Neuronal simulations in MOOSEGUI

Table of Contents

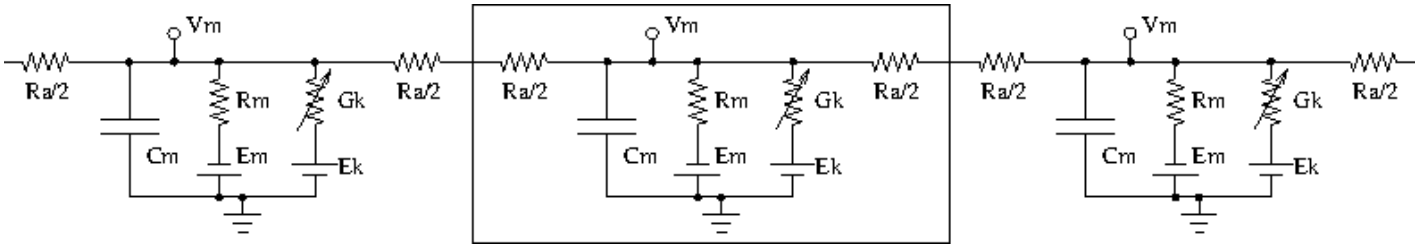
1 Introduction

Neuronal models in various formats can be loaded and simulated in the **MOOSE Graphical User Interface**. The GUI displays the neurons in 3D, and allows visual selection and editing of neuronal properties. Plotting and visualization of activity proceeds concurrently with the simulation. Support for creating and editing channels, morphology and networks is planned for the future.

2 Neuronal models

Neurons are modelled as equivalent electrical circuits. The morphology of a neuron can be broken into isopotential compartments connected by axial resistances Ra denoting the cytoplasmic resistance. In each compartment, the neuronal membrane is represented as a capacitance Cm with a shunt leak resistance Rm. Electrochemical gradient (due to ion pumps) across the leaky membrane causes a voltage drive Em, that hyperpolarizes the inside of the cell membrane compared to the outside.

Each voltage dependent ion channel, present on the membrane, is modelled as a voltage dependent conductance Gk with gating kinetics, in series with an electrochemical voltage drive (battery) Ek, across the membrane capacitance Cm, as in the figure below.



compartments in a neuron

Neurons fire action potentials / spikes (sharp rise and fall of membrane potential Vm) due to voltage dependent channels. These result in opening of excitatory / inhibitory synaptic channels (conductances with batteries, similar to voltage gated channels) on other connected neurons in the network.

MOOSE can handle large networks of detailed neurons, each with complicated channel dynamics. Further, MOOSE can integrate chemical signalling with electrical activity. Presently, creating and simulating these requires pyMOOSE scripting, but these will be incorporated into the GUI in the future.

To understand channel kinetics and neuronal action potentials, run the Squid Axon demo installed along with MOOSEGUI and consult its help/tutorial.

Read more about compartmental modelling in the first few chapters of the Book of Genesis.

Models can be defined in NeuroML, an XML format which is mostly supported across simulators. Channels, neuronal morphology (compartments), and networks can be specified using various levels of NeuroML, namely ChannelML, MorphML and NetworkML. Importing of cell models in the GENESIS .p format is supported for backwards compatibitility.

3 Neuronal simulations in MOOSEGUI

3.1 Quick start

- On first run, the MOOSEGUI creates moose/Demos directory in user's home folder. A few neuronal models are provided in directories inside moose/Demos/neuroml. For example, *File->Load* ~/moose/Demos/neuroml/CA1PyramidalCell/CA1.net.xml, which is a model of hippocampal CA1 pyramidal cell Migliore et al, 2005 (exported using neuroConstruct). A 3D rendering of the neuron appears in **GL Window** tab.
- Use click and drag to rotate, scroll wheel to zoom, and arrow keys to pan the 3D rendering.
- Click to select a compartment on the 3D model, say the fattest cylinder near the center which is the soma / cell body. You may need to zoom/pan a bit.
- Its **Properties** (which you can modify) will appear on the right pane.
- Further, in **Plot configuration** in the right pane, **Plot field** Vm will be selected by default. Click **New plot tab** to create a blank plot and **Add field** to assign Vm of this compartment to the plot.
- Run the model using **Run** button. By default, the model contains a current injection in the soma, which causes action potentials that decay into the dendrites.
- You can switch between plot tabs and colour-coded 3D vizualization of spiking in the **GL Window** tab.
- Manipulate and save plots using the icons at the bottom of the **Plot Window**.

User interface help is available at *Help->User Interface*. Here we delve into neuronal simulations.

3.2 Modelling details

MOOSEGUI uses SI units throughout.

Some salient properties of neuronal building blocks in MOOSE are described below. Variables that are updated at every simulation time step are are listed **dynamical**. Rest are parameters.

Compartment
When you select a compartment, you can view and edit its properties in the right pane. **Vm** and **Im** are plot-able.

Vm
dynamical membrane potential (across Cm) in Volts.
Cm
membrane capacitance in Farads.
Em
membrane leak potential in Volts due to the electrochemical gradient setup by ion pumps.
Im
dynamical current in Amperes across the membrane via leak resistance Rm.
inject
current in Amperes injected externally into the compartment.
initVm
initial Vm in Volts.
Rm
membrane leak resistance in Ohms due to leaky channels.
diameter
diameter of the compartment in metres.
length
length of the compartment in metres.

After selecting a compartment, you can click **See children** on the right pane to list its membrane channels, Ca pool, etc.

HHChannel
Hodgkin-Huxley channel with voltage dependent dynamical gates.

Gbar

peak channel conductance in Siemens.

Ek

reversal potential of the channel, due to electrochemical gradient of the ion(s) it allows.

Gk

dynamical conductance of the channel in Siemens. $Gk(t) = Gbar \times X(t)^{Xpower} \times Y(t)^{Ypower} \times Z(t)^{Zpower}$.

Ik

dynamical current through the channel into the neuron in Amperes. $Ik(t) = Gk(t) \times (Ek - Vm(t))$

X,Y,Z

dynamical gating variables (range 0 to 1) that may turn on or off as voltage increases with different time constants. $dX(t)/dt = X_{inf}/\tau - X(t)/\tau$. Here, X_{inf} and τ are typically sigmoidal/linear/linear-sigmoidal functions of membrane potential Vm, which are described in a ChannelML file and presently not editable from MOOSEGUI. Thus, a gate may open ($X_{inf}(Vm) \rightarrow 1$) or close ($X_{inf}(Vm) \rightarrow 0$) on increasing Vm, with time constant $\tau(Vm)$.

Xpower,Ypower,Zpower

powers to which gates are raised in the Gk(t) formula above.

HHChannel2D

The Hodgkin-Huxley channel2D can have the usual voltage dependent dynamical gates, and also gates that dependent on voltage and an ionic concentration, as for say Ca-dependent K conductance. It has the properties of HHChannel above, and a few more like Xindex as in the GENESIS tab2Dchannel reference.

CaConc

This is a pool of Ca ions in each compartment, in a shell volume under the cell membrane. The dynamical Ca concentration increases when Ca channels open, and decays back to resting with a specified time constant τ. Its concentration controls Ca-dependent K channels, etc.

Ca

dynamical Ca concentration in the pool in mMolar=mol/m^3. $d[Ca^{2+}]/dt = B \times I_{Ca} - [Ca^{2+}]/\tau$

CaBasal/Ca_base

Base Ca concentration to which the Ca decays

tau

time constant with which the Ca concentration decays to the base Ca level.

B

constant in the $[Ca^{2+}]$ equation above.

thick

thickness of the Ca shell within the cell membrane which is used to calculate B (see Chapter 19 of Book of GENESIS.)

3.3 Demos:

Cerebellar granule cell

File->Load ~/moose/Demos/neuroml/GranuleCell/GranuleCell.net.xml . This is a single compartment Cerebellar granule cell with a variety of channels http://www.tnb.ua.ac.be/models/network.shtml (exported from http://www.neuroconstruct.org). Click on its soma, and **See children** for its list of channels. Vary the Gbar of these channels to obtain regular firing, adapting and bursty behaviour (may need to increase tau of the Ca pool).

Purkinje cell

File->Load ~/moose/Demos/neuroml/PurkinjeCell/Purkinje.net.xml . This is a purely passive cell, but with extensive morphology [De Schutter, E. and Bower, J. M., 1994] (exported from http://www.neuroconstruct.org). The channel specifications are in an obsolete ChannelML format which MOOSE does not support.

Olfactory bulb subnetwork

File->Load ~/moose/Demos/neuroml/OlfactoryBulb/numgloms2_seed100.0_decimated.xml . This is a pruned and decimated version of a detailed network model of the Olfactory bulb [Gilra A. and Bhalla U., in preparation] without channels and synaptic connections. We hope to post the ChannelML specifications of the channels and synapses soon.

All channels cell

File->Load ~/moose/Demos/neuroml/allChannelsCell/allChannelsCell.net.xml . This is the Cerebellar granule cell as above, but with loads of channels from various cell types (exported from http://www.neuroconstruct.org). Play around with the channel properties to see what they do. You can also edit the ChannelML files in

~/moose/Demos/neuroml/allChannelsCell/cells$_{channels}$/ to experiment further.

NeuroML python scripts

In directory ~/moose/Demos/neuroml/GranuleCell, you can run 'python FvsI$_{Granule98}$.py' which plots firing rate vs injected current for the granule cell. Consult this python script to see how to read in a NeuroML model and to set up simulations. There are ample snippets in ~/moose/Demos/snippets too.

Author: This document: Aditya Gilra. MOOSE: Numerics: Upi Bhalla, Niraj Dudani; Python bindings: Subhasis Ray; GUI: H. Chaitanya, Harsha Rani, Subhasis Ray; NeuroML import: Aditya Gilra.

Date: 2012-10-01 22:24:14 IST