

# A (brief) introduction to NEURON

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*(Many thanks to David Sterratt (Uni of Edinburgh) for allowing the use of his tutorials and images)*

# Why use NEURON ( 5-10 mins)

*(From the NEURON website, my bold type):*

- is a flexible and powerful **simulator of neurons and networks**
- has important advantages over general-purpose simulators helps users **focus on important biological issues** rather than purely computational concerns
- has a convenient user interface
- has a **user-extendable** library of biophysical mechanisms
- has many enhancements for **efficient network modeling**
- offers customizable initialization and simulation flow control
- is widely used in neuroscience research by experimentalists and theoreticians
- is well-documented and **actively supported**
- is **free, open source**, and runs on (almost) everything

# Use-cases

- Modelling of multicompartmental neurons in which membrane voltage is calculated from ion flows across the membranes
- Connections between cells through synapses (chemical & electrical)
- If you are interested in large networks of 'simple', single compartment neurons, there are other options.

# Use-cases

- For a single compartment cell with simple HH dynamics, you can probably write your own simulation using the ODE solvers in provided matlab/python.
- As your models develop more complexity:
  - Current dependancies e.g. K channels dependant on intracellular Ca
  - Incooperation of the cable equation for multicompartmental neurons
  - Connections via synapses (delays)
- You may find that you are reimplementing lots of mathematical solving, which has been already been done efficiently in NEURON.
- MOD files provide a standard for exchanging channel descriptions (e.g. modeldb)
- NEURON is highly parallelisable (e.g. BBP) for large networks
- There is a python interface

## What do i need to use it?

- It runs on most operating systems (Windows/Linux/Mac). On the NEURON website: - Windows installer - Mac package - Linux .deb, .rpm package
- Eilif Muller has precompiled binaries including Python support  
<http://neuralensemble.org/people/eilifmuller/software.html>

# Resources

- Active questions board
- ModelDB
- The NEURON Book

## **Basics of NEURON (20-25 mins)**



# Overview

- NEURON is complex (I will cover a lot of material in the next slides, don't worry if you don't remember all the details - its the concepts that are important)
- NEURON is old (& built on even older software)
- (These are positives and negatives)

## 2 Parts: HOC and NMODL files

- Two main types of language:
  - *Interpreted* languages (Python/matlab) are interactive, but slow
  - *Compiled* languages (Fortran/C/C++/...) are fast, but not interactive
- NEURON uses both:
  - **HOC** - which controls the 'structure' of the simulation
  - **NMODL** - a compiled language for defining the dynamics of channels/synapses mathematically (e.g. Hodgkin-Huxley type channels). We will not cover NMODL in this tutorial.

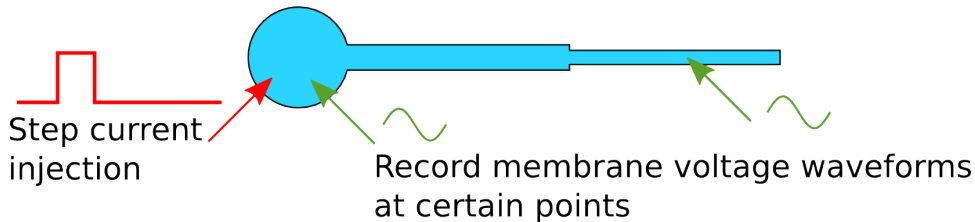
# HOC Interpreter

- HOC is an interactive interpreter which controls the *structure* of the simulation:
  - creating morphologies
  - choosing which channels to apply and where, changing certain parameters (channel densities)
  - connecting cells together with synapses
  - creating stimuli: current clamps, voltage clamps
  - defining what you want to record: voltages, internal states
  - setting simulation parameters: stimulation time-steps,
  - running the simulation

## Example simulation: Soma + Axon, HH Channels, with current injection

- We will walk through the steps required to simulate a neuron, which has a soma and an axon, stimulate it with a current clamp, and visualise the somatic membrane voltage.

Neuron with Soma & Axon  
(Hodgkin-Huxley channels)



# HOC - Graphical User Interface

NEURON has a graphical user interface:

```
$ nrngui  
oc>
```

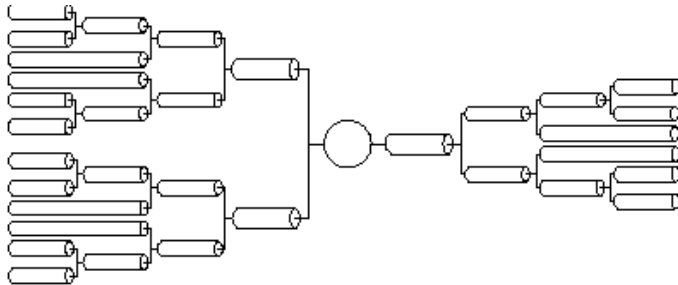


Or NEURON can be used entirely from the commandline and within scripts:

```
$ nrnoc  
oc>
```

# Morphologies I (Overview)

- Neuron morphologies are represented as a tree of *unbranched cylinders* called **Sections** which describe the *gross* morphology of the neuron.
- e.g.



## Morphology II (Building & Connecting Sections)

- **Sections** are created with the *create* <section-name> command
- **Length** and **diameter** of the sections are set as properties for each section.

```
// Create 3 Sections:
oc> create soma
oc> create axon_proximal
oc> create axon_distal

// Setup the sizes of each Section:
oc> soma L = 12.3
oc> soma diam = 12.3

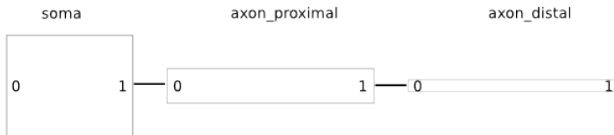
oc> axon_proximal diam = 1.0
oc> axon_proximal L = 50

oc> axon_distal diam = 0.5
oc> axon_distal L = 20
```

## Morphology II (Building & Connecting Sections)

- **Sections** are connected together with the *connect* function.
- '0' defines one end of the **Section**, '1' defines the other.

```
// Setup the connections:  
oc> connect soma(1.0), axon_proximal(0.0)  
oc> connect axon_proximal(1.0), axon_distal(0.0)
```





## Morphologies III (Segments)

- To solve simulations for better spatial accuracy, **Sections** can be subdivided into **segments**.
- Each **segment** has its own voltage and state variables
- (Hines & Carnevale recommend using an odd number of **segments**)

```
oc> axon_proximal nseg = 11  
oc> axon_distal nseg = 3
```

## HOC: *psection()*

```
oc>axon_proximal psection()  
axon_proximal { nseg=11  L=50  Ra=35.4  
/*location 0 attached to cell 1*/  
/* First segment only */  
insert capacitance { cm=1}  
insert morphology { diam=1}  
}
```

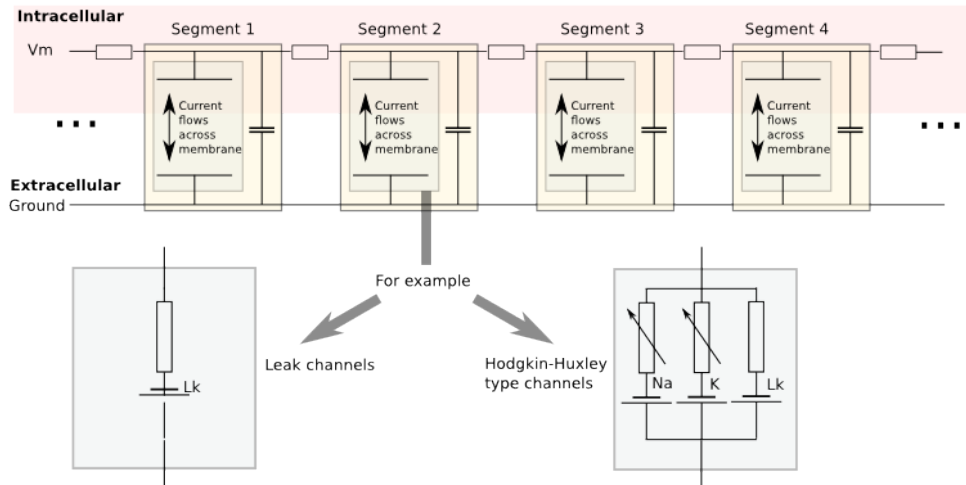
This can be used with *foreach*:

```
oc> forall psection()  
// <shows 'psection()' for every section>....
```

# Channels I (Overview)

- Neurons are interesting because of their active membrane channels
- Channels define the currents flowing across the membrane (e.g. sodium, potassium, leak)
- In NEURON:
  - it comes with some predefined channel definitions (*pas*, *hh*)
  - it is possible to define your own using NMODL files (not covered here)
- Normally we only need to define the currents flowing accross the membrane - NEURON automatically handles membrane capacitance and axial resistances

# Channels II (Segments)



## Channels III (Using channels)

- Channels are *inserted* into each Section
- Channels can have parameters that can be changed in HOC, (e.g. conduction density)
- E.g.

```
// Insert the channel into the soma Section
oc> soma insert hh

// View and change some properties:
oc> soma.gnabar_hh
    0.12
oc> soma.gnabar_hh = 0.2
// (in S/cm2)
```

## Channels IV (Summary):

```
oc> soma psection()  
soma { nseg=1  L=12.3  Ra=35.4  
      axon_proximal connect soma (1), 0  
      /* First segment only */  
      insert morphology { diam=12.3}  
      insert capacitance { cm=1}  
      insert hh { gnabar_hh=0.2 gkbar_hh=0.036 gl_hh=0.0003 el_hh=-54.3}  
      insert na_ion { ena=50}  
      insert k_ion { ek=-77}  
}
```

## Stimuli (Overview)

- NEURON is very flexible in the stimulation protocols that can be used
- Most commonly used are:
  - Current Clamp (*IClamp*)
  - Voltage Clamp (*SEClamp*, *VClamp*)

## Stimuli (Current Clamp)

- For example, a current clamp called 'stim' at the centre of the soma:

```
oc> objref stim
oc> soma stim = new IClamp(0.5)
oc> stim.del = 100
oc> stim.dur = 100
oc> stim.amp = 0.1
```

*(NEURON documentation gives details of properties of specific objects)*

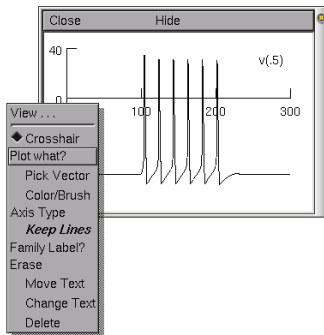


# Running the simulation

- NEURON simulations are run:
  - with the 'run()' command from *hoc*
  - clicking 'Init & Run' from the GUI
- By default, running the simulation will not plot anything....

# Plotting the results

- We want to plot the internal states of the simulation (e.g. membrane voltage, current flows, state variables)
- This is easiest done by using the NEURON GUI
- (It is also possible to save results to file using code)



# Exercises (45 mins)

- We will work through the tutorial from David Sterratt and Andrew Gillies.
- Section **A**: investigates a single compartment neuron containing HH channels, stimulated with a current clamp
- Section **B**: extending this to a multicompartmental neuron
- These can be found at: <http://www.anc.ed.ac.uk/school/neuron/>

**Wrap Up (10 mins)**

## Useful things to know about NEURON

- NEURON contains an 'adaptive-timestep' integrator, which can dramatically improve simulation time in some circumstances. This is enabled simply by adding `cvar.active(1)` before calling `run()`
- NEURON has a python interface. This allows you to use the hoc Interpreter from within Python, use objects and access stored data as numpy-arrays.  
**HOWEVER!** There are limitations on 'clearing-the-workspace'

## **'Competitors' to NEURON**

- GENESIS, MOOSE

## Other Tools in the ecosystem

- morphforge
- NeuroML & neuroConstruct
- NineML
- neuronvisio

# Any Questions

??



# Who am I

- I am not a NEURON guru
- 3rd year Ph.D student (4 years using NEURON for modelling work)
- Teaching-Assistant for Neural-Computation course at Edinburgh Uni
- One of the developers of NineML (incl. NEURON interface)
- Author of *morphforge* - a high-level interface to NEURON in python