Using NEURON to model cells Tutorial

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Introduction

The **NEURON Simulation Environment** is designed for modeling individual neurons and networks of neurons.

It is particularly well-suited to explore problems which are closely linked to experimental data.

NEURON was build and is maintained by Ted Carnevale and Michael Hines, lately the Blue Brain Project is becoming heavily involved with the development of the software

Neuron is written in C & C++, the interface with the simulator is with HOC, but a Python wrapper was build and now commonly used instead of HOC (NEURON as a python package). In addition User-defined mechanisms such as voltage- and ligand-gated ion channels are used in order to expand NEURON (NMODL files, need to be compiled).

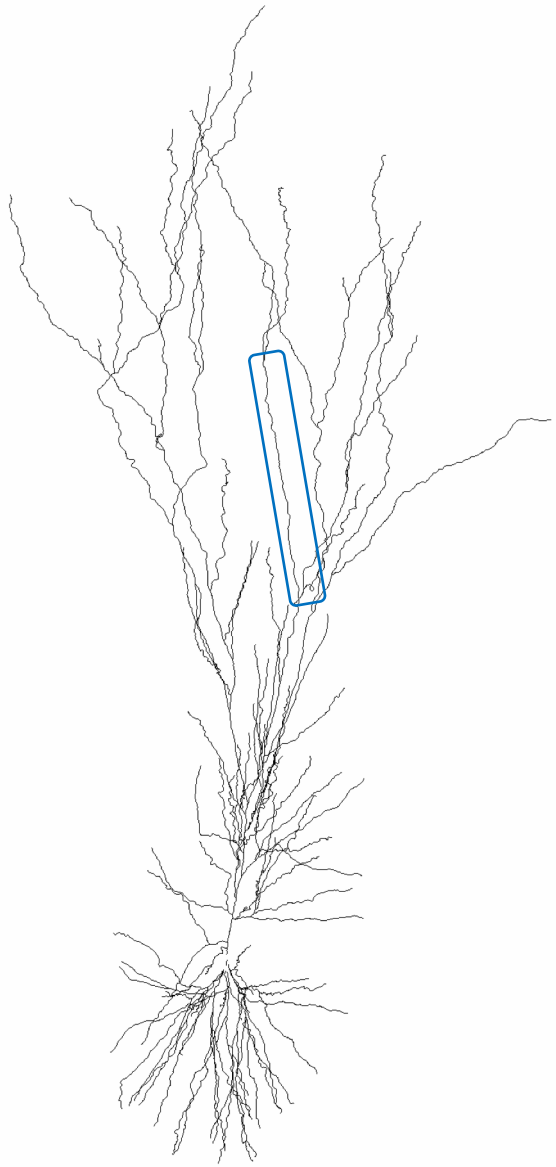
In this presentation we will show the following examples:

- Single compartment model
- Ball and Stick model and the replication of a published result (Gidon et al.)
- Multicompartmental L5 Pyramidal cell and two published results (Hay et al., Doron et al.)

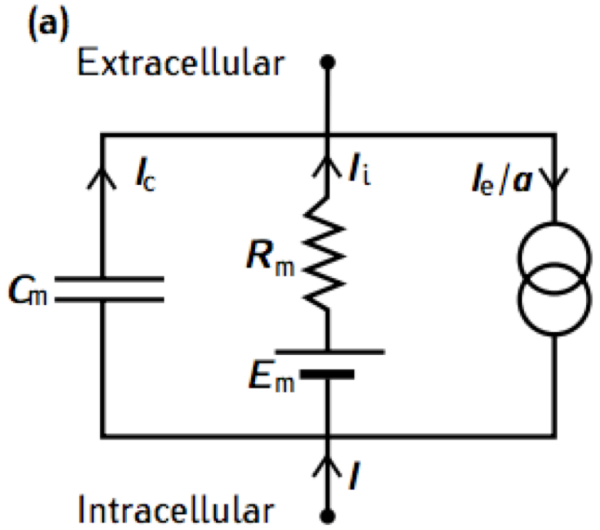
Introduction

Basic concepts of Neuron models:

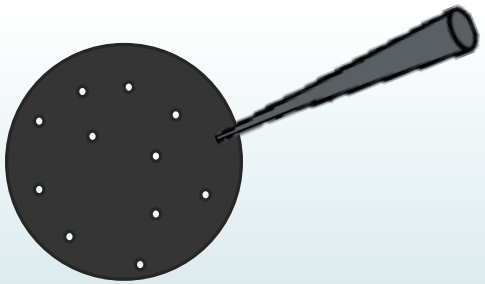
- **Model** - a Neuron object, it can have soma, basal dendrites (dend) and apical dendrite (apic).
- **Section** - more of a morphological definition, a section is usually a dendrite between 2 bifurcation points.
- **Segment** - one RC circuit that resemble (approximate) the computation in a piece of membrane.
- **Clamps** - an object that represent an experimental electrode.
- **Synapses** - object that resemble a single synapse (we will see it later, and how it's activated in the simulation).
- **Point Process** - a more general idea, it's an object that seats on the segment (RC circuit), and simulate a channel or synapse.



Single compartment neuron - single RC circuit



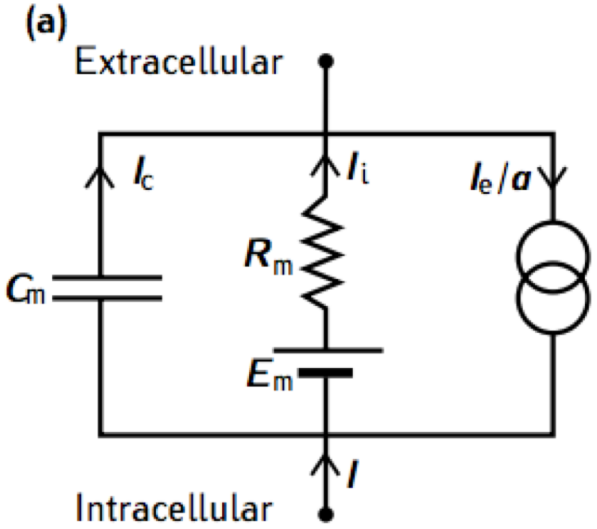

```
from neuron import h, gui
# create model
Soma = h.Section(name="soma")
soma.L = 10  # length µm
soma.diam = 10  # diameter µm
soma.insert('pas'). # add passive properties
soma.g_pas = 1/10000  # set the specific membrane
                        resistance to 10000 ohm*cm^2
```



```
# current current clamp
stim = h.IClamp(soma(0.5))
stim.delay = 20. # start of the current injection (ms)
stim.dur   = 100  # duration (ms)
stim.amp   = 0.01  # amplitude (nA)
```

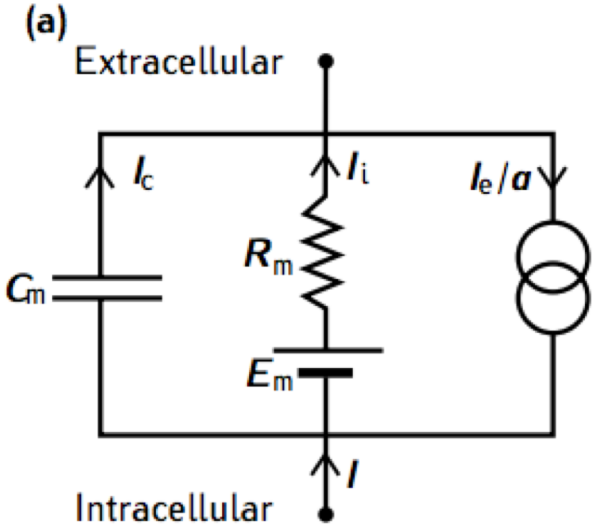
0_soma_passive.ipynb

Single compartment neuron - recording



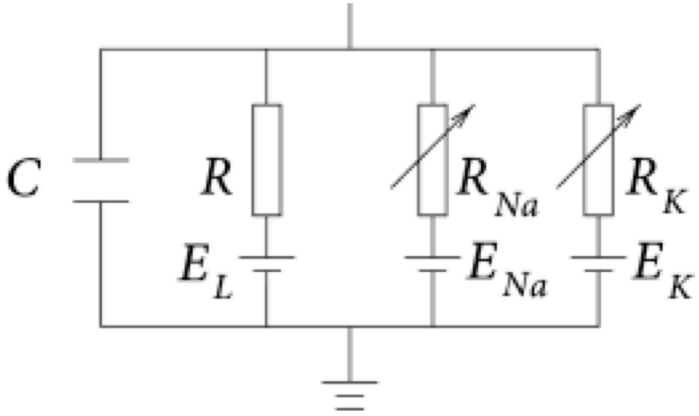

```
# record injected current soma voltage (and time)
soma_v = h.Vector()
soma_v.record(soma(0.5)._ref_v)
stim_current = h.Vector()
stim_current.record(stim._ref_i)
t = h.Vector()
t.record(h._ref_t)


# run simulation
h.tstop = 220  # simulation time (ms)
h.dt = 0.025.
h.v_init = -70. # initial voltage (mV)
h.run()
```

Single compartment neuron - synapse




```
# add a synapse
synapse = h.Exp2Syn(soma(0.5))
synapse.tau1 = 0.3  # rise time constant
synapse.tau2 = 1.8  # decay time constant
Stim = h.NetStim()
stim.number = 1
stim.noise = 0  # no noise
stim.interval = 1
net_con = h.NetCon(stim, synapse)
net_con.weight[0]= 0.0004  # the maximal conductance
                           of the synapse
```

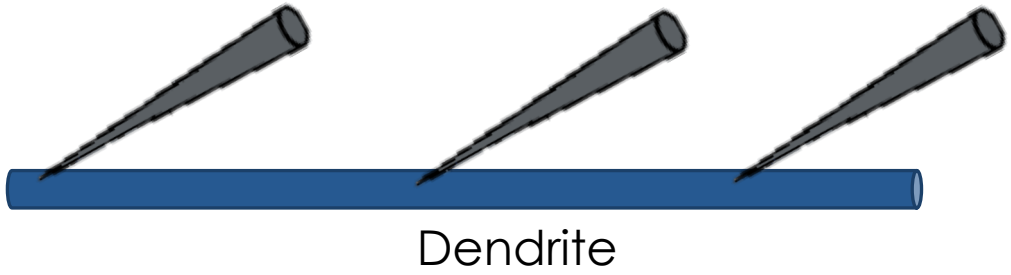
Single compartment neuron – active conductances

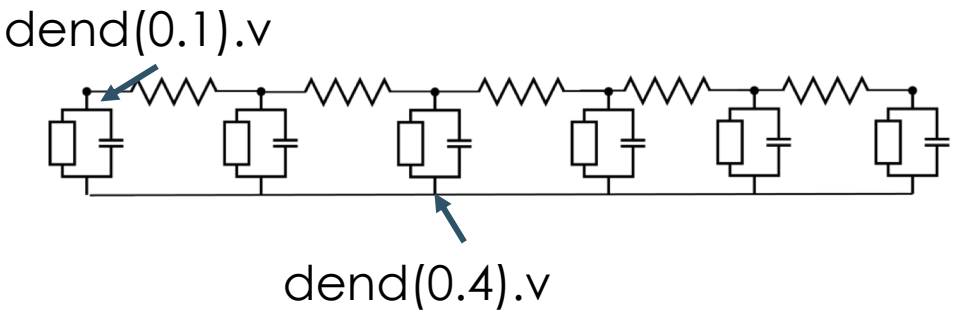


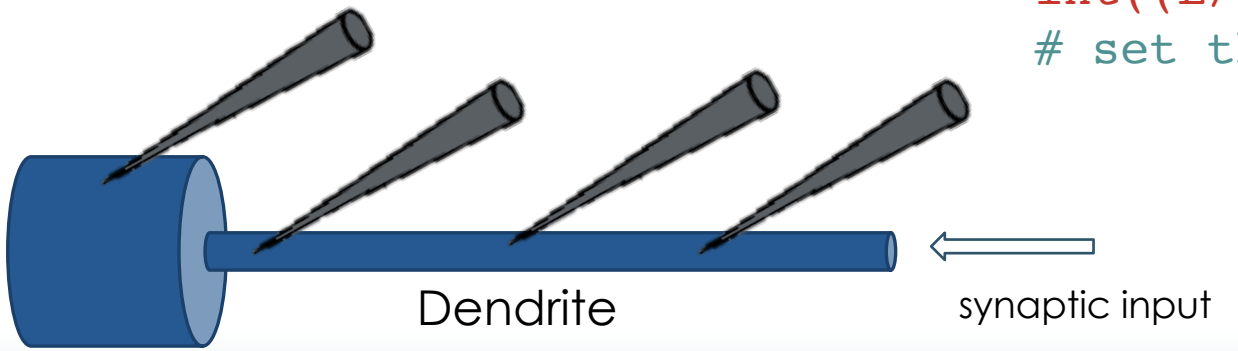

```
from neuron import h, gui
# create model
Soma = h.Section(name="soma")
soma.L = 10  # length µm
soma.diam = 10  # diameter µm
soma.insert("pas"). # add passive properties
soma.g_pas = 1/10000  # set the specific membrane
                        resistance to 10000 ohm*cm^2
soma.insert(”kv")  # add potassium channel
                     (from a mod file)
soma.gbar_kv = 2000 # set the potassium conductance
soma.insert(”na") # add sodium channel
                    (from a mod file)
soma.gbar_na = 8000 # set the sodium conductance
h.celsius = 30. # set temperature
```

1_soma_active.ipynb

Moving towards the cable model





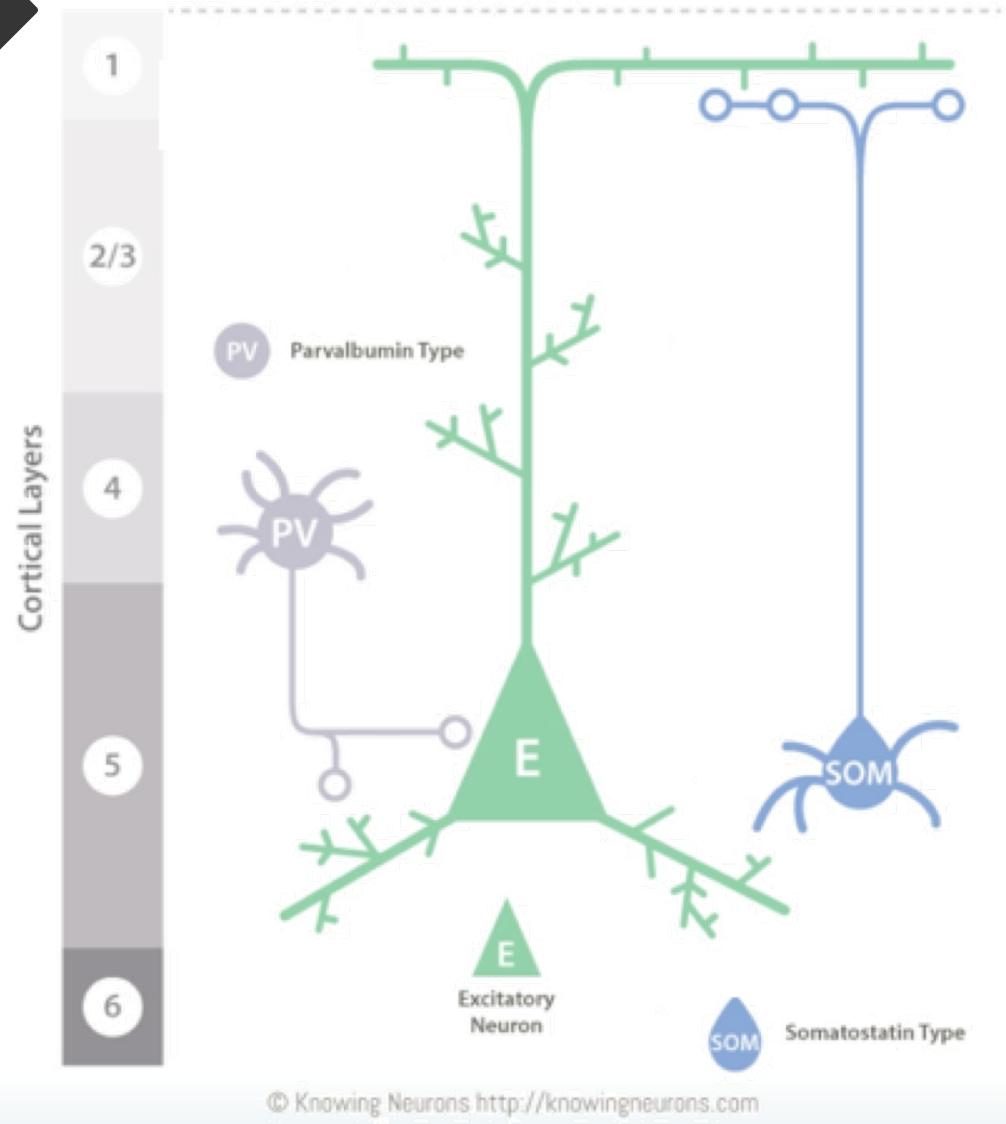


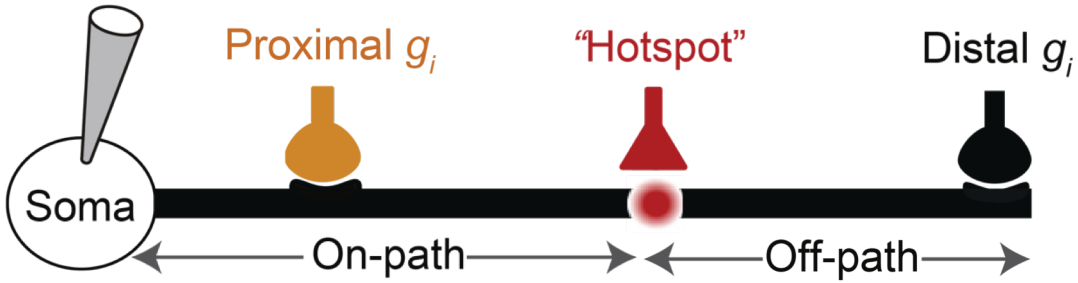

```
# create dendrite
dend = h.Section(name="dend")
dend.L = 500  # um
dend.diam = 1  # um
dend.Ra = 100  # ohm*cm
dend.insert("pas")
dend.g_pas = 1/10000
dend.connect(soma, 1, 0). # connect the end of
The dendrite to the beginning of the soma
h"forall { nseg =
int((L/(0.1*lambda_f(100))+0.9)/2)*2 + 1  }")
# set the number of segments
```

2_soma_dend_step_current.ipynb
3_soma_dend_synapse.ipynb

Note: d_lambda rule – NEURON book p50

Inhibition location

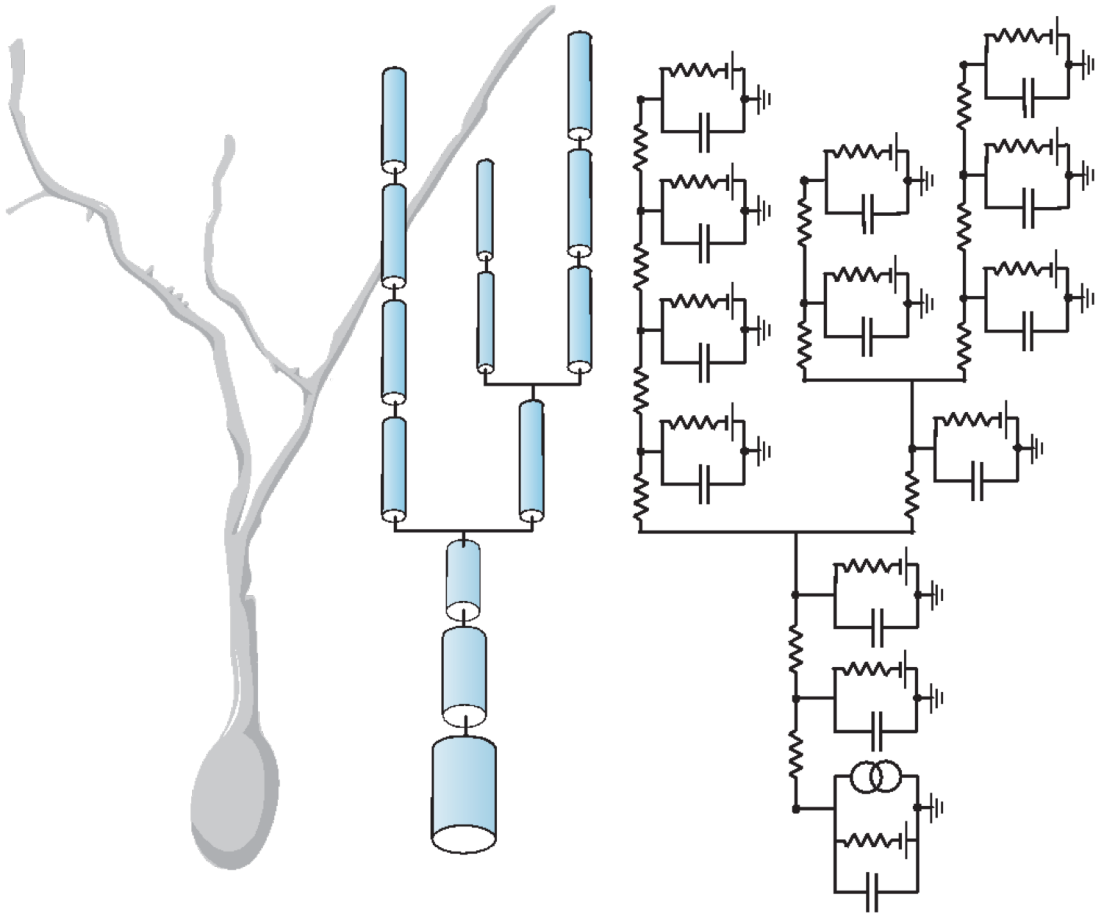


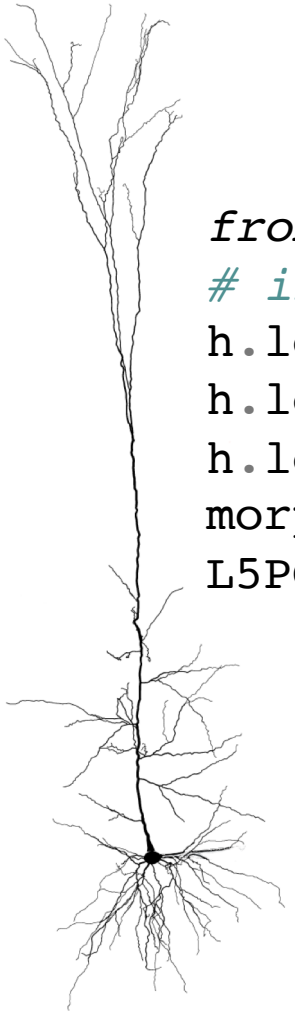


4_inhibition_location_Gidon_et_al.ipynb

"Principles Governing the Operationof Synaptic Inhibition in Dendrite" Albert Gidon, Idan Segev. Neuron, 2012

Layer 5b Pyramidal Cell

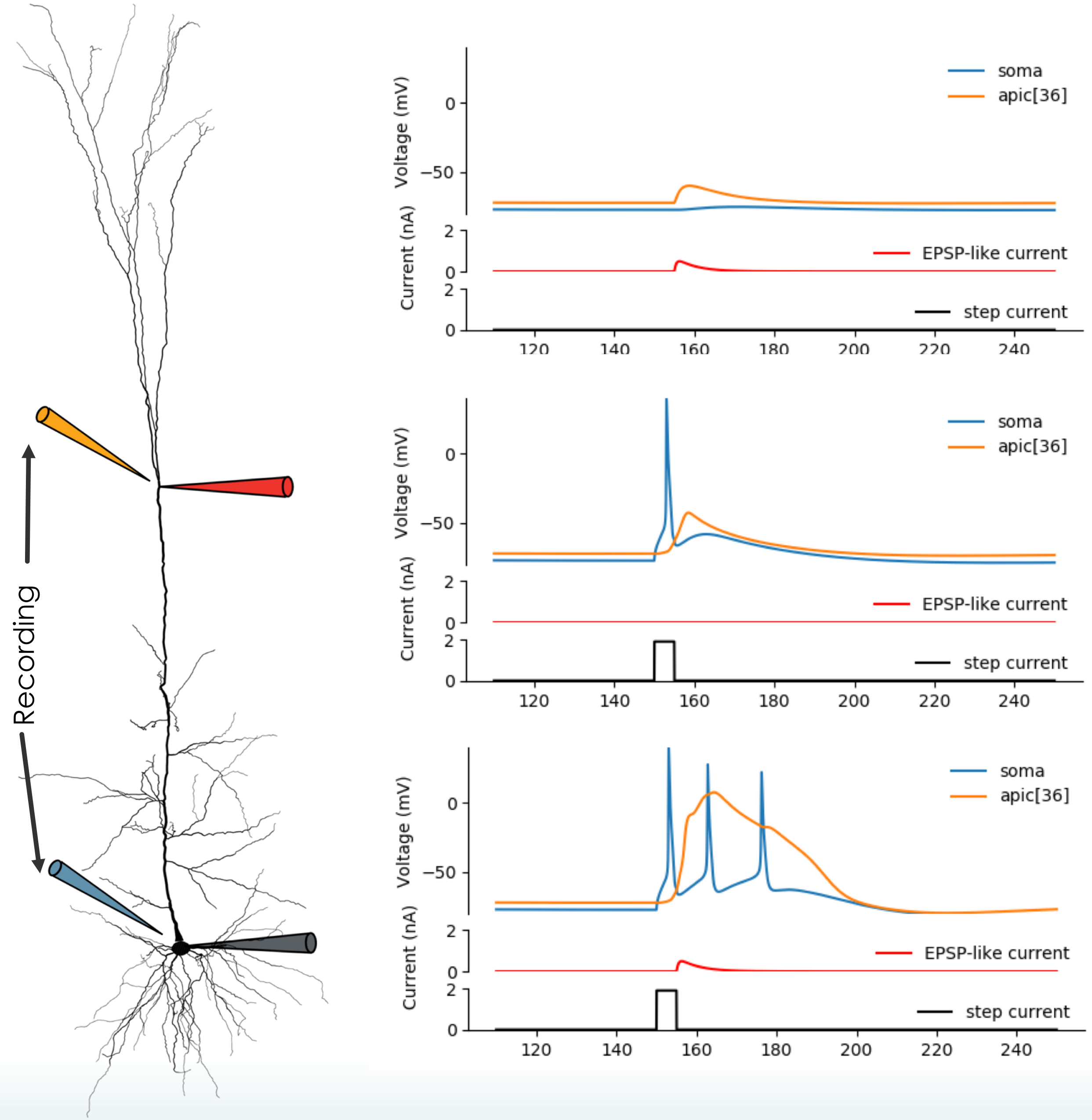




```
from neuron import h, gui
# instantiating cell
h.load_file("import3d.hoc")
h.load_file("models/L5PCbiophys3.hoc")
h.load_file("models/L5PCtemplate.hoc")
morph_fname = "morphologies/cell1.asc"
L5PC = h.L5PCtemplate(morph_fname )
```

6_L5_PC_Hay_et_al.ipynb

"Models of Neocortical Layer 5b Pyramidal Cells Capturing a Wide Range of Dendritic and Perisomatic Active Properties", Etay Hay , Sean Hill, Felix Schürmann, Henry Markram, Idan Segev. PLOS Computational Biology, 2011




```
# Only EPSP-like current
   syn.imax = 0.5
   stim.amp = 0
   h.run();
   plot_result(...)
```

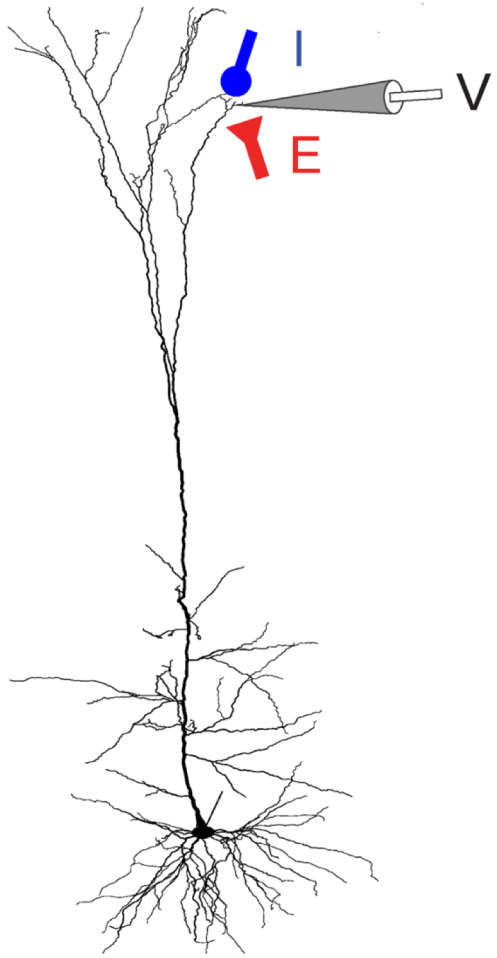
```
# Only small step current
   syn.imax = 0
   stim.amp = 1.9
   h.run();
   plot_result(...)
```

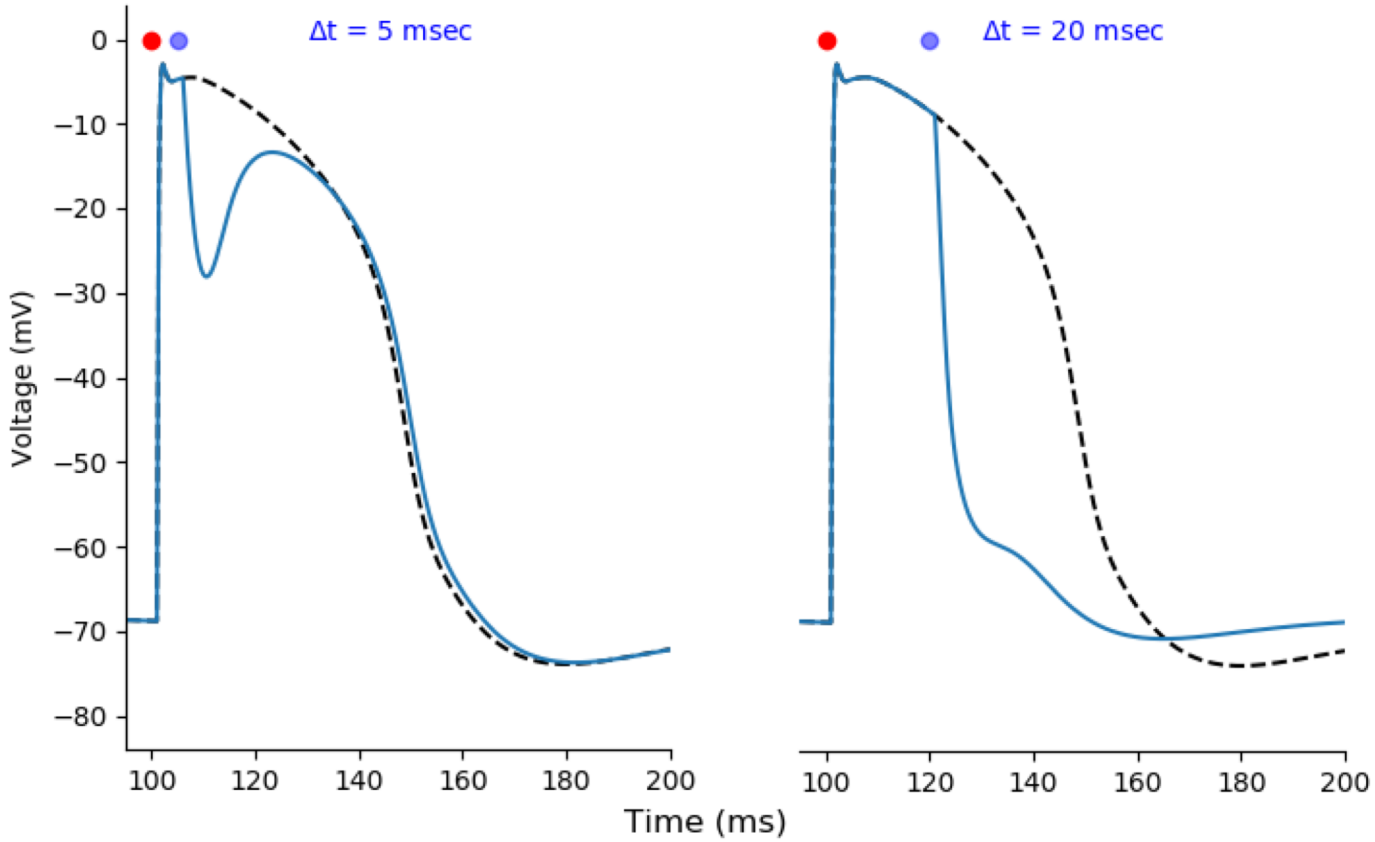
```
# both currents
   syn.imax = 0.5
   stim.amp = 1.9
   h.run()
   plot_result(...);
```

7_calcium_spike_Hay_et_al.ipynb

"Models of Neocortical Layer 5b Pyramidal Cells Capturing a Wide Range of Dendritic and Perisomatic Active Properties", Etay Hay , Sean Hill, Felix Schürmann, Henry Markram, Idan Segev. PLOS Computational Biology, 2011

Timed inhibition





8_timed_inhibition_Doron_et_al.ipynb

"Timed Synaptic Inhibition Shapes NMDA Spikes, Influencing Local Dendritic Processing and Global I/O Properties of Cortical Neurons" Michael Doron, Giuseppe Chindemi, Eilif Muller, Henry Markram, Idan Segev. Cell Reports, 2017