulations: the basics

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)
```

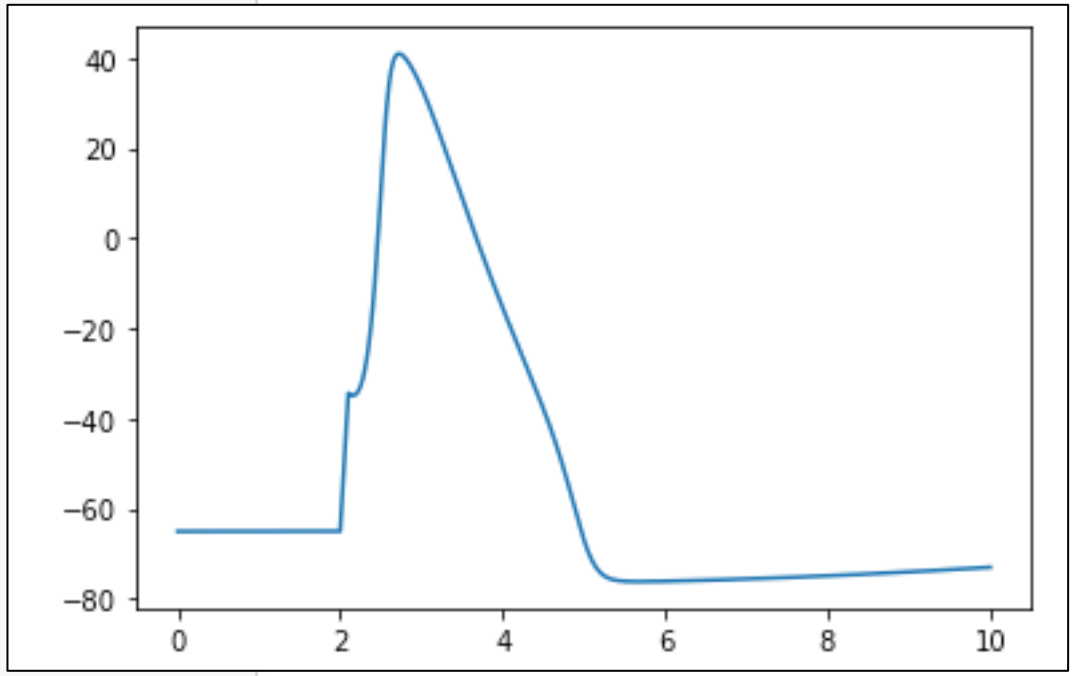
Advance one timestep:

```
h.fadvance()
```

Example: Hodgkin-Huxley

Note: Here we trigger the action potential by injecting a current. We could alternatively include a model of a synapse and trigger the synapse using an `h.NetStim`. See the documentation for more information.

```
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 * µm
h.hh.insert(soma)

ic = h.IClamp(soma(0.5))
ic.delay = 2 * ms
ic.dur = 0.1 * ms
ic.amp = 1

t = h.Vector().record(h._ref_t)
v = h.Vector().record(soma(0.5)._ref_v)

h.finitialize(-65 * mV)
h.continuerun(10 * ms)

plt.plot(t, v)
plt.show()
```

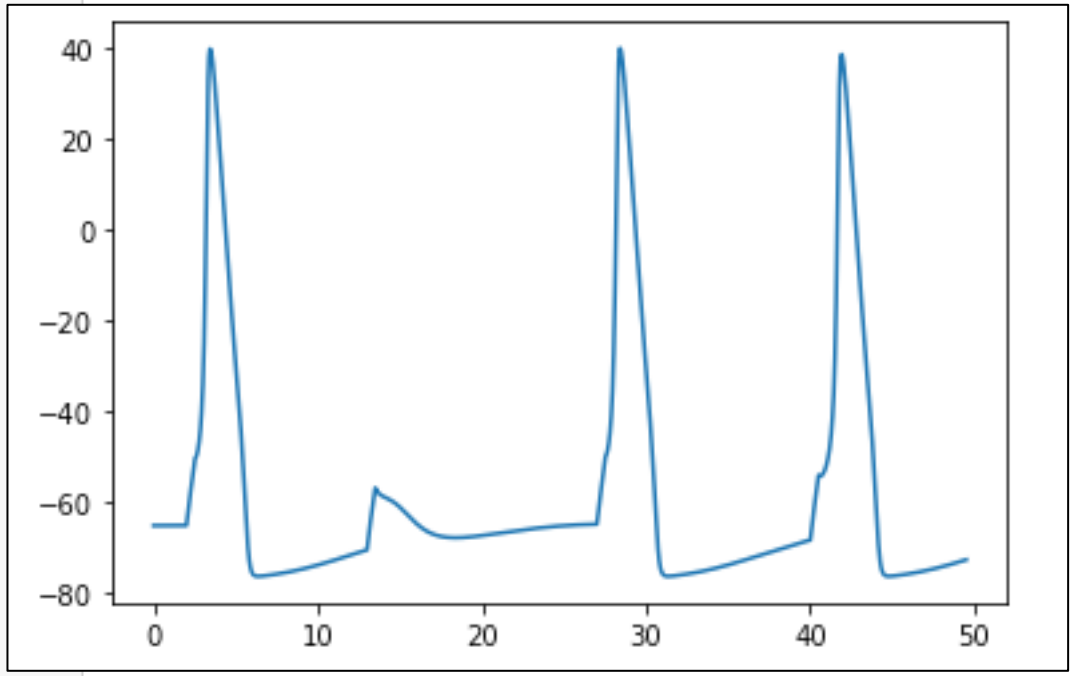


Example: spike detection

Many inputs

Recording spikes

```
from neuron import h
from neuron.units import ms, mV, µm
import matplotlib.pyplot as plt
h.load_file("stdrun.hoc")

axon = h.Section(name='axon')
h.hh.insert(axon)

iclamps = []
for input_time in [2 * ms, 13 * ms, 27 * ms, 40 * ms]:
    ic = h.IClamp(axon(0.5))
    ic.delay = input_time
    ic.dur = 0.5 * ms
    ic.amp = 50
    iclamps.append(ic)

t = h.Vector().record(h._ref_t)
v = h.Vector().record(axon(0.5)._ref_v)
nc = h.NetCon(axon(0.5)._ref_v, None, sec=axon)
spike_times = h.Vector()
nc.record(spike_times)

h.finitialize(-65 * mV)
h.continuerun(49.5 * ms)

print("spike times:", list(spike_times))
plt.plot(t, v)
plt.show()
```




```
spike times: [3.225000000100012, 28.20000000009893, 41.70000000010092]
```

Networks of neurons

- Suppose we have the simple model:

```
from neuron import h
from neuron.units import ms, mV

class Cell:
    def __init__(self):
        self.soma = h.Section(name="soma", cell=self)
        self.all = self.soma.wholetree()
        h.hh.insert(self.all)
```

- and two cells:

```
neuron1 = Cell()
neuron2 = Cell()
```

Networks of neurons

- If the first cell has a sufficient current clamp injection, we know that it will fire, but how can we get that to send a signal to another cell?
- We do this with a synapse.
- On the post-synaptic side:

```
postsyn = h.ExpSyn(neuron2.soma(0.5))
postsyn.e = 0   # reversal potential
```

- On the pre-synaptic side, specify a source pointer, the corresponding post-synaptic side, the transmission delay, and synaptic weight:

```
syn = h.NetCon(neuron1.soma(0.5)._ref_v, postsyn, sec=neuron1.soma)
syn.delay = 1
syn.weight[0] = 5
```

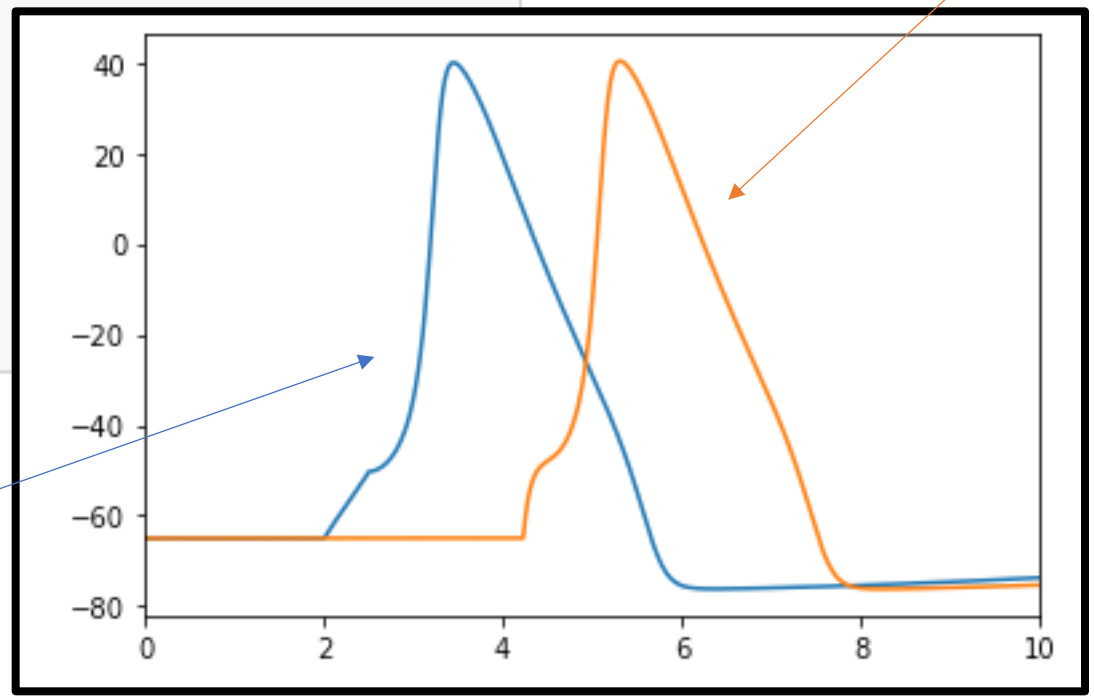
Networks of neurons

Record, run, and plot as normal:

```
t = h.Vector().record(h._ref_t)
v1 = h.Vector().record(neuron1.soma(0.5)._ref_v)
v2 = h.Vector().record(neuron2.soma(0.5)._ref_v)

h.finitialize(-65 * mV)
h.continuerun(10 * ms)

plt.plot(t, v1, t, v2)
plt.xlim((0, 10))
plt.show()
```

due to the synapse

due to the iclamp
(code not shown)



Storing and loading data with pandas

- Saving as CSV with pandas:

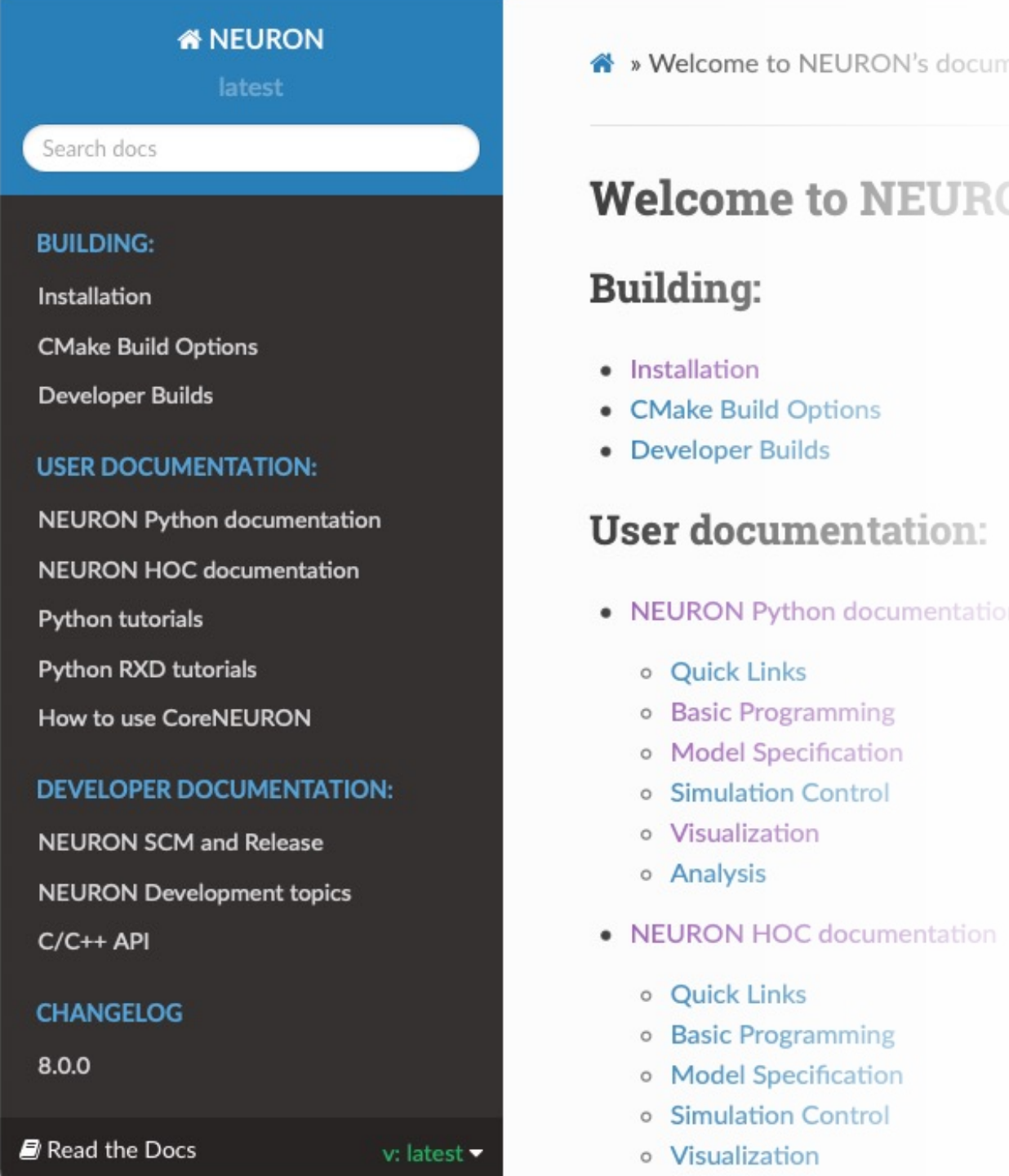
t and v are `h.Vector` instances

```
import pandas as pd
pd.DataFrame({"t": t, "v": v}).to_csv("data.csv", index=False)
```

- Loading from CSV with pandas:

```
import pandas as pd
data = pd.read_csv("data.csv")
t = h.Vector(data["t"])
v = h.Vector(data["v"])
```

```
t,v
0.0,-65.0
0.025,-64.99925452909274
0.05,-64.9985207095132
0.075,-64.99779768226396
0.0999999999999999,-64.99708468737194
0.1249999999999999,-64.9963810528078
0.15,-64.99568618464123
```



NEURON Resources

Unified documentation

- tinyurl.com/neuron-docs

Forum

- tinyurl.com/neuron-forum

NEURON models on ModelDB

- tinyurl.com/neuron-models

CNS 2020 Tutorial

- tinyurl.com/neuron-cns2020