

NeuroML with PyMOOSE

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libNeuroML meeting
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History:

NeuroML import in MOOSE β 1.3

- Siji George (Upi lab)
- Uses libNeuroML v0.2:

<http://neuroml.svn.sourceforge.net/viewvc/neuroml/TestLibNeuroML/v0.2/libneuroml/>

- C++, libxml2
- moose/branches/moose-Beta-1.3.0/external/neuroML_src
- moose/branches/moose-Beta-1.3.0/neuroML_IO
- moose/branches/moose-Beta-1.3.0/DEMOS/NeuroML_Reader
 - Granule, Purkinje, CA1 (Ca pool, K_AHP, etc)

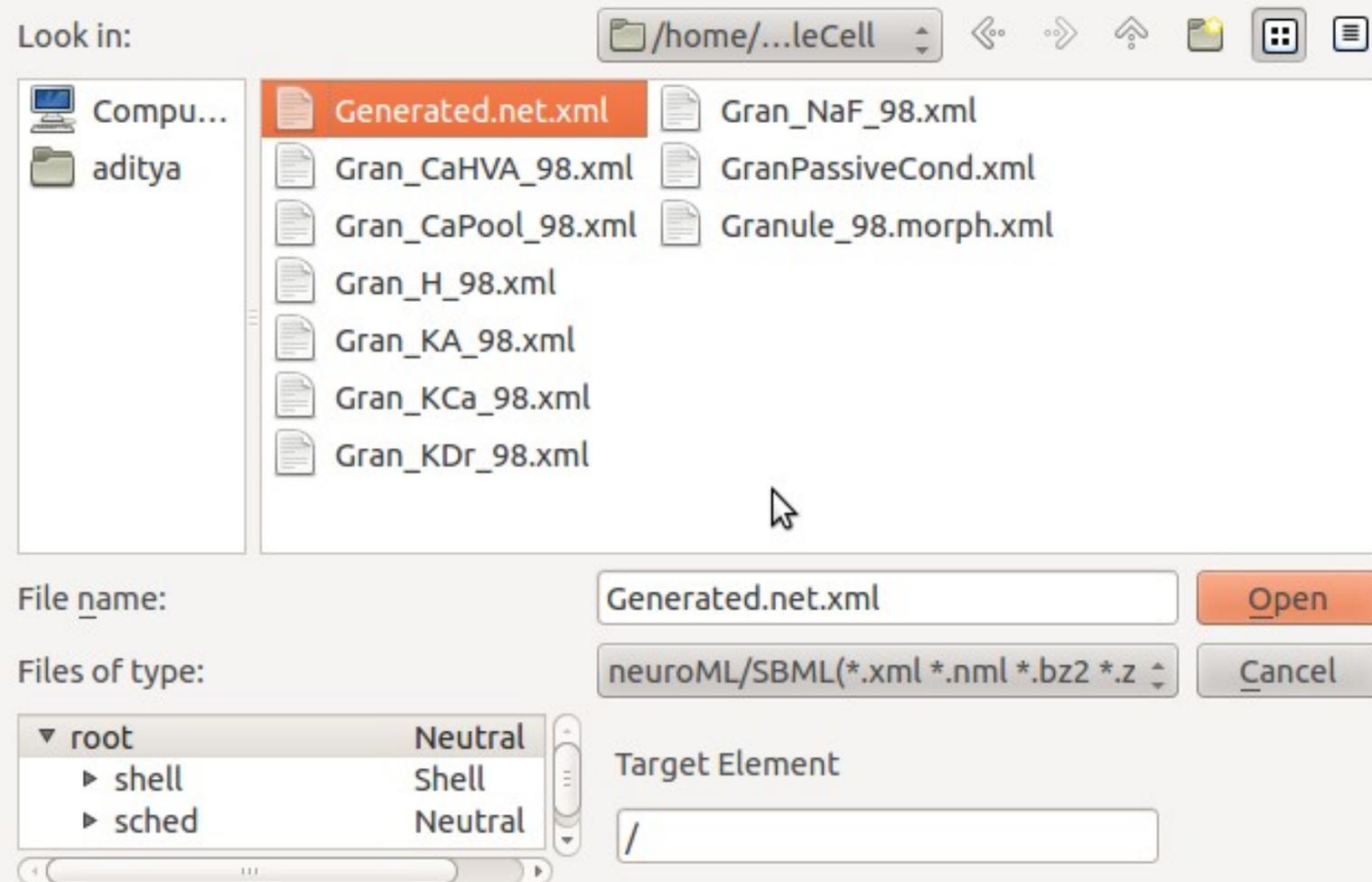
Why python importer then?

- libNeuroML v0.2: no NetworkML
- Bhalla & Bower mitral cell '93 (284 comps):
 - GENESIS→NEURON (Andrew Davison)
 - NEURON→NeuroML morphology exporter exports <cablegroup> tags to group cables
 - libNeuroML v0.2 only supports <meta:group> tags inside <cable> tags.
 - Redundancy in NeuroML1 – bad?
- Bug importing a validated H channel
- Python easier than debugging C++

Importer MOOSE β 1.4 – Aditya

- ElementTree module
 - Included / standard in Python2.5
 - Mostly compatible with the faster cElementTree or lxml, can switch later
- ChannelML, MorphML, NetworkML from file/node.
- Load channels, then cells into /library. Then create populations & projections. OR
- Load NeuroML file and load cells / channels from it, or separate files in its directory.

MOOSE β 1.4 GUI – Chaitanya



Chaitanya

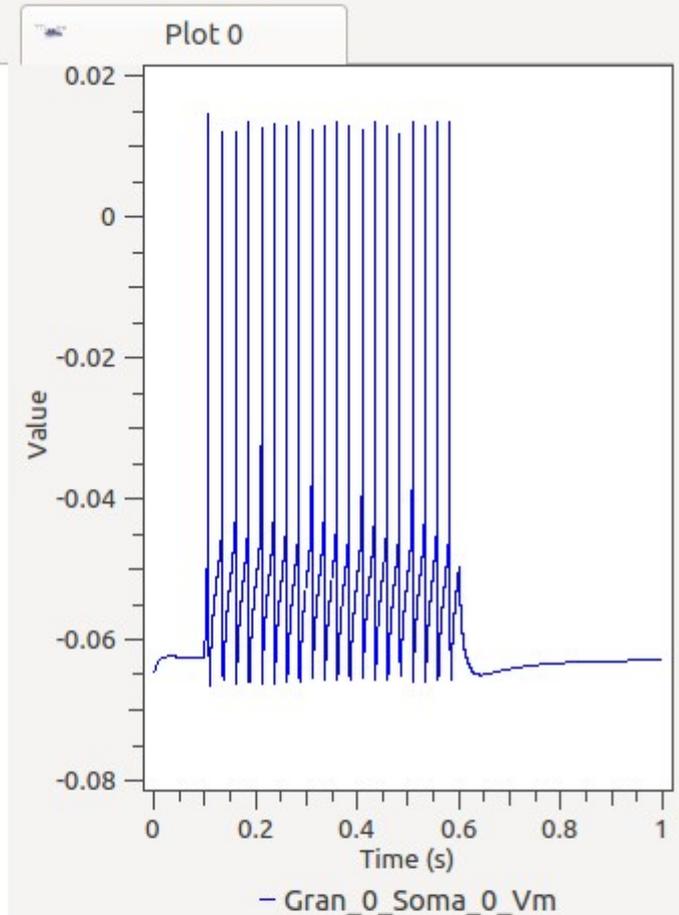
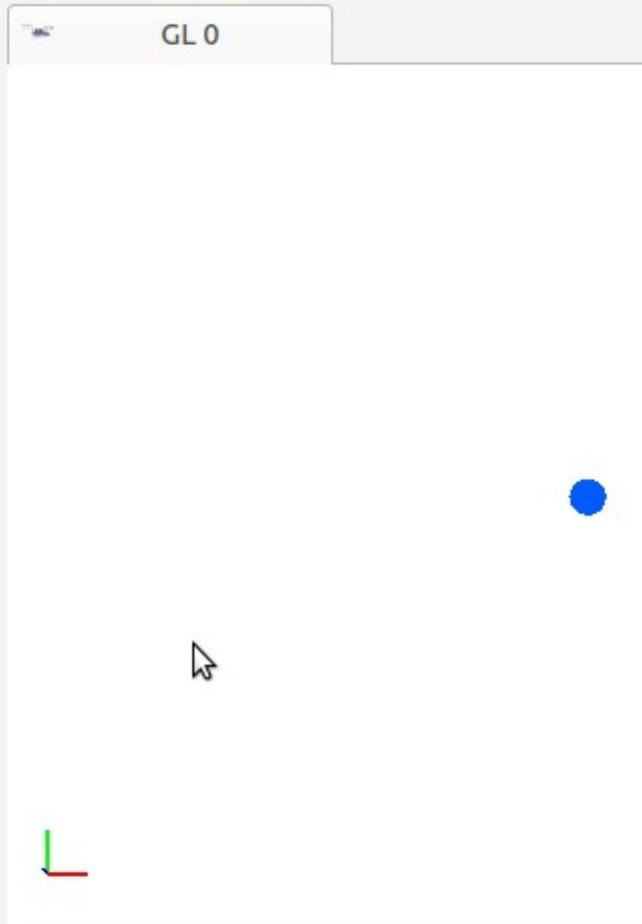
File View Edit Run Help

Run Time: 1.000e+00 Current Time: 1.0



Element Tree

- ▼ root Neutral
 - ▶ shell Shell
 - ▶ sched Neutral
 - ▶ library Neutral
 - proto Neutral
 - data Neutral
 - gl Neutral
 - ▼ Gran_0 Cell
 - ▼ Soma_0 Compartment
 - Gran_KDr_98 HHChannel
 - Gran_H_98 HHChannel
 - Gran_CaHVA_98 HHChannel
 - Gran_KCa_98 HHChannel2D
 - Gran_KA_98 HHChannel
 - Gran_NaF_98 HHChannel
 - Gran_CaPool_98 CaConc
 - ▼ elec Neutral
 - pulsegen_Gran_10pA PulseGen
 - iclamp_Gran_10pA DiffAmp



MOOSE Shell

```

creating inputs in /elec ...
Loaded model
/home/aditya/pymoose_svn/trunk/DEMOS/NeuroML_neuroConstruct/GranuleCell/Generated.net.x
ml of type NEUROML
Adding table /data/Gran_0_Soma_0_Vm
Clearing plot Gran_0_Soma_0_Vm
Resetting curves
Adding table /data/Gran_0_Soma_0_Vm
  
```

Property Editor - Soma_0

Field	Value	Plot
name	Soma_0	
Vm	-0.0629481	Plot 0
Cm	3.14159e-12	None
Em	0.0	None

Chaitanya

Click on compartment to open properties in Property Editor. Use arrow keys to pan model. Click and drag to rotate. Scroll to zoom. To visualize more cell

OB model – Aditya: Usage

```
from moose.neuroml import *

load_channels()

    CML = ChannelML({'temperature':CELSIUS})
    CML.readChannelMLFromFile('../channels/lh_cb.xml')

cellSegmentDict = load_cells()

    MML = MorphML({'temperature':CELSIUS})
    mitral_dict =
        MML.readMorphMLFromFile('../cells/mitral_bbmit1993davison_neuroML
            _L1_L2_L3_mod.xml',{})
    cellSegmentDict.update(mitral_dict)

## populationDict = { 'populationname1':(cellname,{instanceid1:moosecell, ... }) , ... }

## projectionDict = { 'projectionname1':(source,target,
[(syn_name1,pre_seg_moosepath,post_seg_moosepath),...]) , ... }

(populationDict,projectionDict) = \

NML.readNetworkMLFromFile(filename,cellSegmentDict,params=tweaks)
```

Aditya

ChannelML1 issues

- Global properties like temperature (meta?)
- Lookup table channels – Na in BBmit93
- Destexhe et al 's receptor-saturating synapse (implemented in MOOSE)

<http://cns.iaf.cnrs-gif.fr/files/synapse.pdf>

MorphML1 issues

- `<cablegroup>`s inside `<cables>` (NEURON export)

versus

- `<meta:group>` tags within `<cable>`
 - Former: easy to implement
 - Latter: easy to read / understand model
 - XSLT converter between these?

MorphML1 issues

- `<segment>` and `<cable>`
 - 1 segment to a compartment?
- Soma with dendrites at opp ends:
 - `<segment>` has opt attrib `cable`
 - `<cable>` & `fract_along_parent` attrib.
 - Need to parse `<segments>` and `<cables>` to get connectivity
- Attrib for every segment: connect proximal vs distal to parent.

NetworkML1 issues

- Rotation of cell instances
- Inhomogeneous populations?
 - Override say RMP of individual cells
 - cell_type as a list in <population>
 - Collections of populations with same potential synaptic locations
 - Projections should not be affected

Implementation issues

- Rotation of cell instances by <meta:notes>
- Asym compartment converted to sym compartment by Hines solver in MOOSE: axial of parent to raxial of child segment
- Changing params of channel in MorphML not implemented
- Need clean separation of NeuroML reader to in-memory model VS sim-dependent model creation code!

XSLT to X3D – Aditya

- Enhancements to the XSL file by Padraig:
 - NetworkML support:
 - Populations and projections
 - Cells as spheres / morphology if present
 - Cell morphology with dendritic widths
- On the NeuroML website
- Olfactory bulb model (Aditya) visualized in X3D ...

Mitral Cells [Bhalla & Bower 1993]

10 gloms, 20 cells, 400 ORNs-->mit per mit

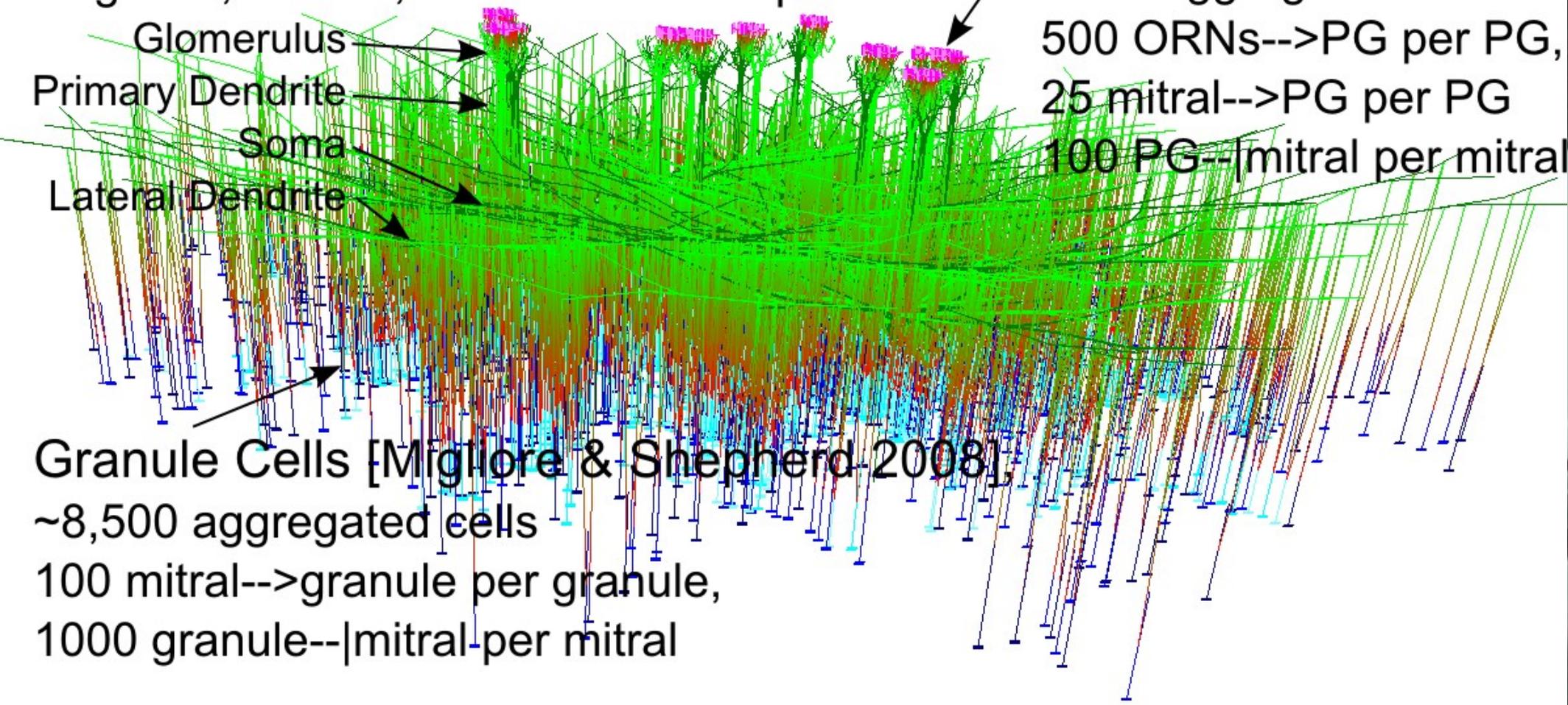
Glomerulus
Primary Dendrite
Soma
Lateral Dendrite

PG Cells [self],

~400 aggregated cells
500 ORNs-->PG per PG,
25 mitral-->PG per PG
100 PG--|mitral per mitral

Granule Cells [Migliore & Shepherd 2008],

~8,500 aggregated cells
100 mitral-->granule per granule,
1000 granule--|mitral per mitral



Aditya

Post simulation analysis tool

Moogli – Chaitanya

.p (genesis)

.xml
(Neuroml /
Morphml)

.csv
(general)

.h5 (hdf5)

Moogli

.png
(snapshots)

.avi
(movies)

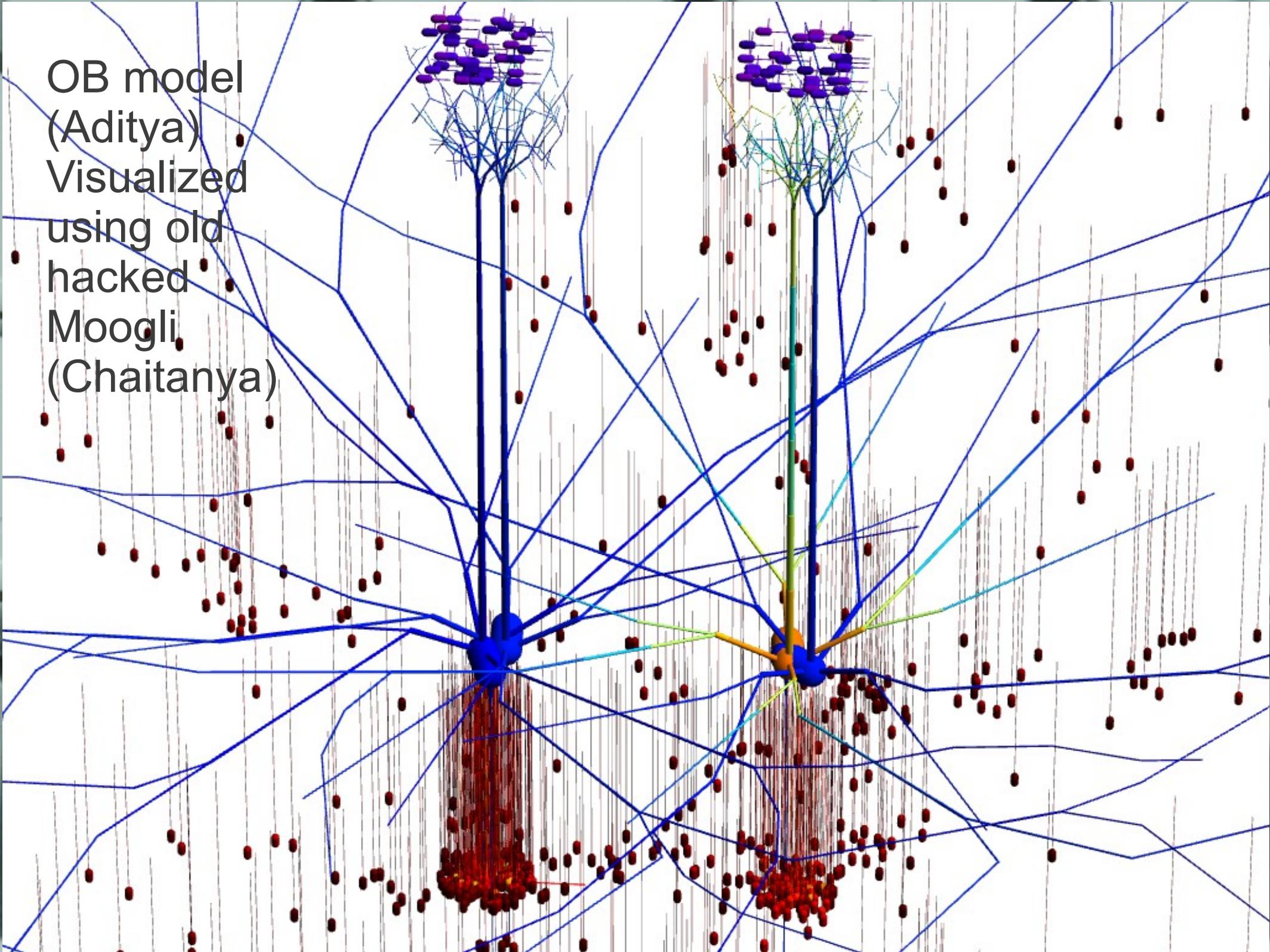
Inspection of
morphology

Plots

- hdf5 import: file includes morphology of the cell(s) being visualized.
- NEO support coming

Chaitanya

OB model
(Aditya)
Visualized
using old
hacked
Moogli
(Chaitanya)



LEMS

- Core set of ComponentTypes should correspond to existing objects in simulators
 - Performance issues: Niraj – hsolve
- Markov channels implemented in MOOSE
 - Vishaka, Niraj
 - Kinetic Schemes directly translate? – Niraj

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