

Large scale cortical models in NeuroML format on Open Source Brain

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University College London
CNS 2018, Seattle

Overview

NeuroML

Open Source Brain

Cortical models on OSB

Issues with current usage

NeuroMLlite

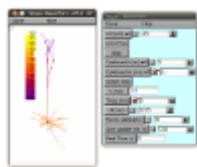
NeuroML

Standardised XML language for computational neuroscience

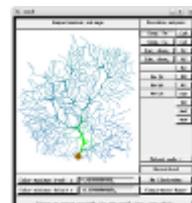
Version 1.x allowed specification of:

- Detailed neuronal morphologies
- Ion channels
- Synapses
- 3D network structure

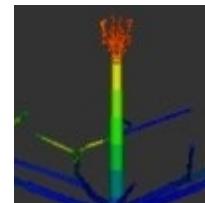
30+ simulators/applications/databases/libraries support
NeuroML



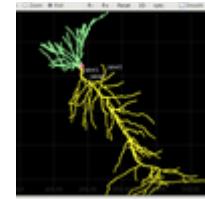
NEURON



GENESIS



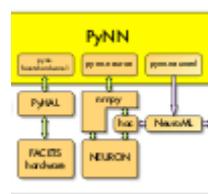
MOOSE



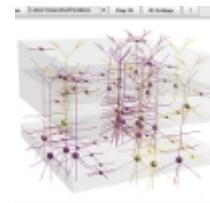
PSICS



NeuroSpaces



PyNN



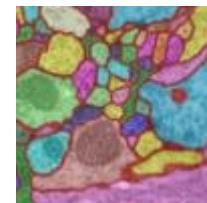
neuroConstruct



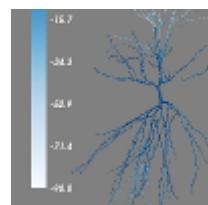
OpenWorm



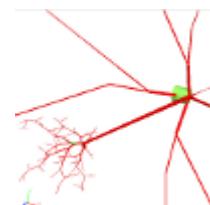
LFPy



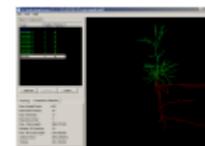
CATMAID



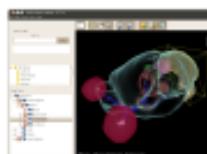
Neuronvisio



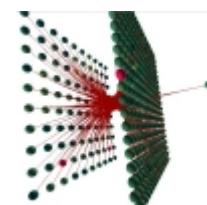
Moogli



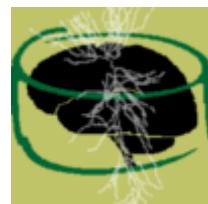
NeuronLand



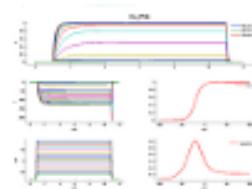
Whole Brain Catalog



NeurAnim



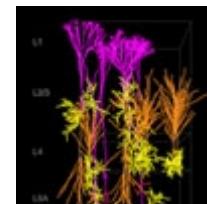
NeuroMorpho



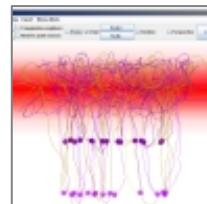
Channelpedia



TREES toolbox



NeuGen



CX3D

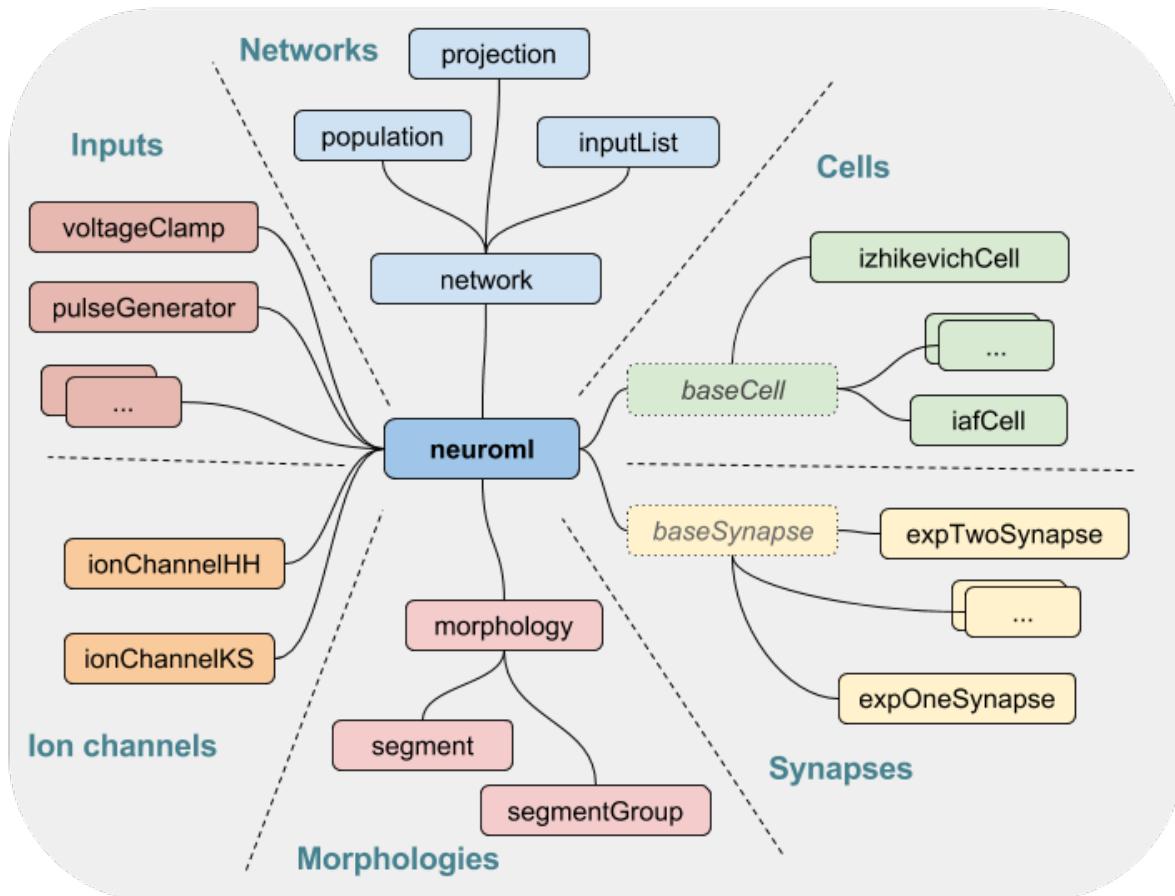


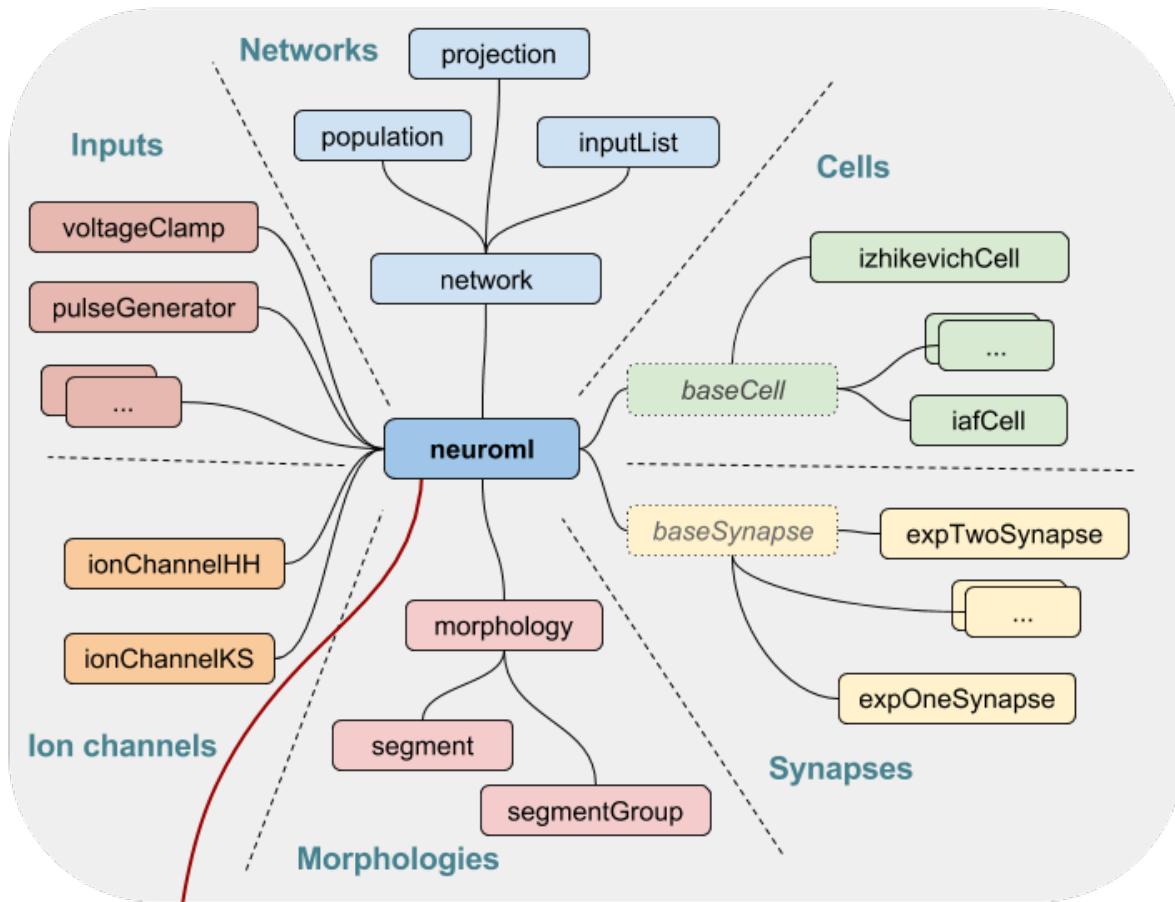
[NeuroML]



OPEN SOURCE BRAIN



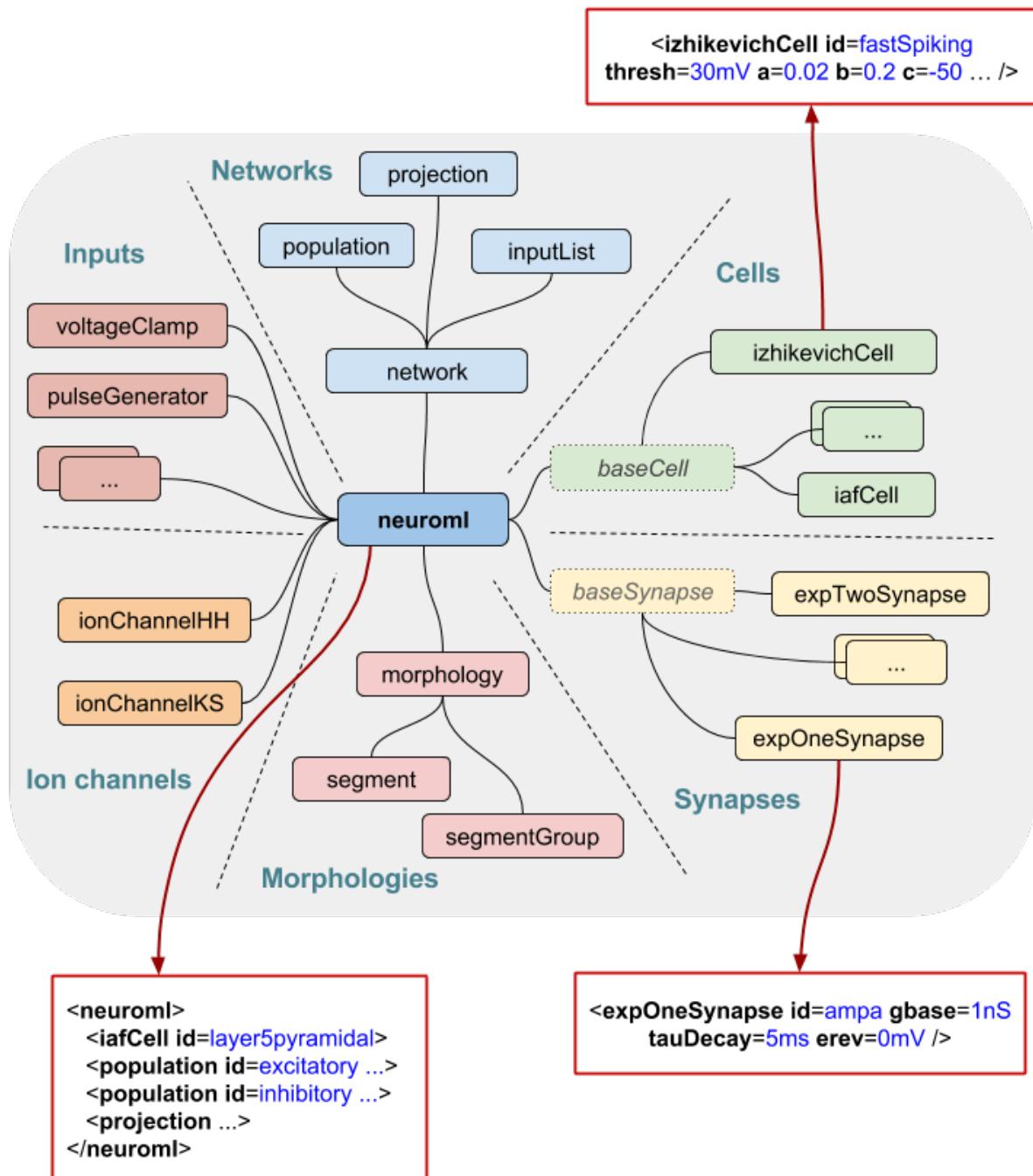




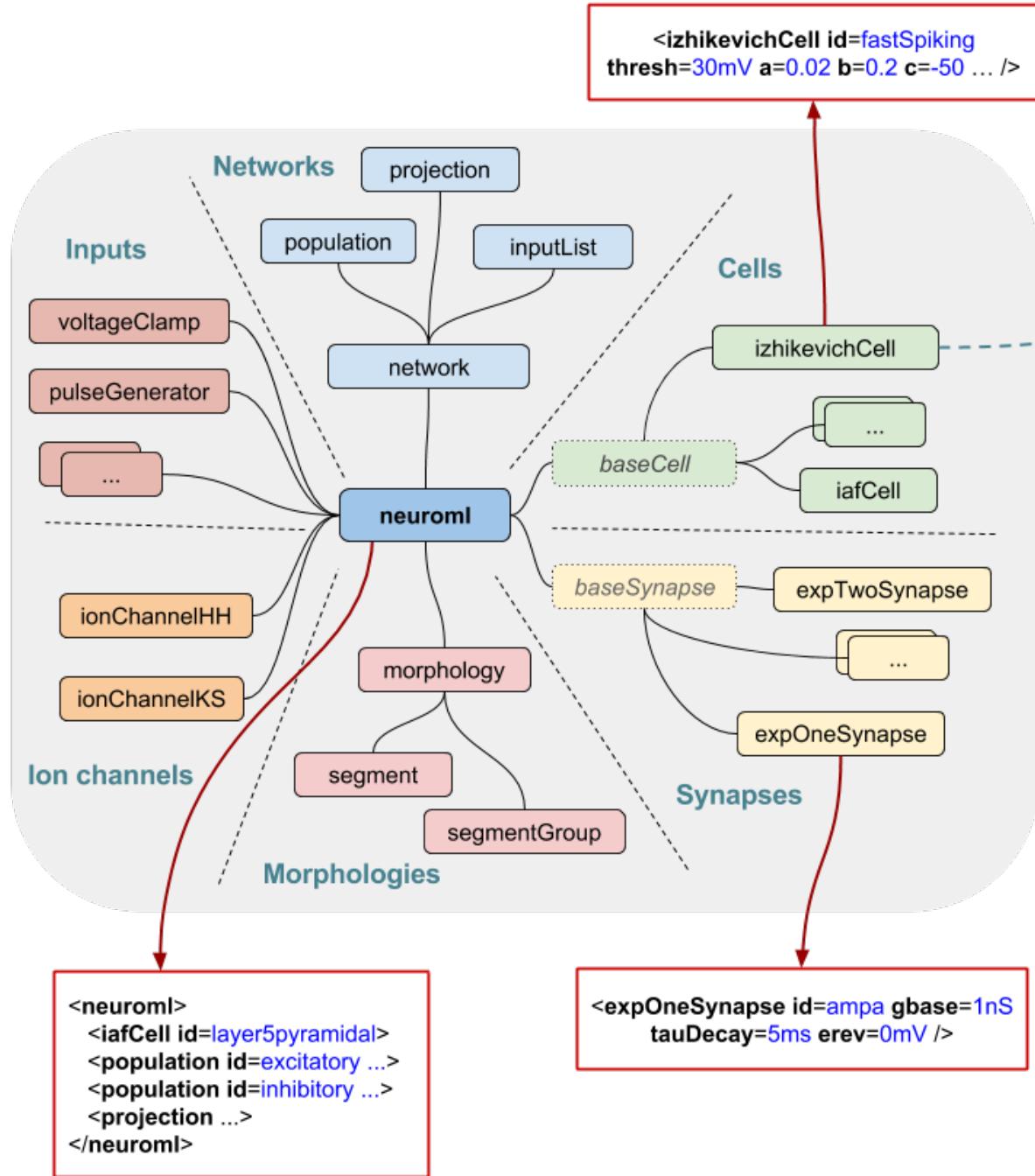
```

<neuroml>
  <iafCell id=layer5pyramidal>
  <population id=excitatory ...>
  <population id=inhibitory ...>
  <projection ...>
</neuroml>

```



NeuroML 2

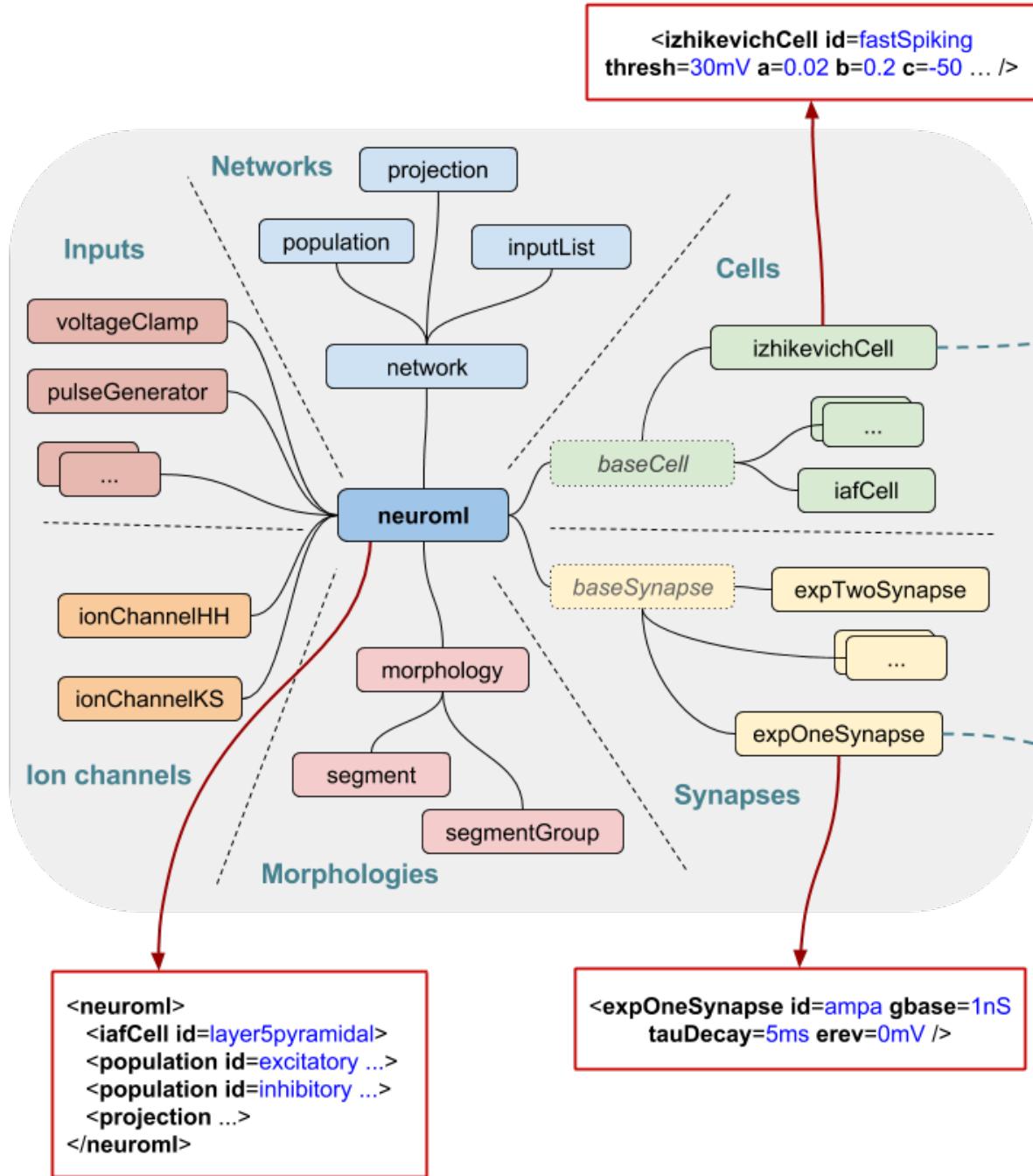


LEMS

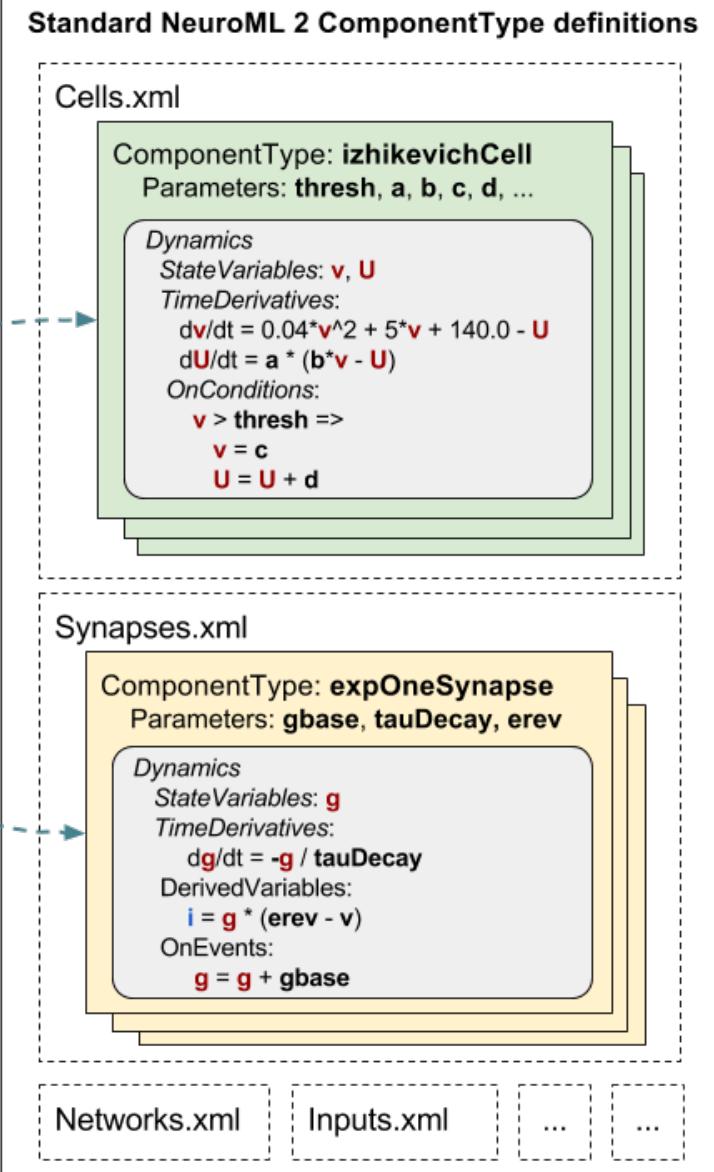
ComponentType: **izhikevichCell**
Parameters: **thresh, a, b, c, d, ...**

Dynamics
StateVariables: **v, U**
TimeDerivatives:
 $\frac{dv}{dt} = 0.04*v^2 + 5*v + 140.0 - U$
 $\frac{dU}{dt} = a * (b*v - U)$
OnConditions:
 $v > \text{thresh} \Rightarrow$
 $v = c$
 $U = U + d$

NeuroML 2



LEMS



The Open Source Brain repository

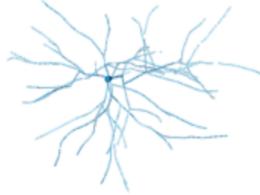
 **OPEN SOURCE BRAIN**  [Explore OSB](#) [Sign in](#) [Sign Up](#)

 Modelling the brain, together

Open Source Brain is a resource for sharing and collaboratively developing computational models of neural systems.

Try exploring one of these models:


Primary Auditory Cortex Network


L23 Cell

...


Izhikevich Spiking Neuron Model


Hodgkin-Huxley Neuron


CA1 Pyramidal Cell

Explore OSB to see all the rest, create an account to add your own models and **run simulations!**

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The Open Source Brain Initiative 2017. Website powered by Redmine

Supported by


The Open Source Brain repository

Wellcome Trust funded project

Open source model development repository for computational neuroscience

Structured database of well tested **spiking neuron & network models** in standardised formats

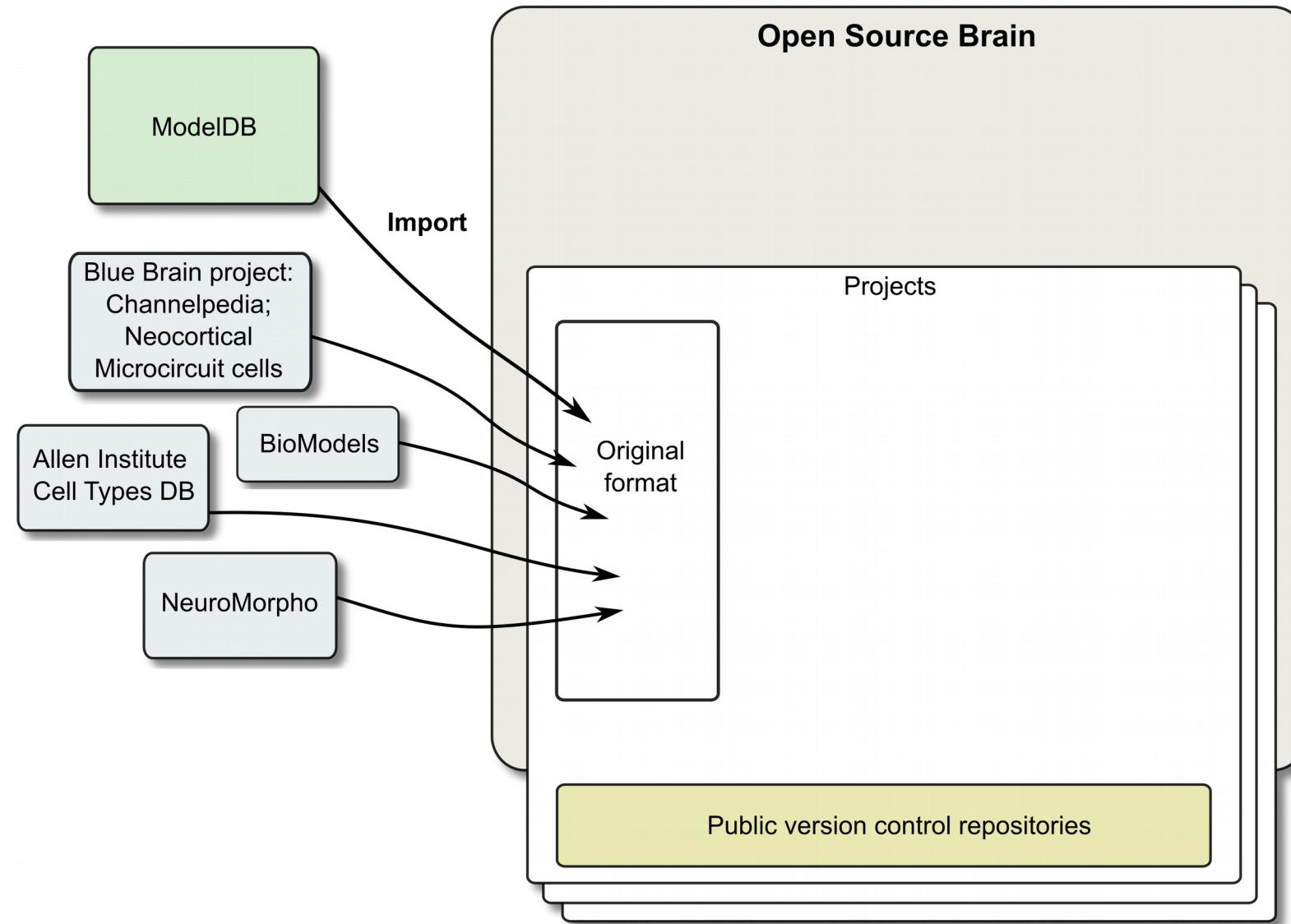
Allow anyone to comment on, extend, reuse models & run them across multiple simulators: **a collaboration platform**

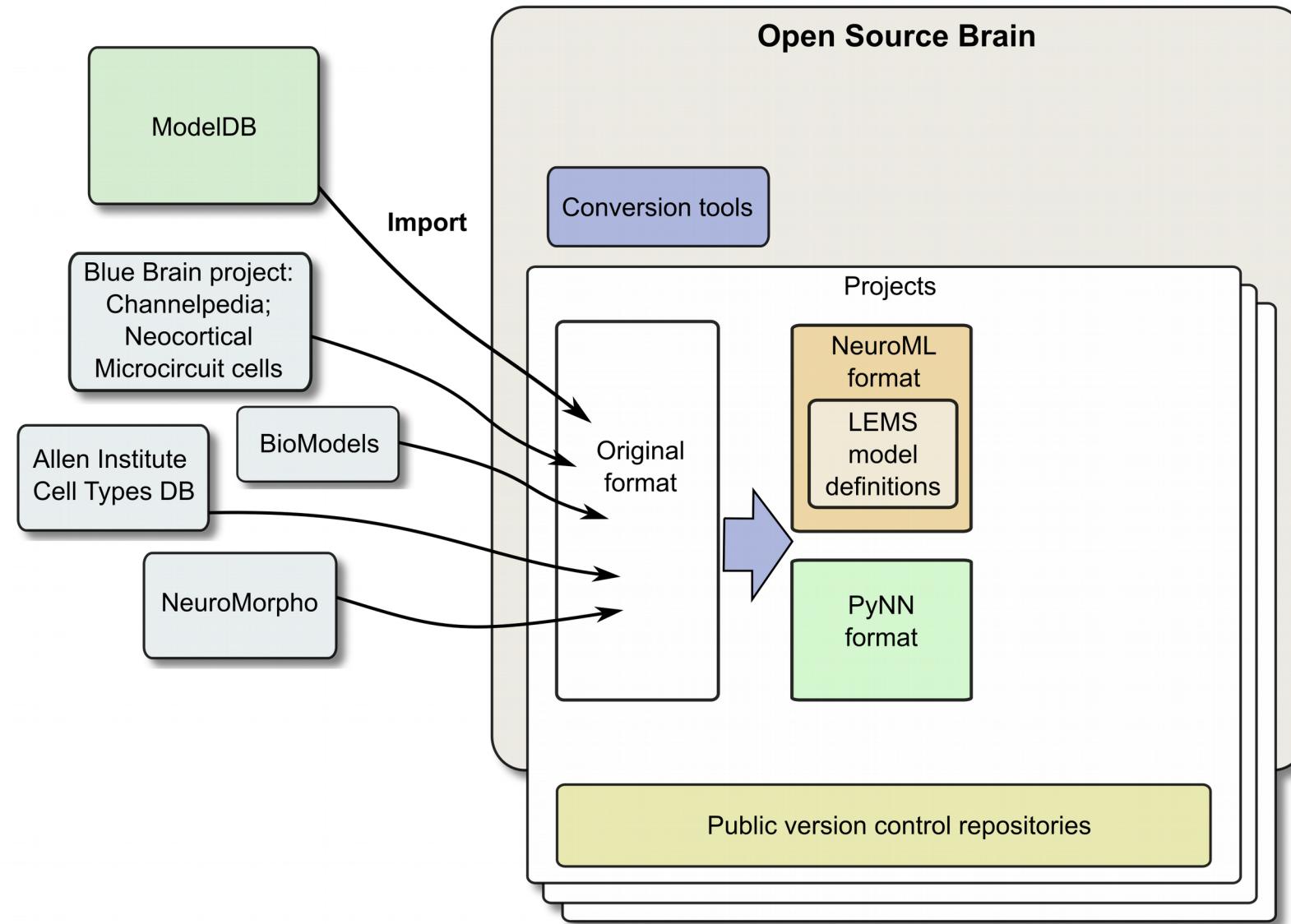
Uses tools & best practices from Open Source software development

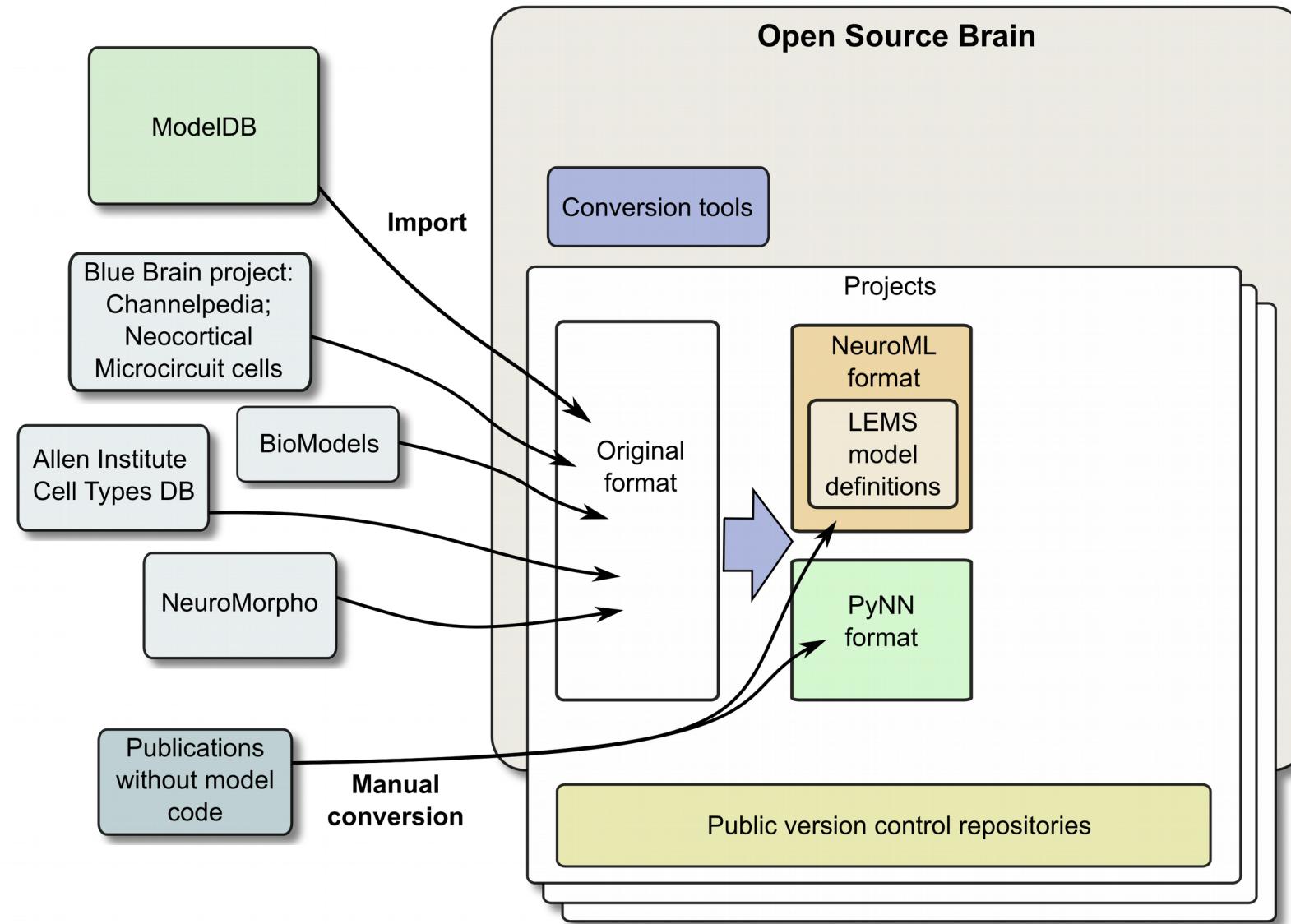
Open Source Brain

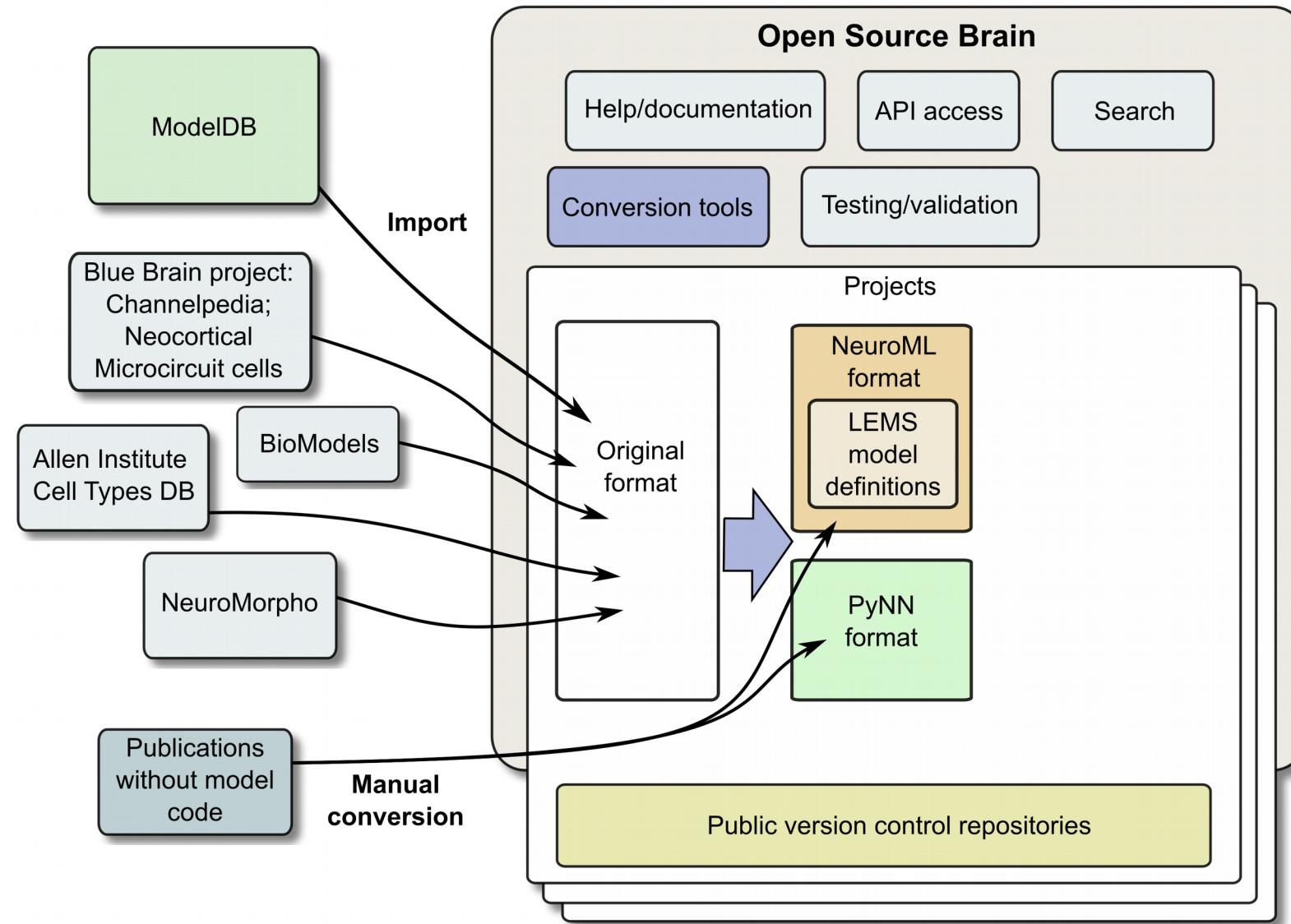
Projects

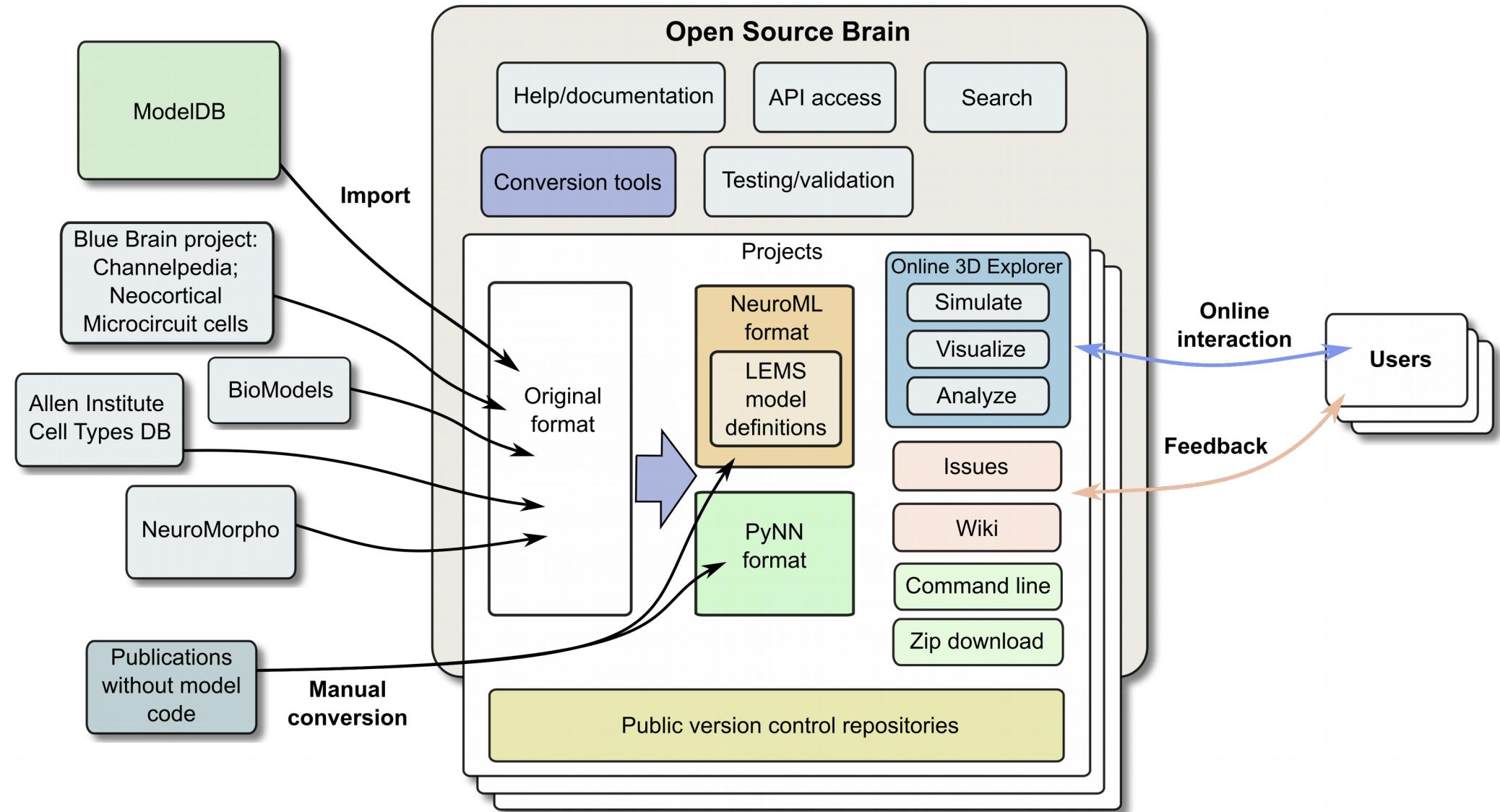
Public version control repositories

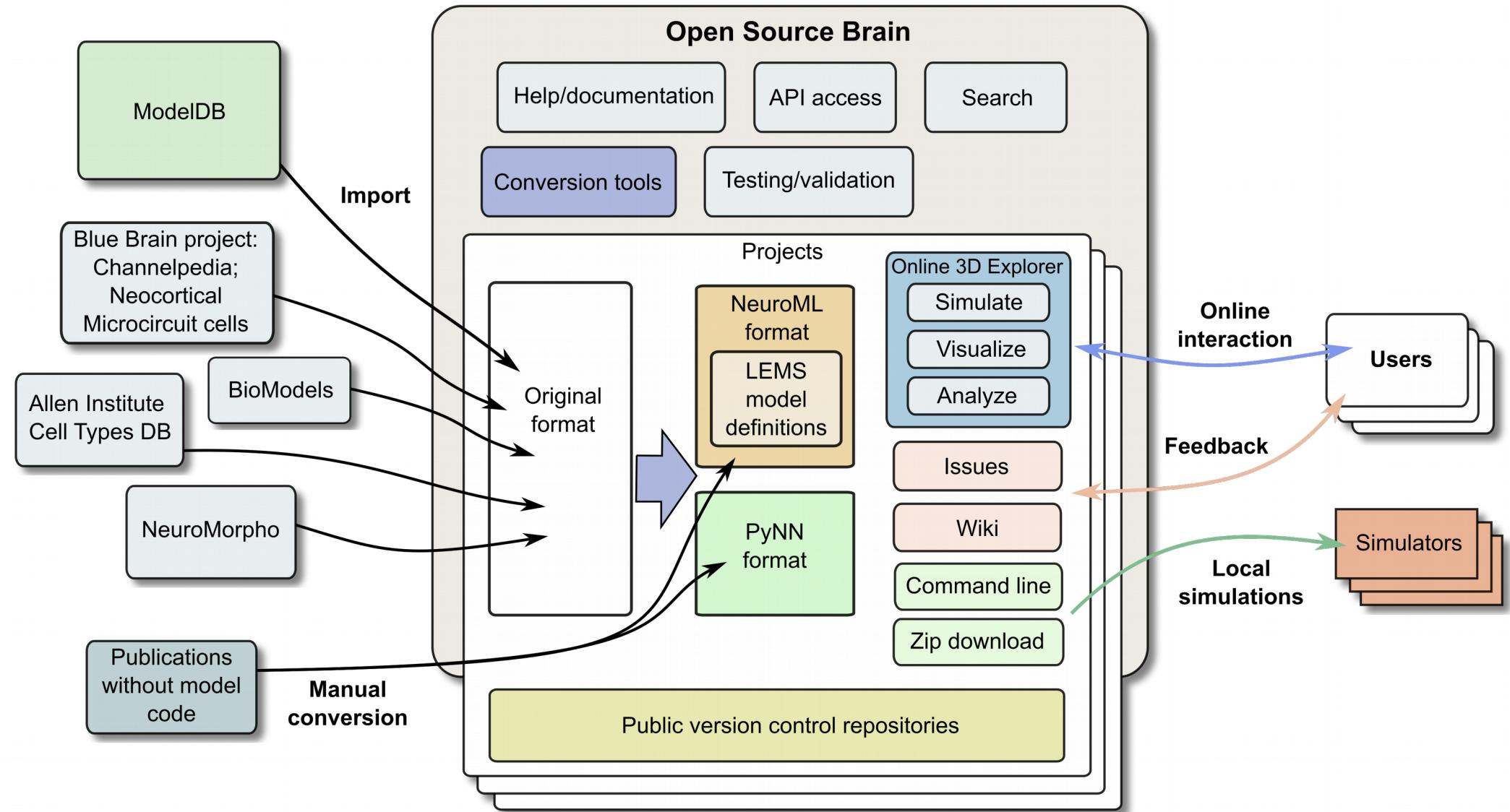


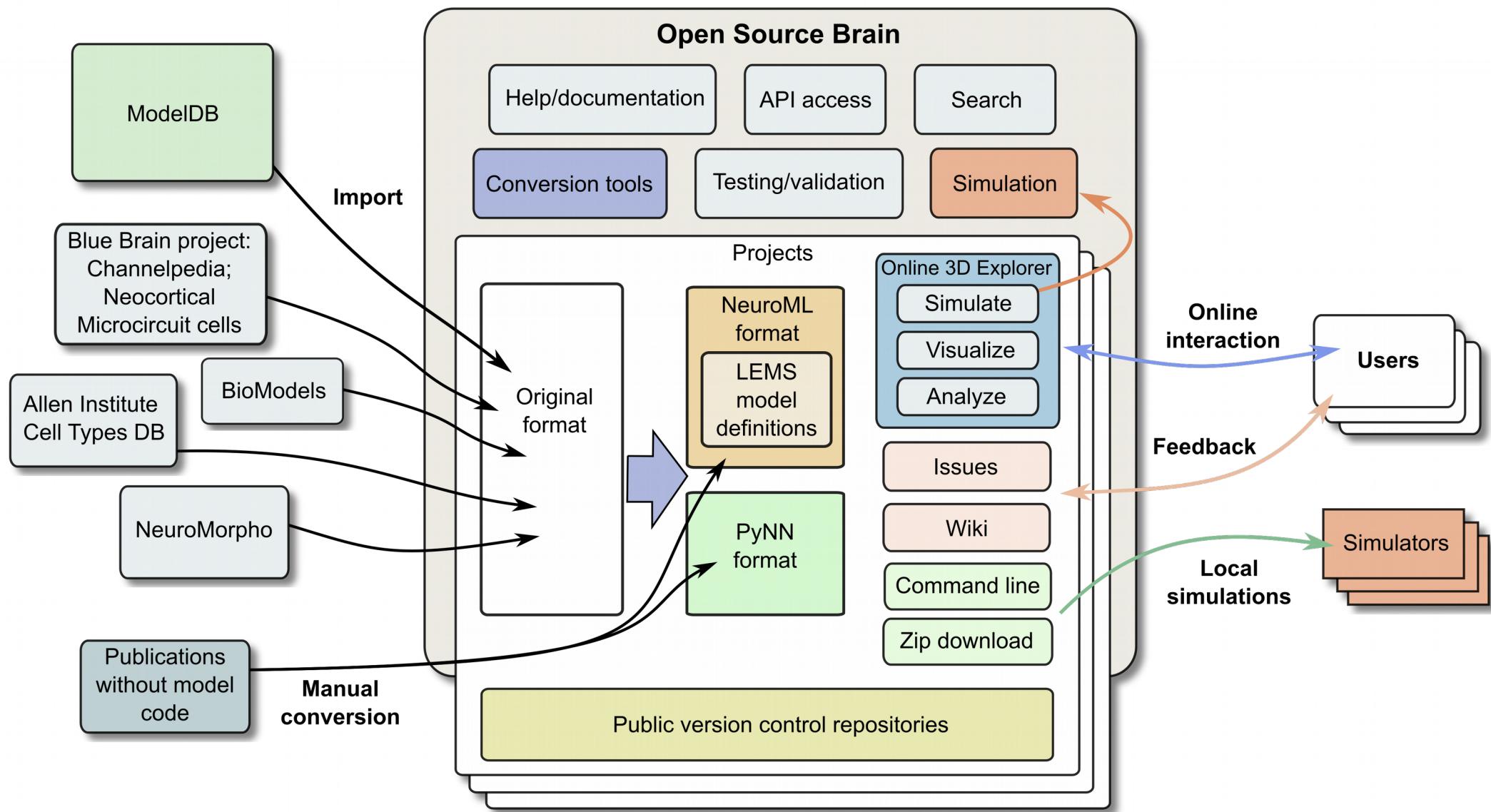


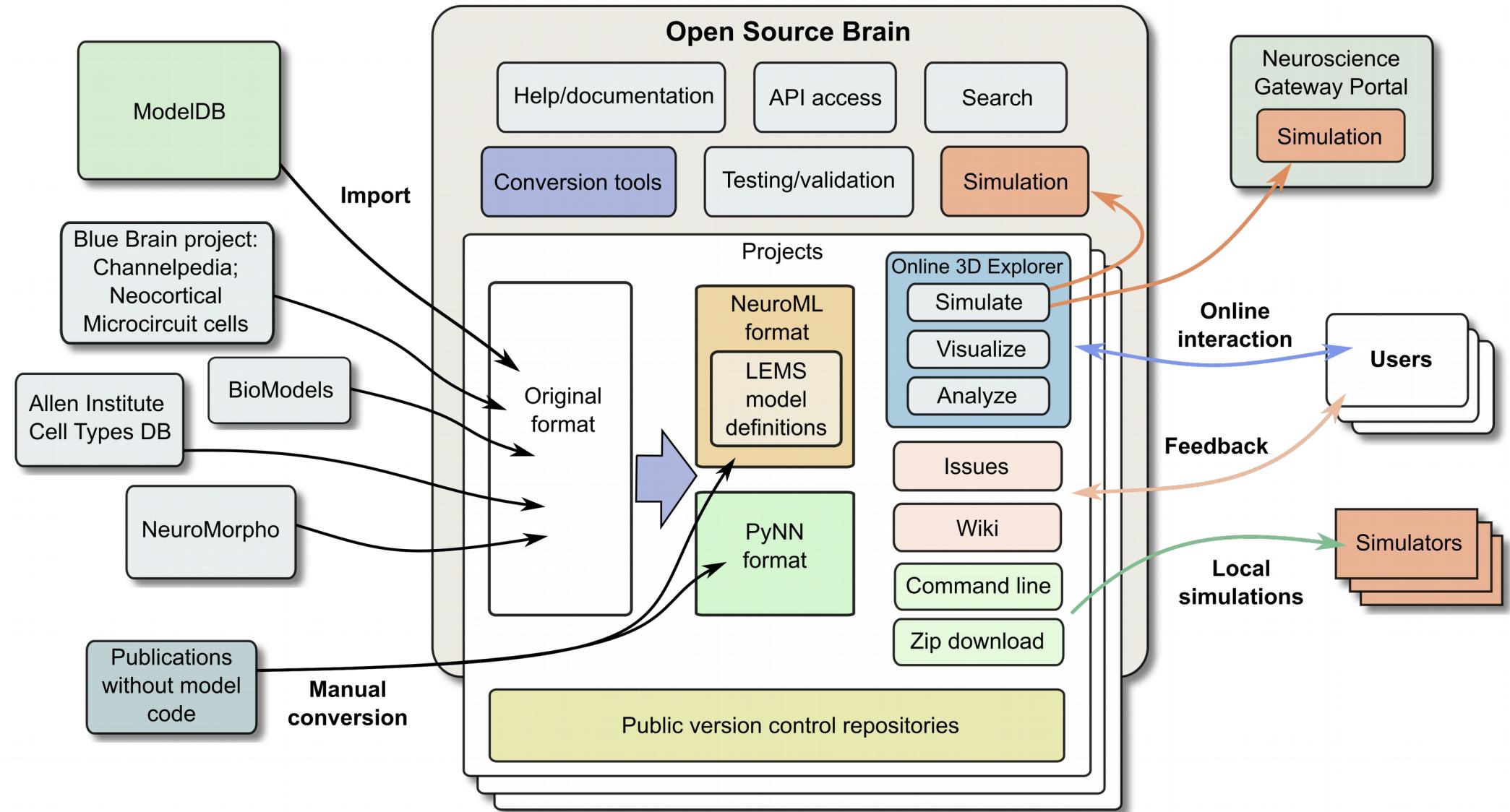


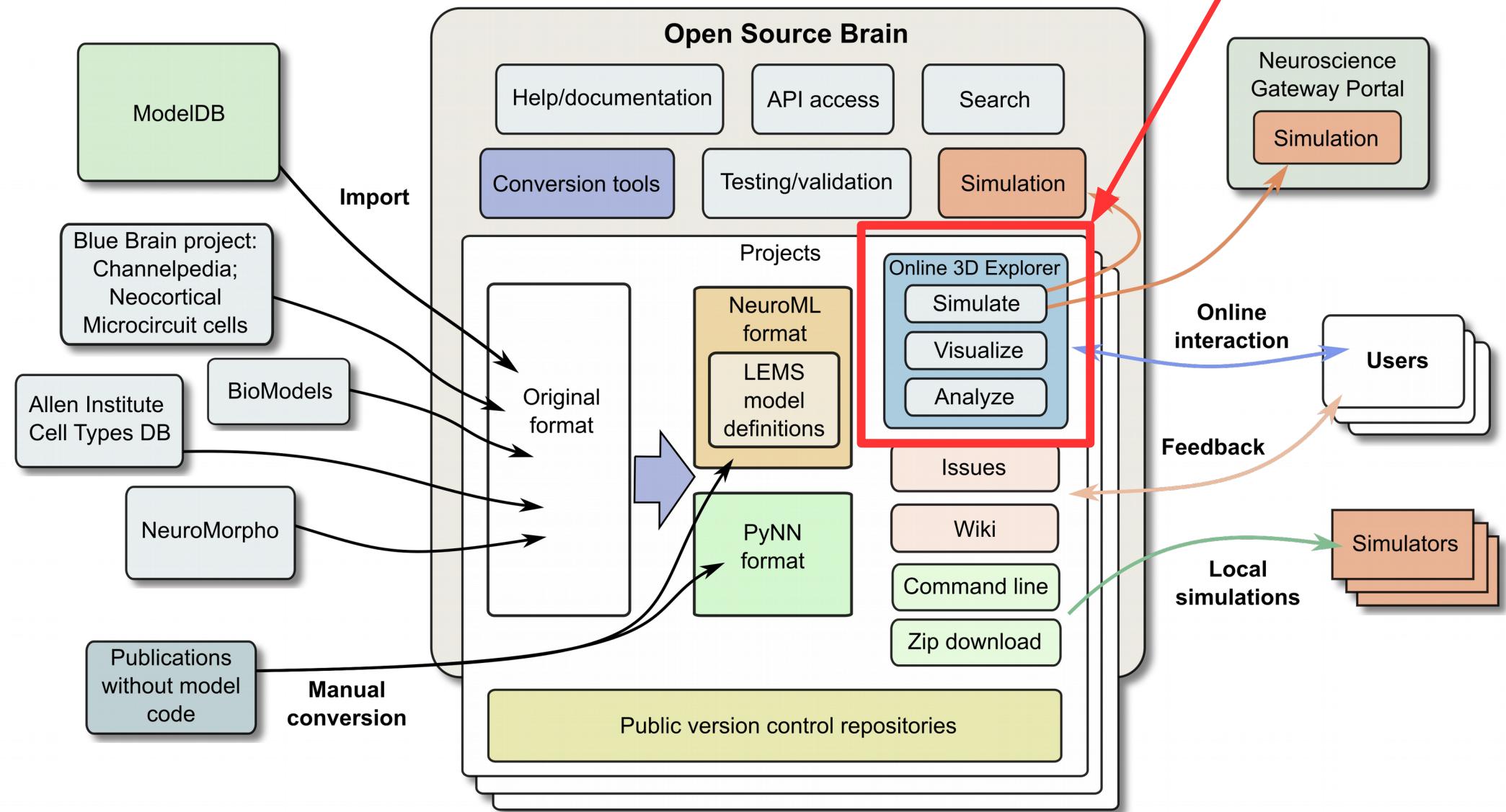








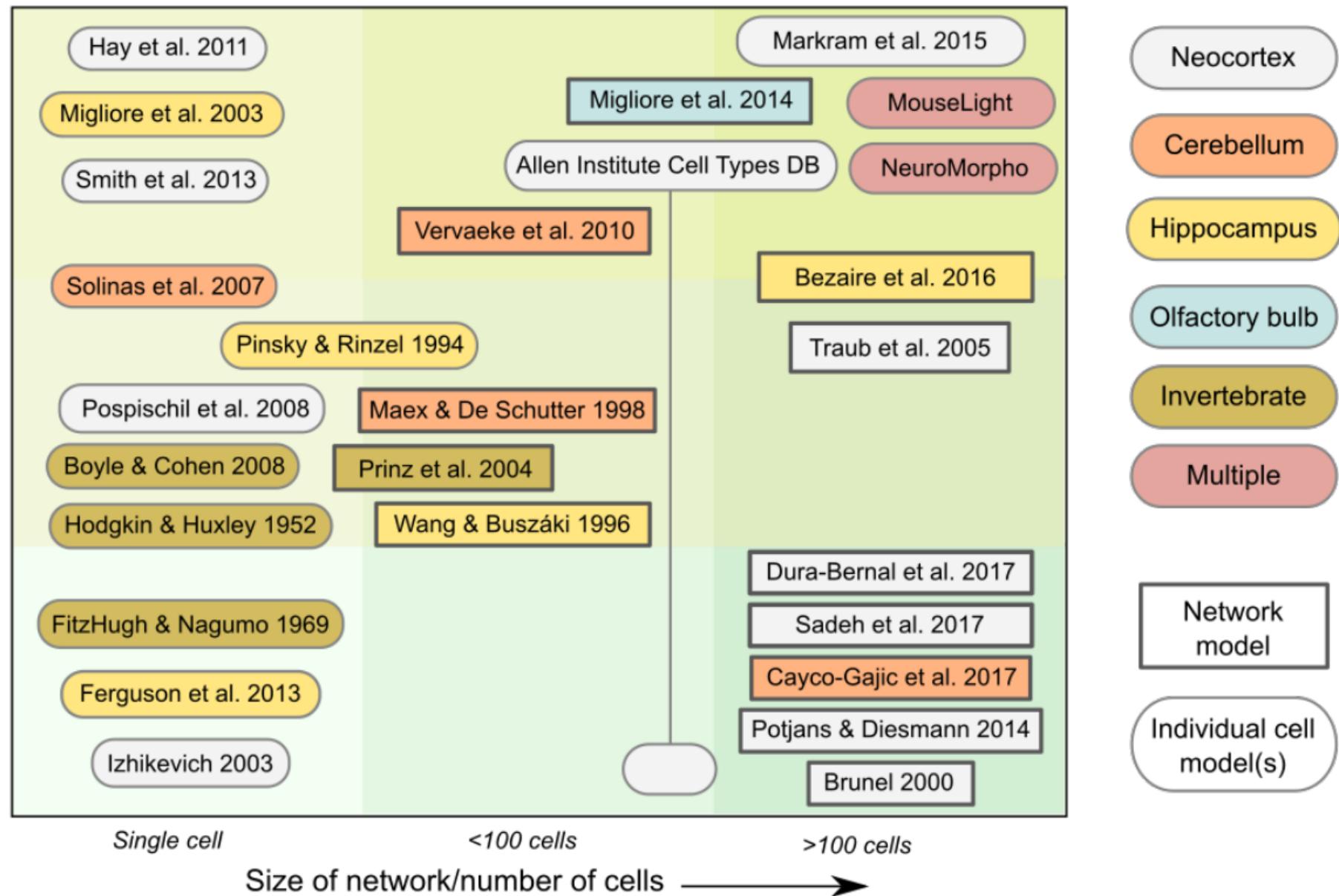




What's there at the moment

A

Model biophysical detail
Detailed neuronal morphology
Abstract morphology
Conductance based 1 comp.
(Extended) I&F





New Results

 [Previous](#) [Next](#)

Open Source Brain: a collaborative resource for visualizing, analyzing, simulating and developing standardized models of neurons and circuits

Padraig Gleeson, Matteo Cantarelli, Boris Marin, Adrian Quintana, Matt Earnshaw, Eugenio Piasini, Justas Birgiolas, Robert C Cannon, N Alex Cayco-Gajic, Sharon Crook, Andrew P Davison, Salvador Dura-Bernal, Andras Ecker, Michael L Hines, Giovanni Idili, Stephen Larson, William W Lytton, Amit Majumdar, Robert A McDougal, Subhashini Sivagnanam, Sergio Solinas, Rokas Stanislovas, Sacha J van Albada, Werner Van Geit, R Angus Silver

doi: <https://doi.org/10.1101/229484>

This article is a preprint and has not been peer-reviewed [what does this mean?].

[Abstract](#)[Info/History](#)[Metrics](#) [Preview PDF](#)

Abstract

Computational models are powerful tools for investigating brain function in health and disease. However, biologically detailed neuronal and circuit models are complex and implemented in a range of specialized languages, making them inaccessible and opaque to many neuroscientists. This has limited critical evaluation of models by the scientific community and impeded their refinement and widespread adoption. To address this, we have combined advances in standardizing models, open source software development and web technologies to develop Open Source Brain, a platform for visualizing, simulating, disseminating and collaboratively developing standardized models of neurons and circuits from a range of brain regions. Model structure and parameters can be visualized and their dynamical properties explored through browser-controlled simulations, without writing code. Open Source Brain makes neural models transparent and accessible and facilitates testing, critical evaluation and refinement, thereby helping to improve the accuracy and reproducibility of models, and their dissemination to the wider community.

Posted January 11, 2018.

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Video

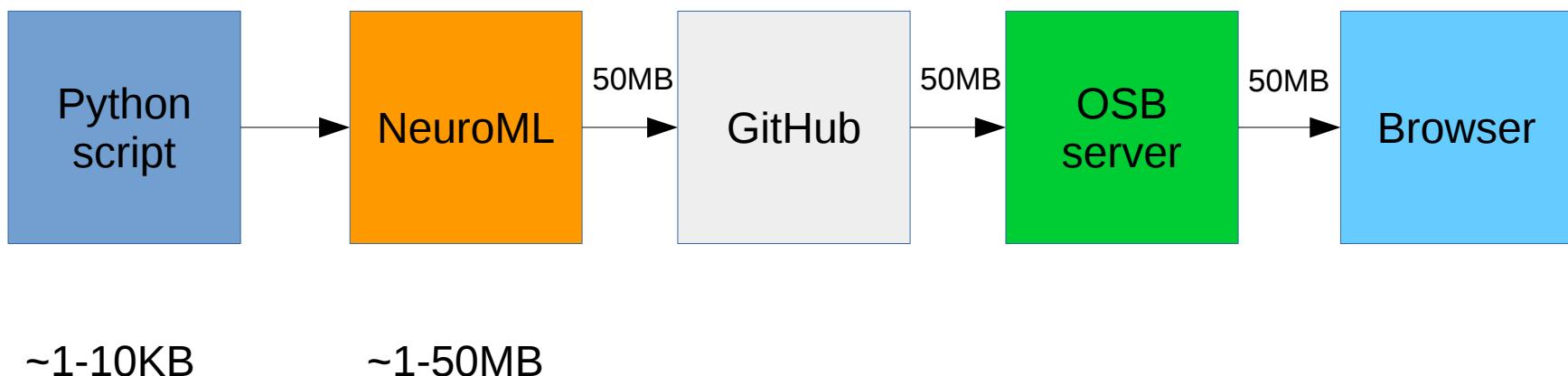
What's missing

Currently NeuroML files are generated offline (e.g. from Python script) & single instance of network can be seen on OSB



What's missing

Bottleneck is size of NeuroML instance

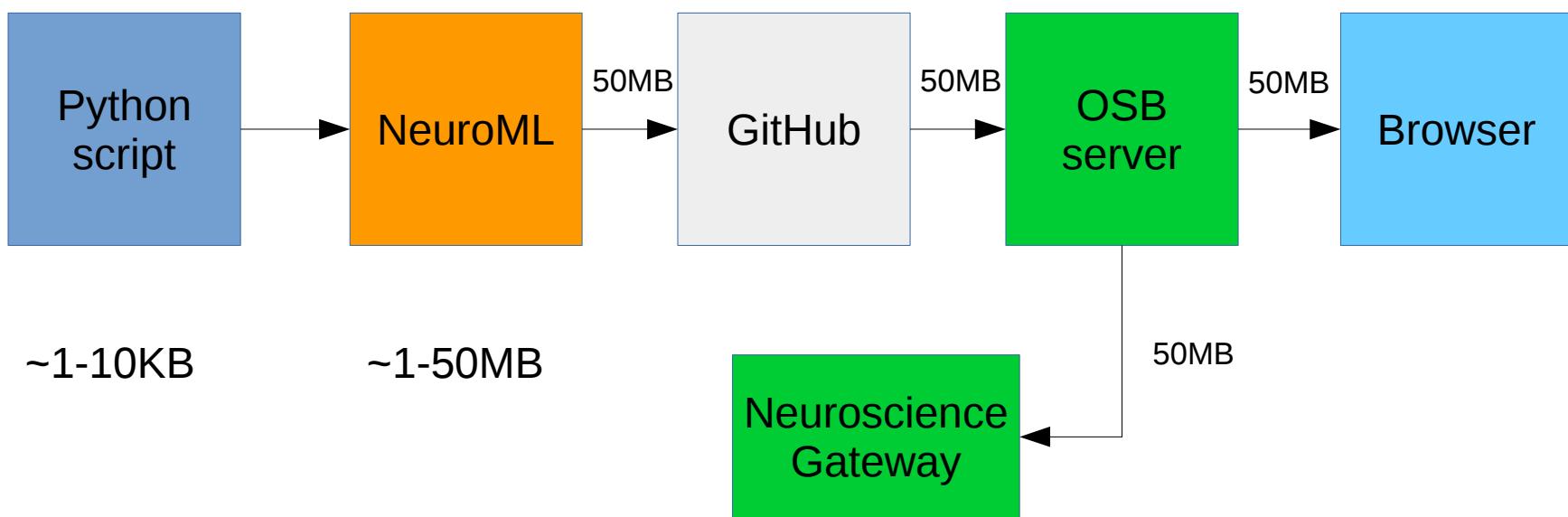


~1-10KB

~1-50MB

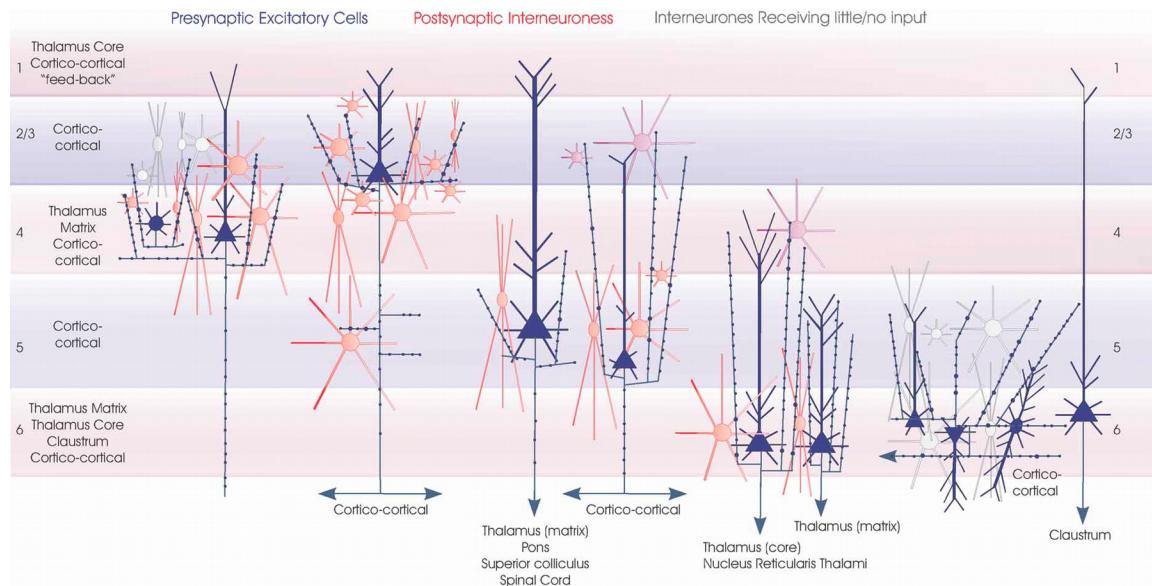
What's missing

Bottleneck is size of NeuroML instance

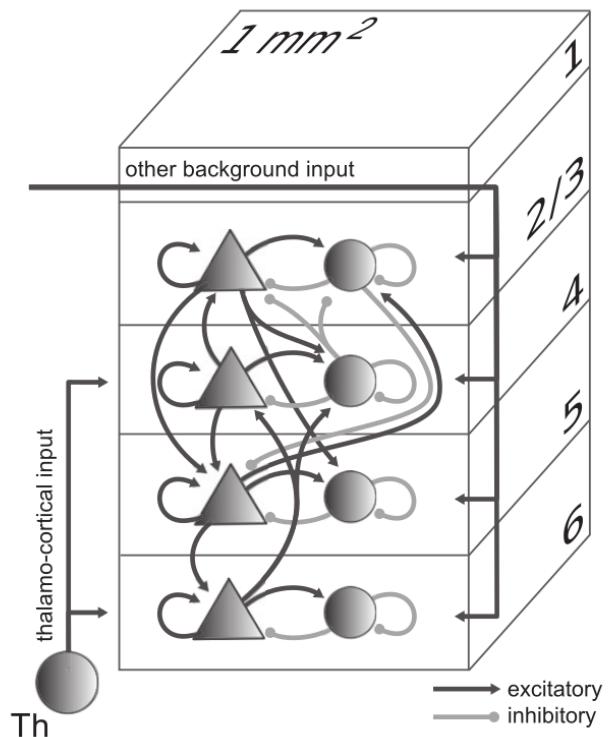


What's missing

There is a lot of experimental data out there on (cortical) connectivity, as well as high level/conceptual models of network structure

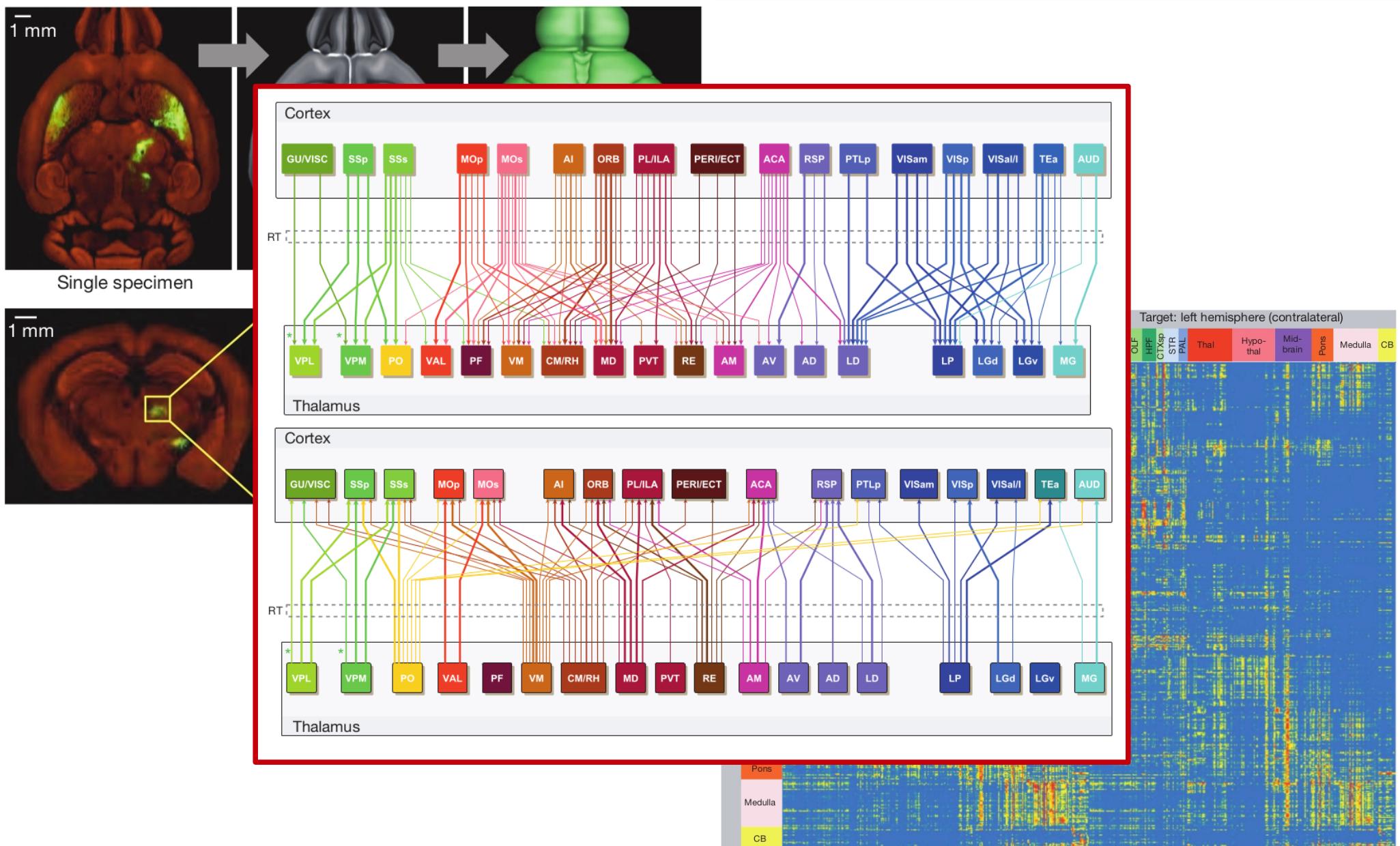


Functional maps of neocortical local circuitry,
Thomson & Lamy, Front. Neurosci. 2007

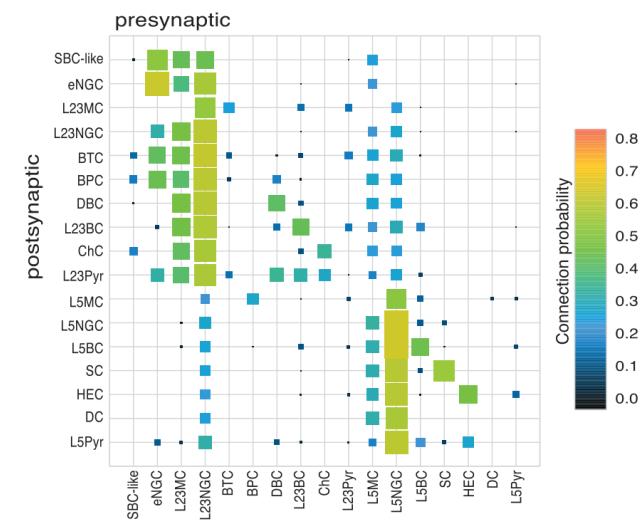
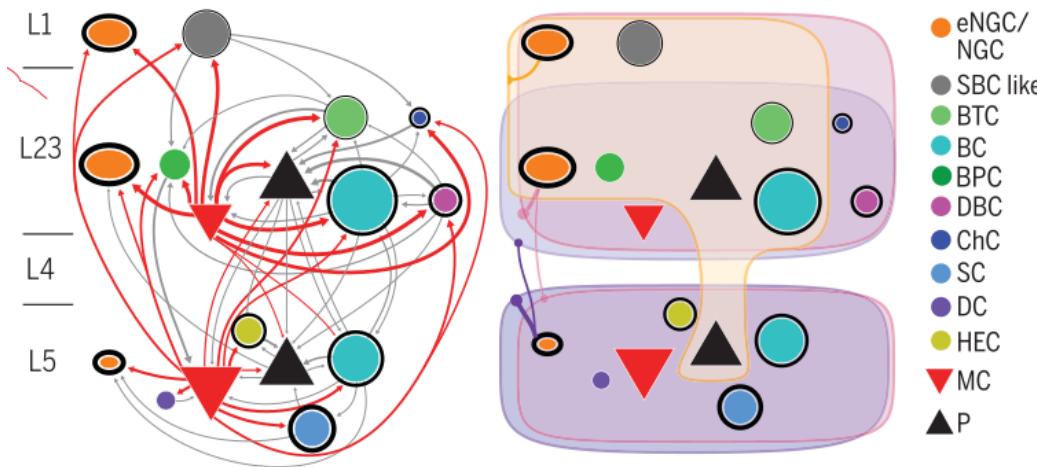
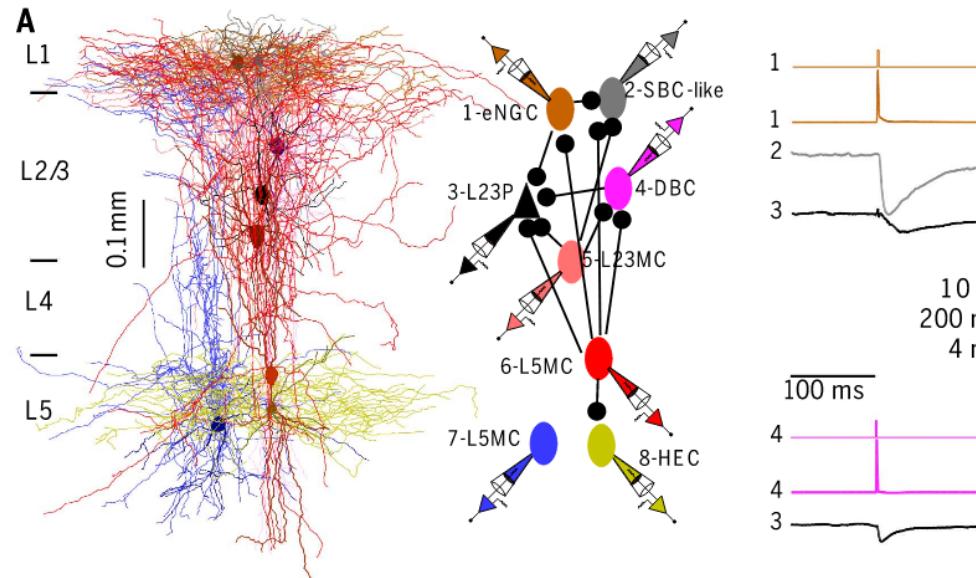


The cell-type specific cortical microcircuit: relating structure and activity in a full-scale spiking network model,
Potjans & Diesmann, Cereb. Cortex 2014

Experimental data: Allen Mesoscale Connectome



Experimental data: multiple whole-cell recording & morphological reconstruction



Principles of connectivity among morphologically defined cell types in adult neocortex, Jiang et al. Science 2015

Solution: NeuroMLlite...

Simple high level representation of network

JSON format (easier to read/write than XML)

Python classes for editing

Solution: NeuroMLlite...

JSON

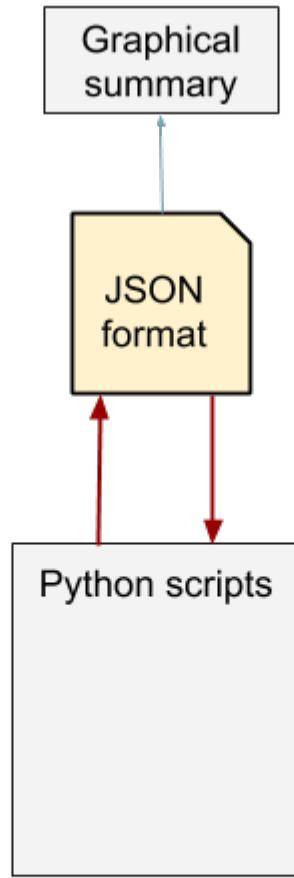
```
{  
  "TestNetwork": {  
    "populations": [  
      {"pop0": {  
        "size": 5,  
        "component": "iaf",  
      }},  
      {"pop1": {  
        "size": 10,  
        "component": "iaf",  
      }}  
    ],  
    "projections": [  
      {"proj0": {  
        "presynaptic": "pop0",  
        "postsynaptic": "pop1",  
        "synapse": "ampa",  
        "random_connectivity": {  
          "probability": 0.5  
        }  
      }}  
    ]  
  }  
}
```

Python

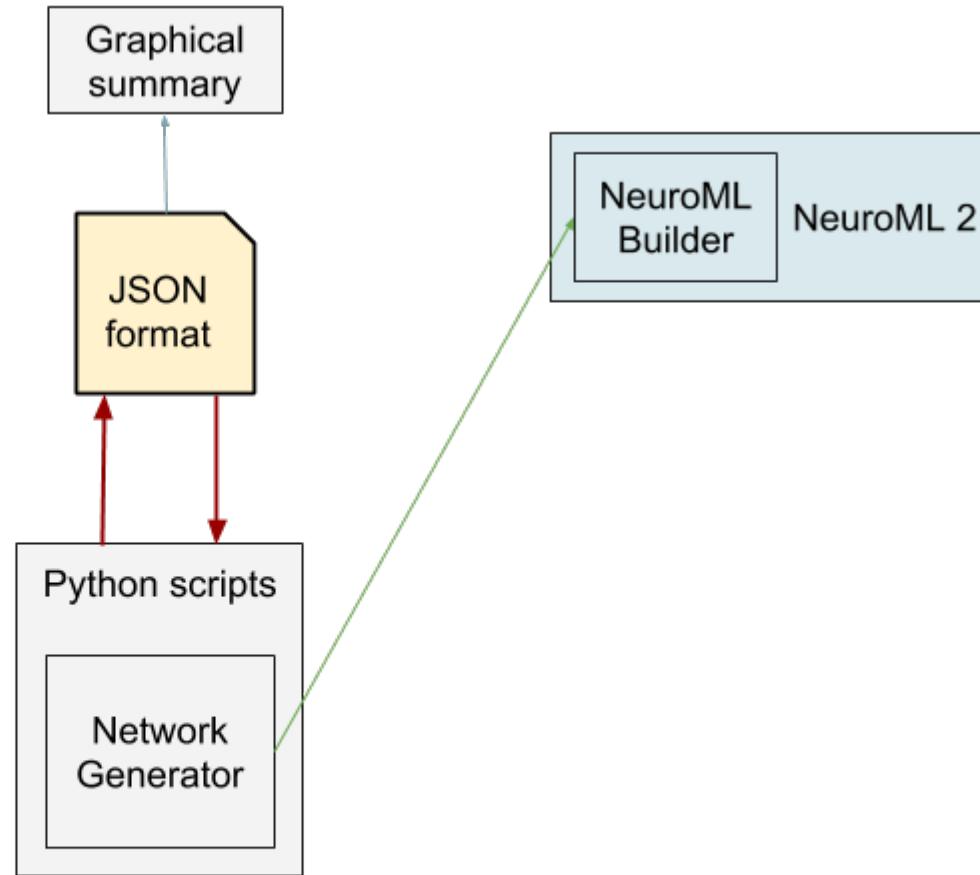
```
p0 = Population(id='pop0', size=5, component='iaf')  
p1 = Population(id='pop1', size=10, component='iaf')  
  
proj = Projection(id='proj0',  
                  presynaptic=p0.id,  
                  postsynaptic=p1.id,  
                  synapse='ampa',  
                  random_connectivity=  
                  RandomConnectivity(probability=0.5))
```



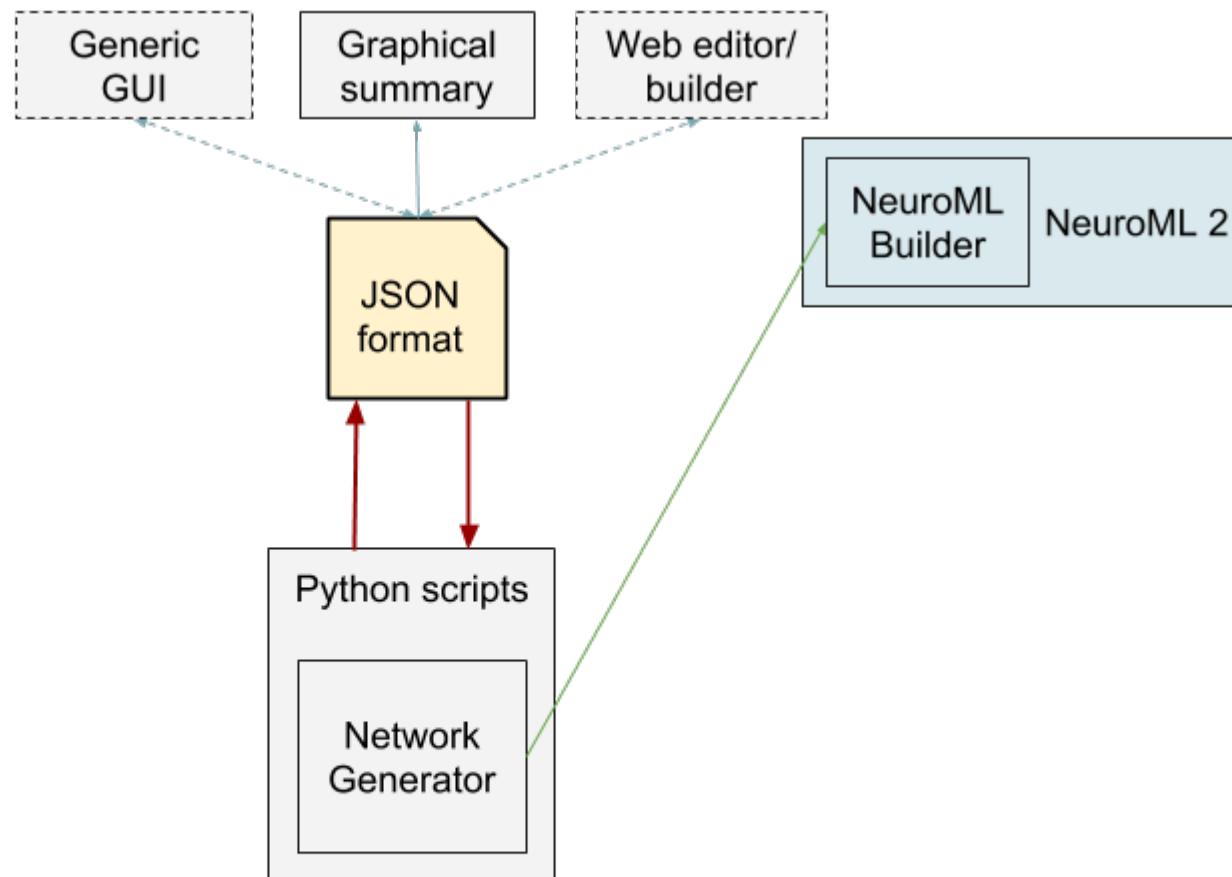
Solution: NeuroMLlite...



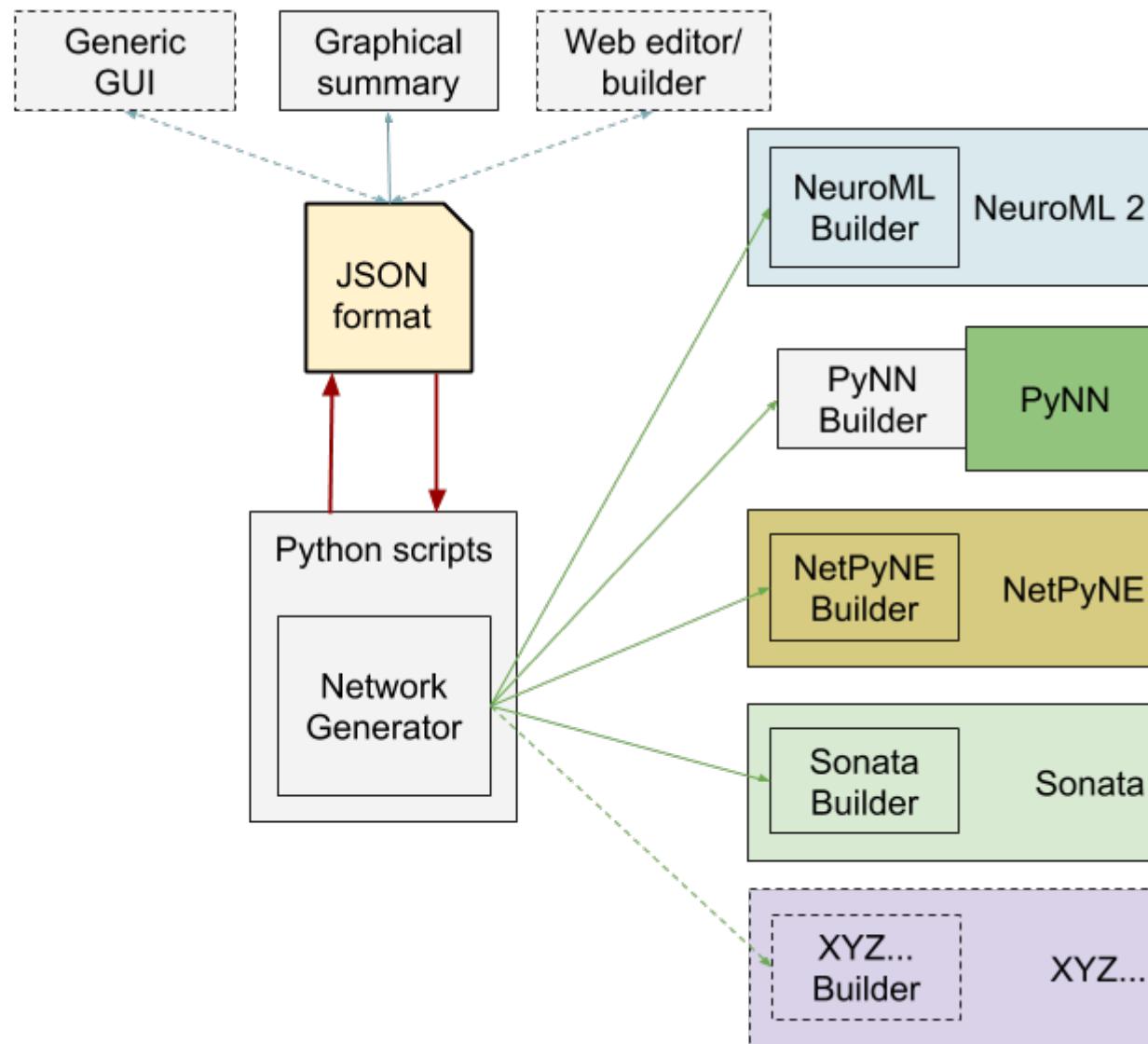
Solution: NeuroMLlite...



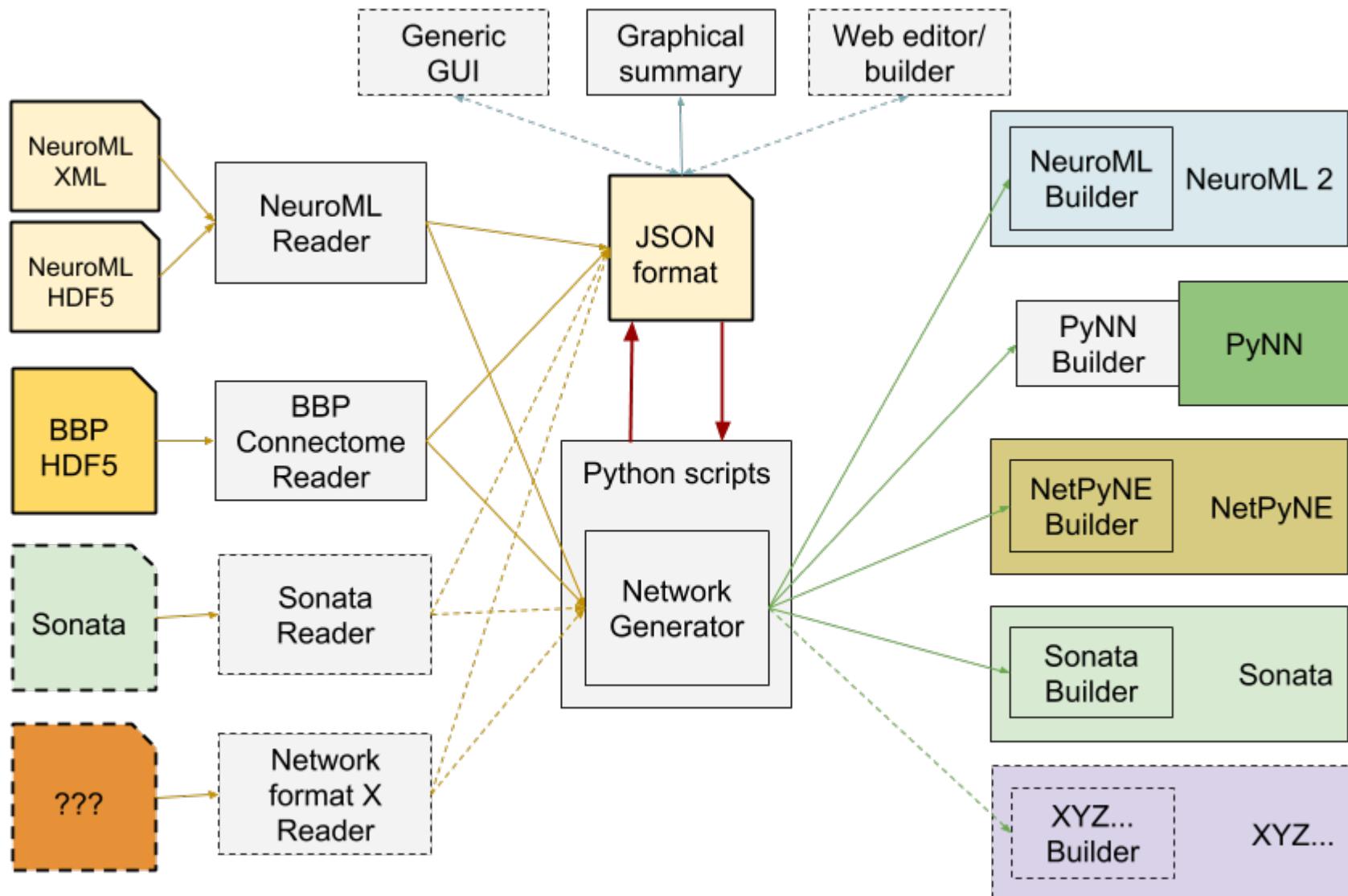
Solution: NeuroMLlite...



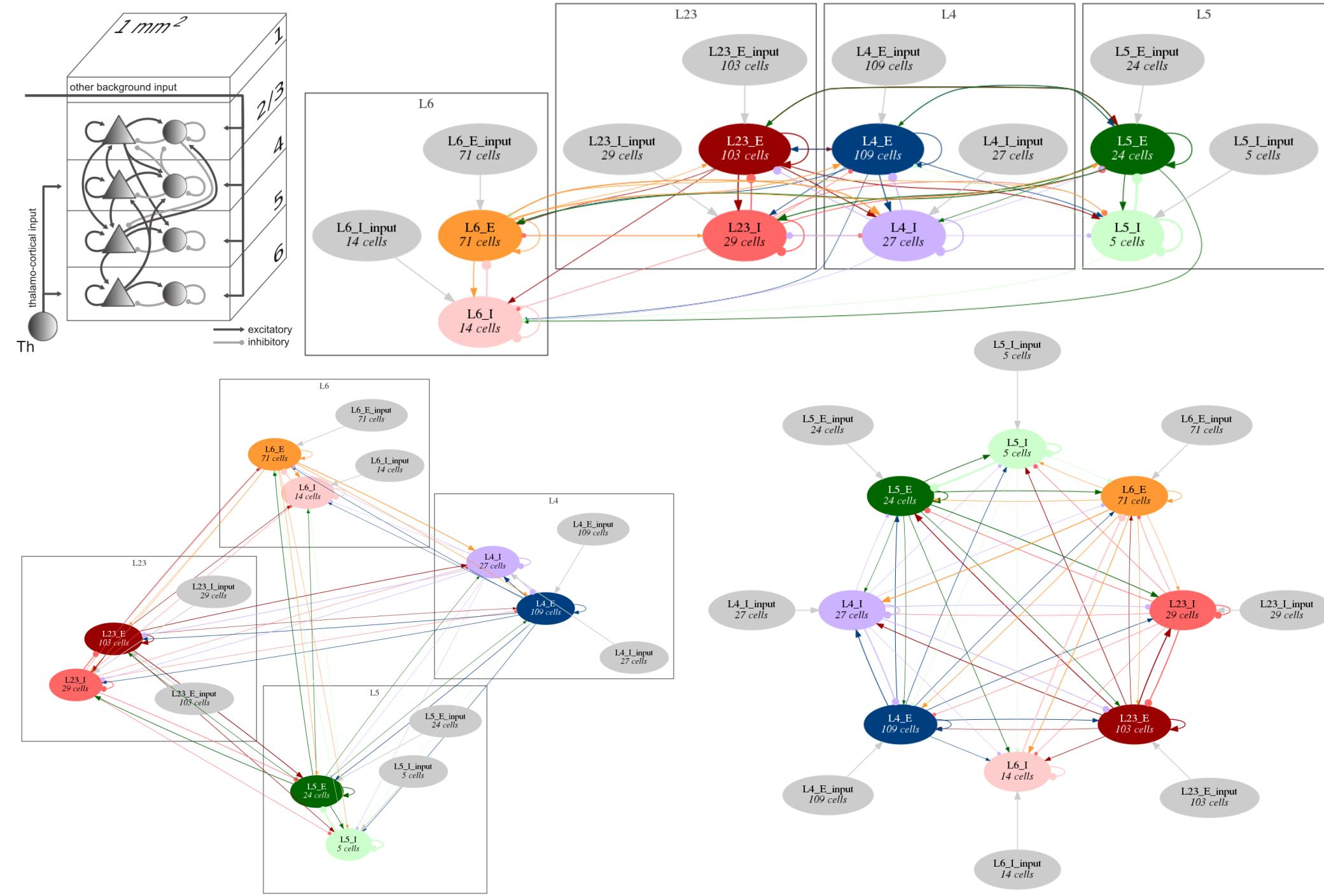
Solution: NeuroMLlite...



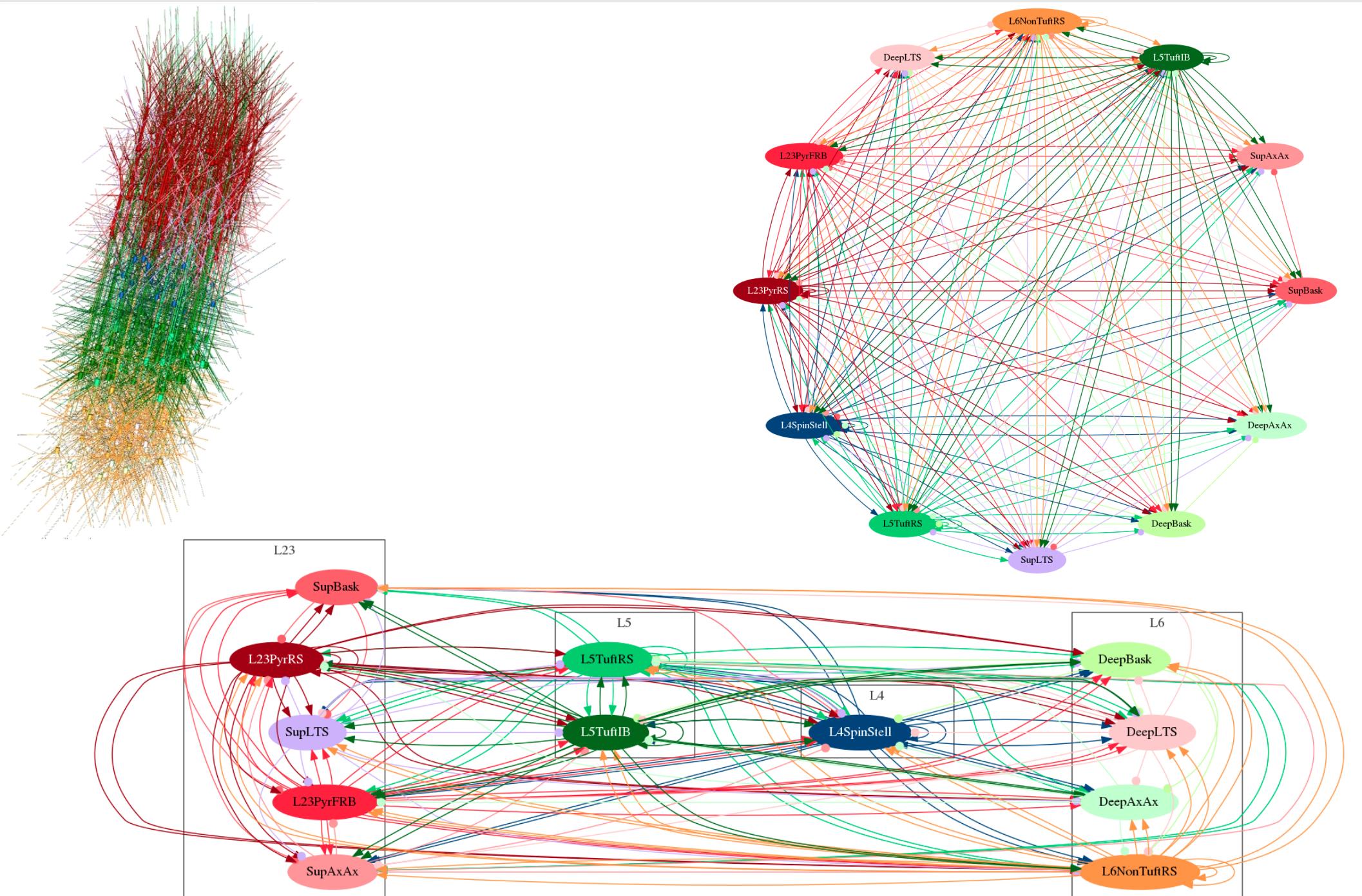
Solution: NeuroMLlite...



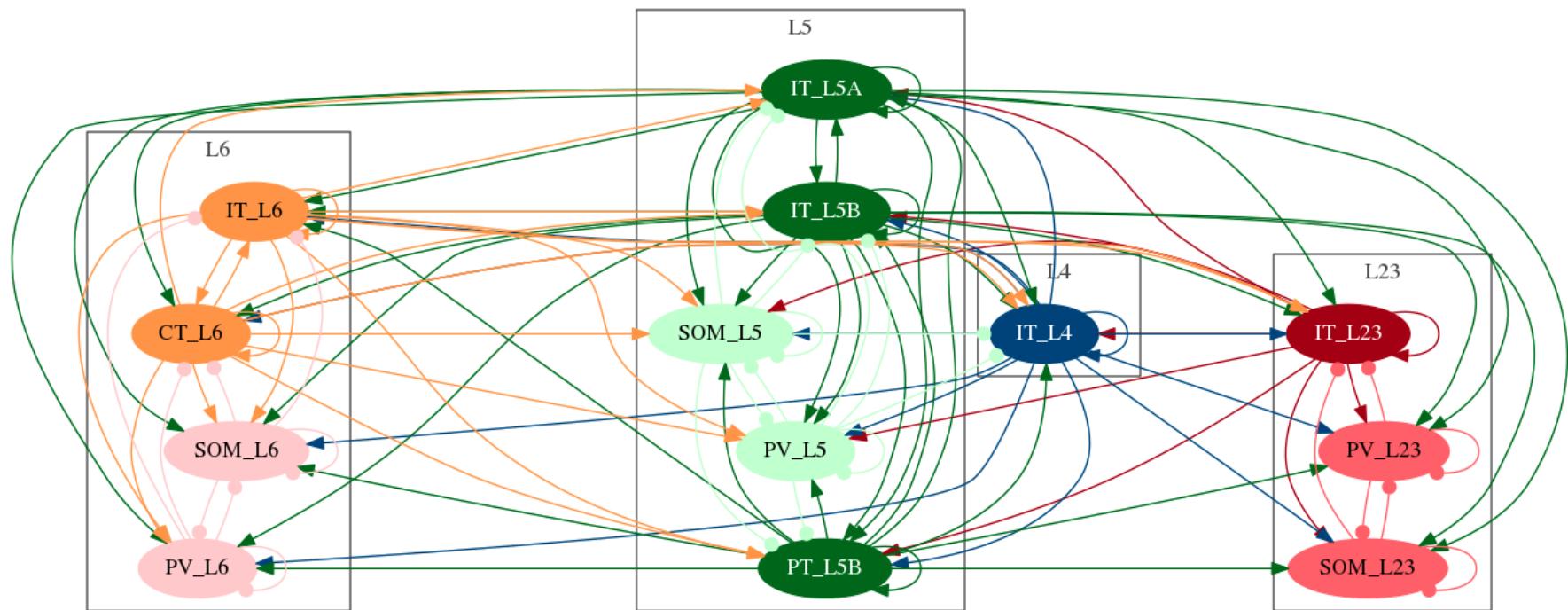
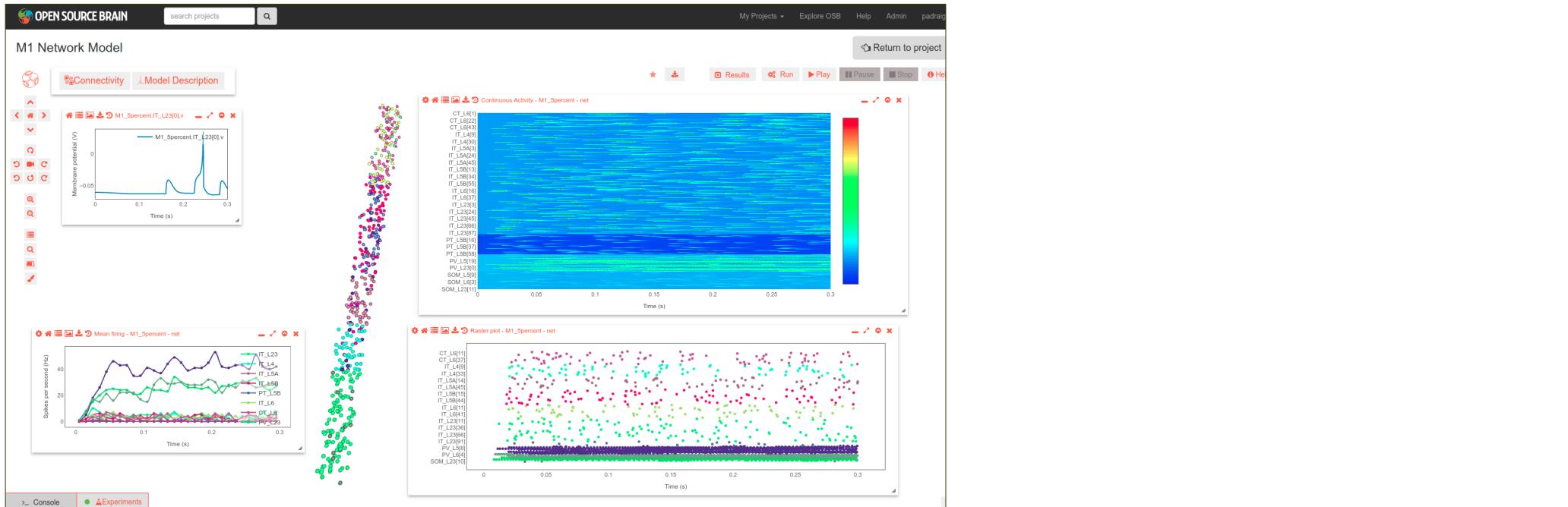
NeuroMLlite example: Potjans and Diesmann 2014



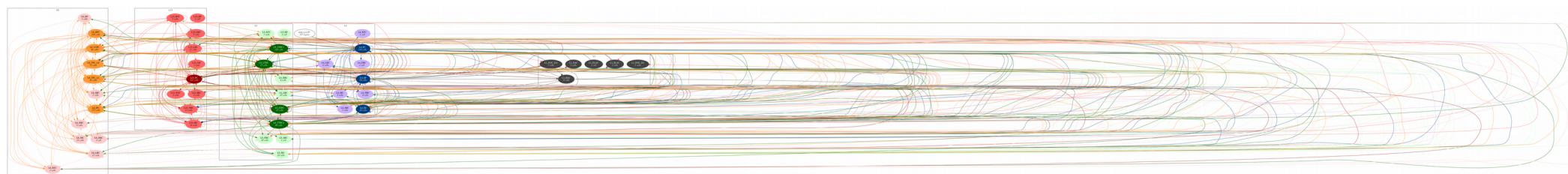
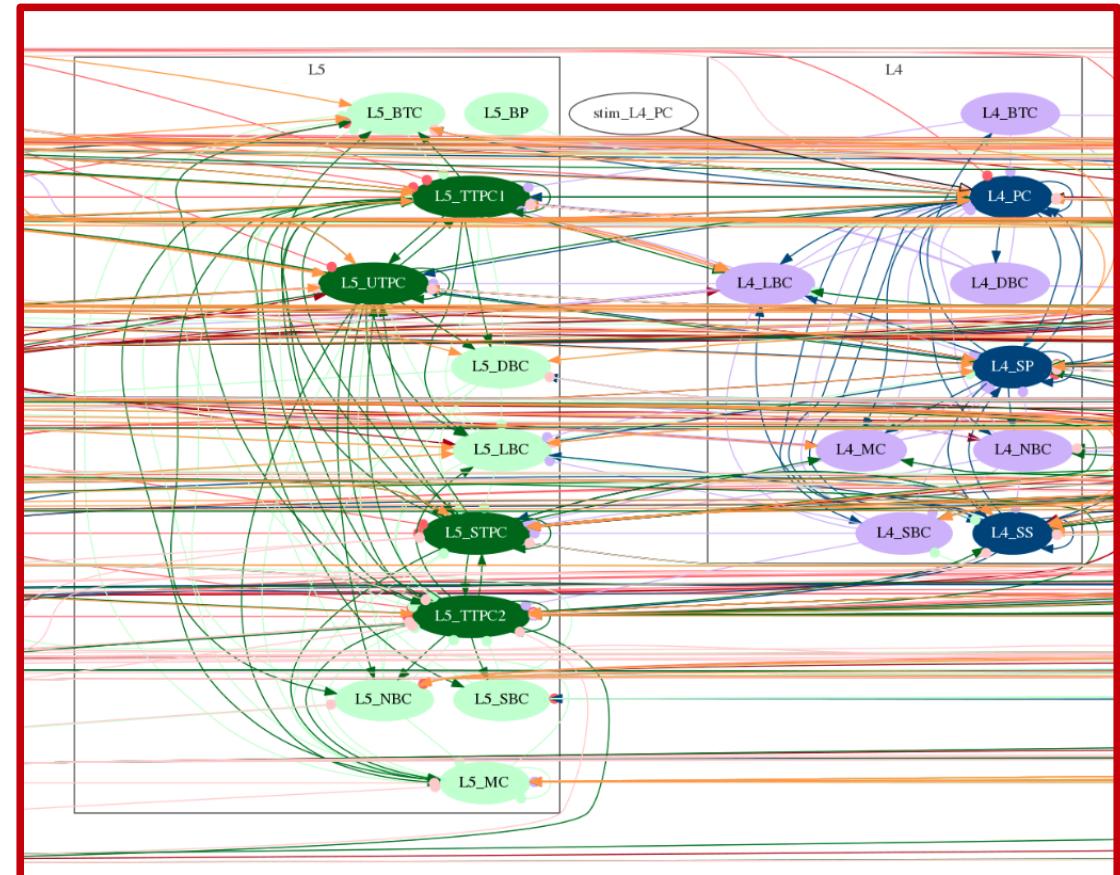
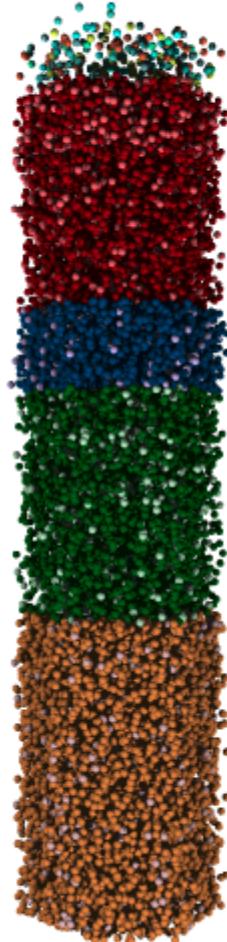
NeuroMLlite example: Traub et al. 2005



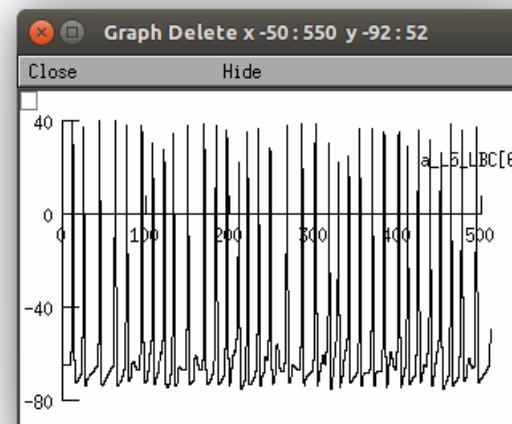
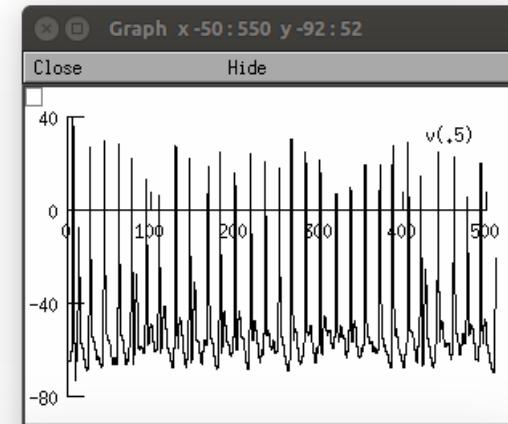
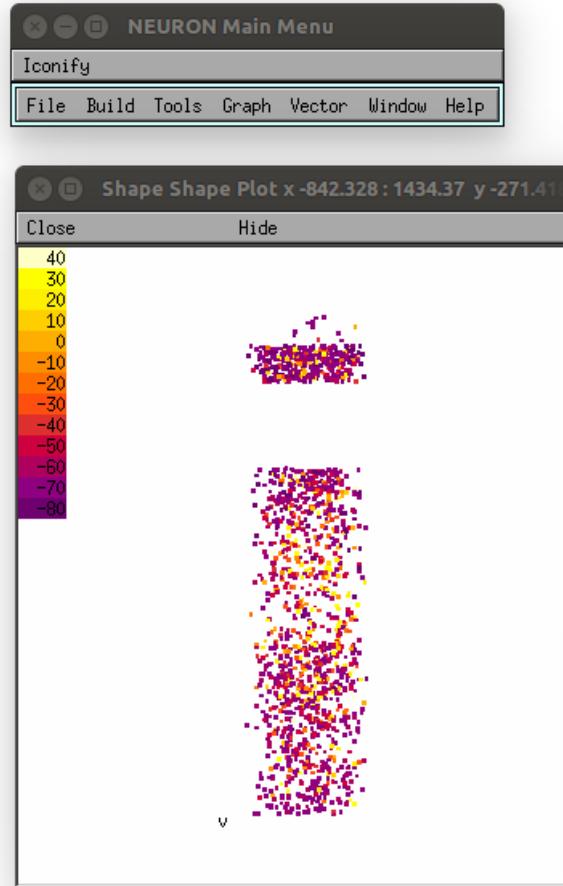
NeuroMLlite example: Dura-Bernal et al. M1 network



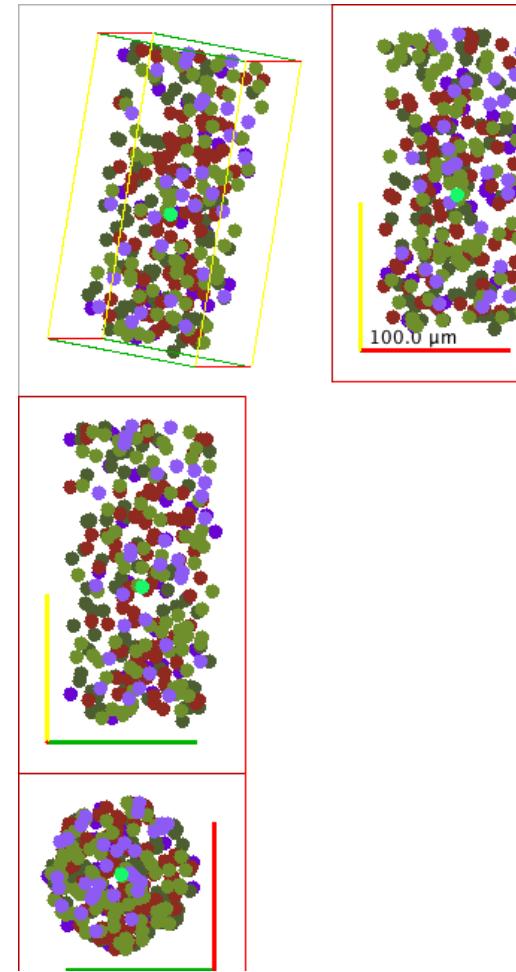
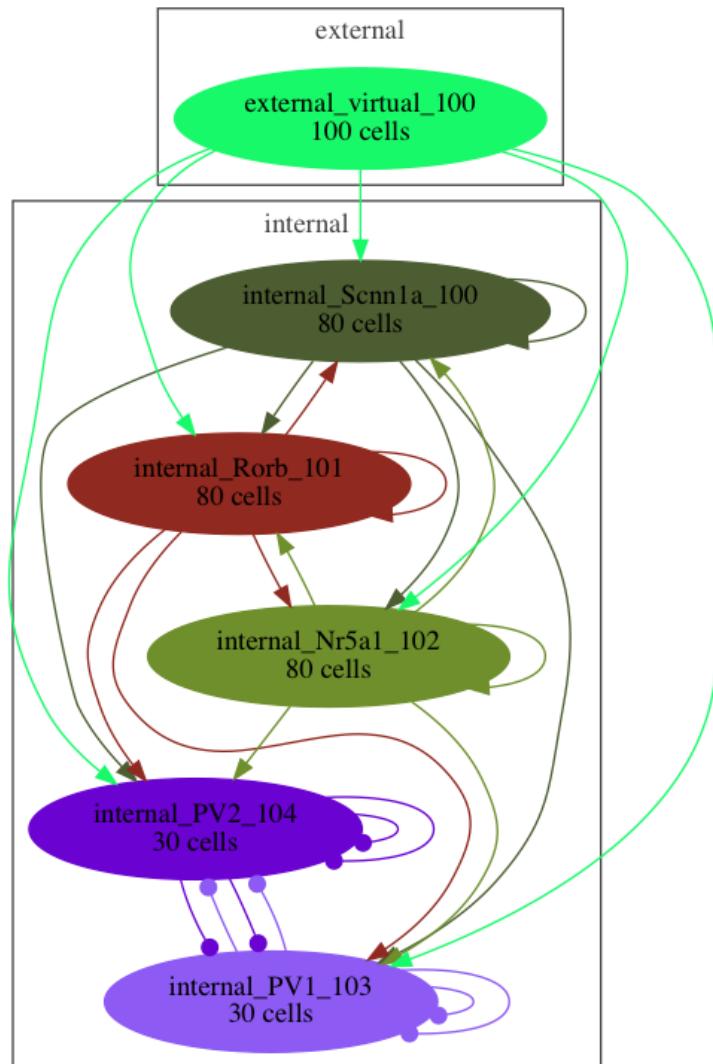
NeuroMLlite example: Blue Brain Project column



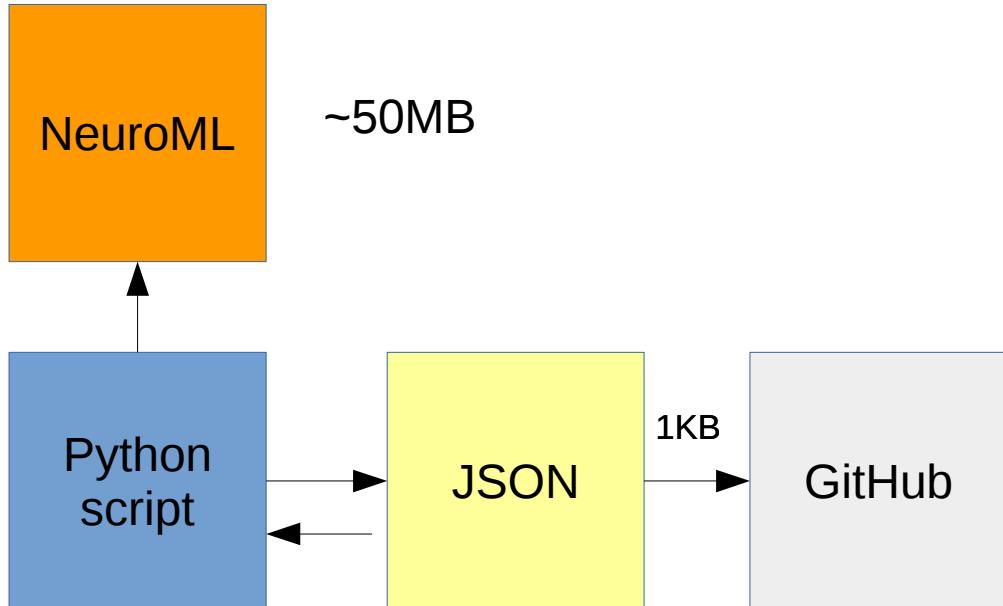
NeuroMLlite example: Blue Brain Project column



NeuroMLlite example: Sonata import

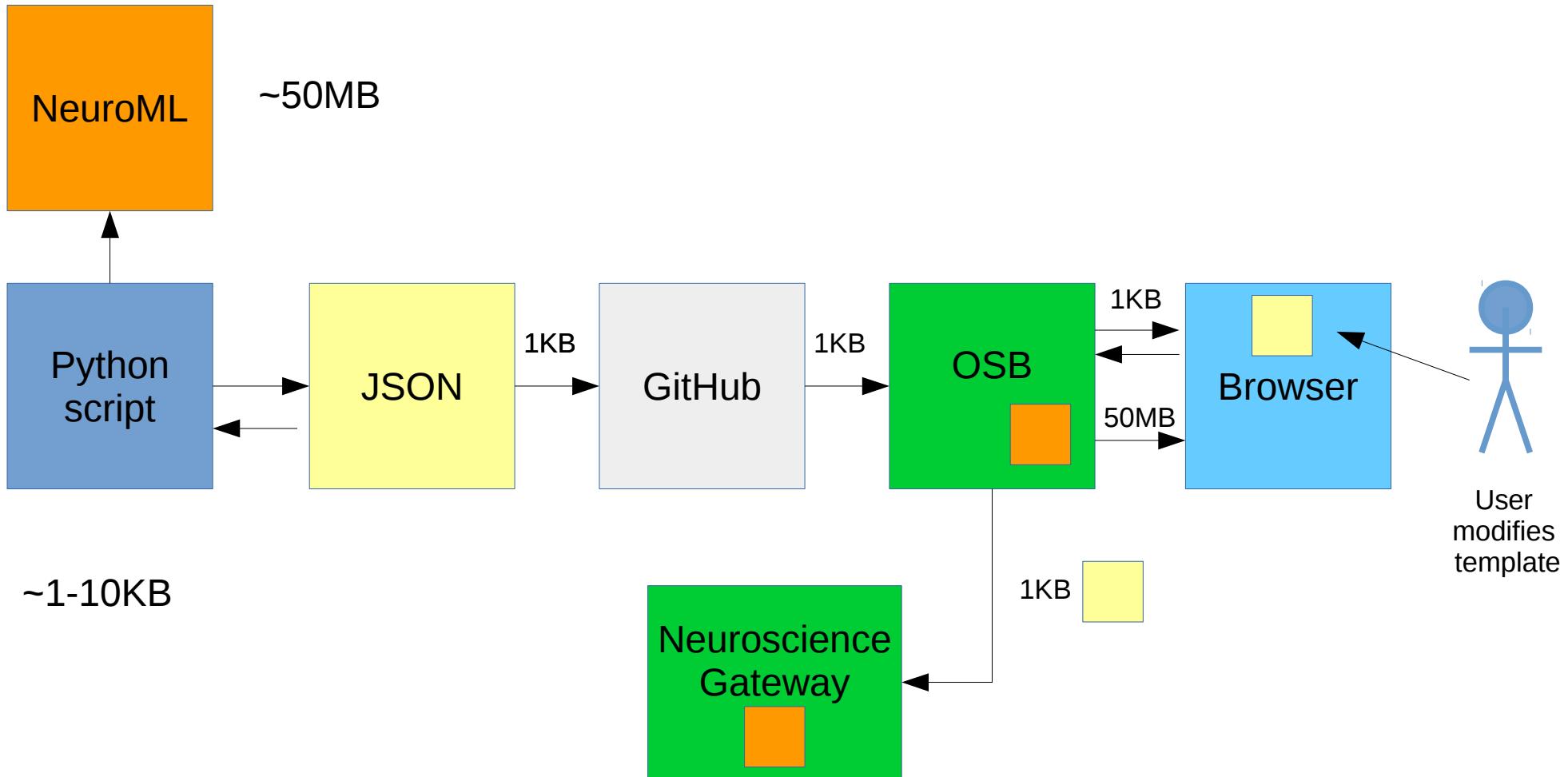


Improved workflow on OSB with NeuroMLlite



~1-10KB

Improved workflow on OSB with NeuroMLlite



NetPyNE like interface on OSB?

DEFINE YOUR NETWORK EXPLORE YOUR NETWORK SIMULATE AND ANALYSE

Populations
Define here the populations of your network

+ Population0 Population1

General Spatial Distribution Cell List

X-axis range (um)
Normalized

Min x-axis 0 Max x-axis 1

Y-axis range (um)
Normalized

Min y-axis 0 Max y-axis 1

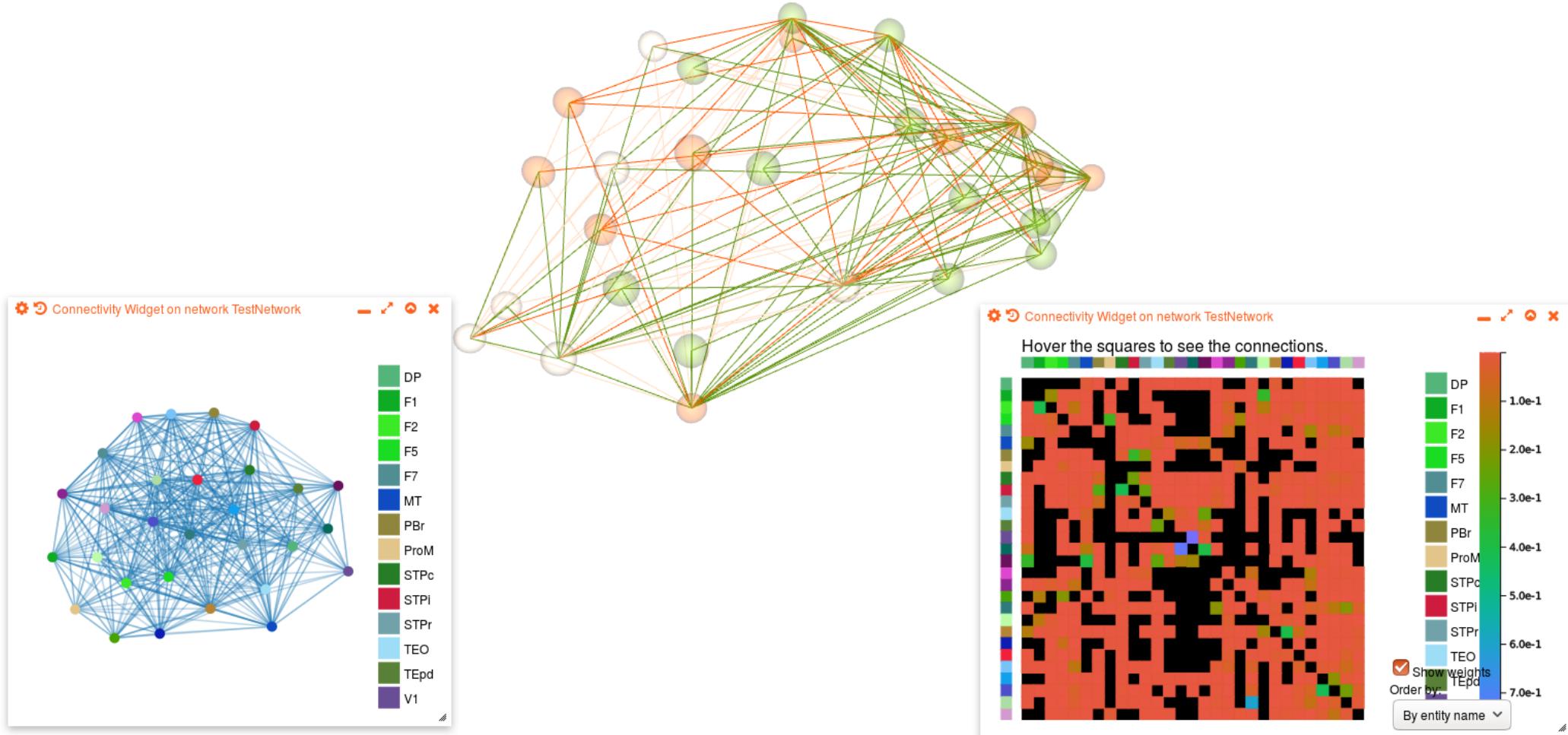
Z-axis range (um)
Normalized

Min z-axis 0 Max z-axis 1

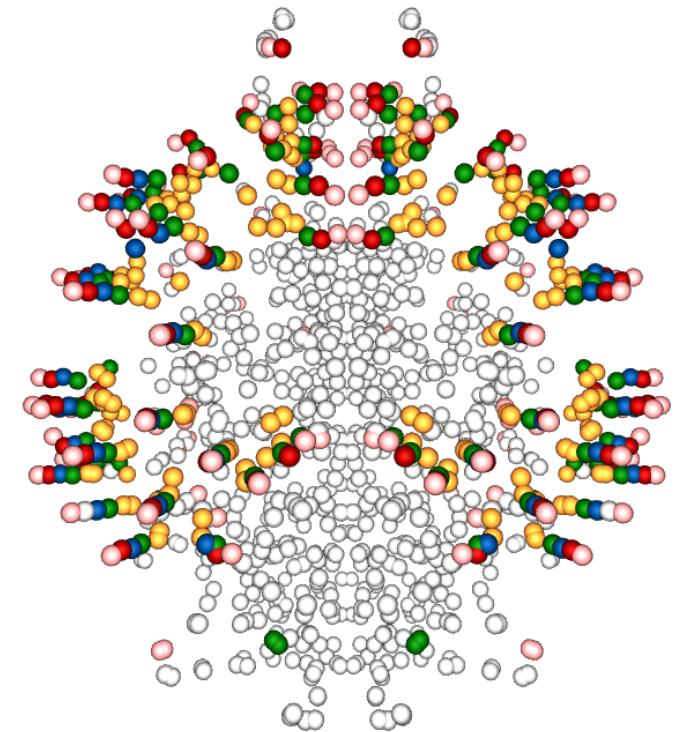
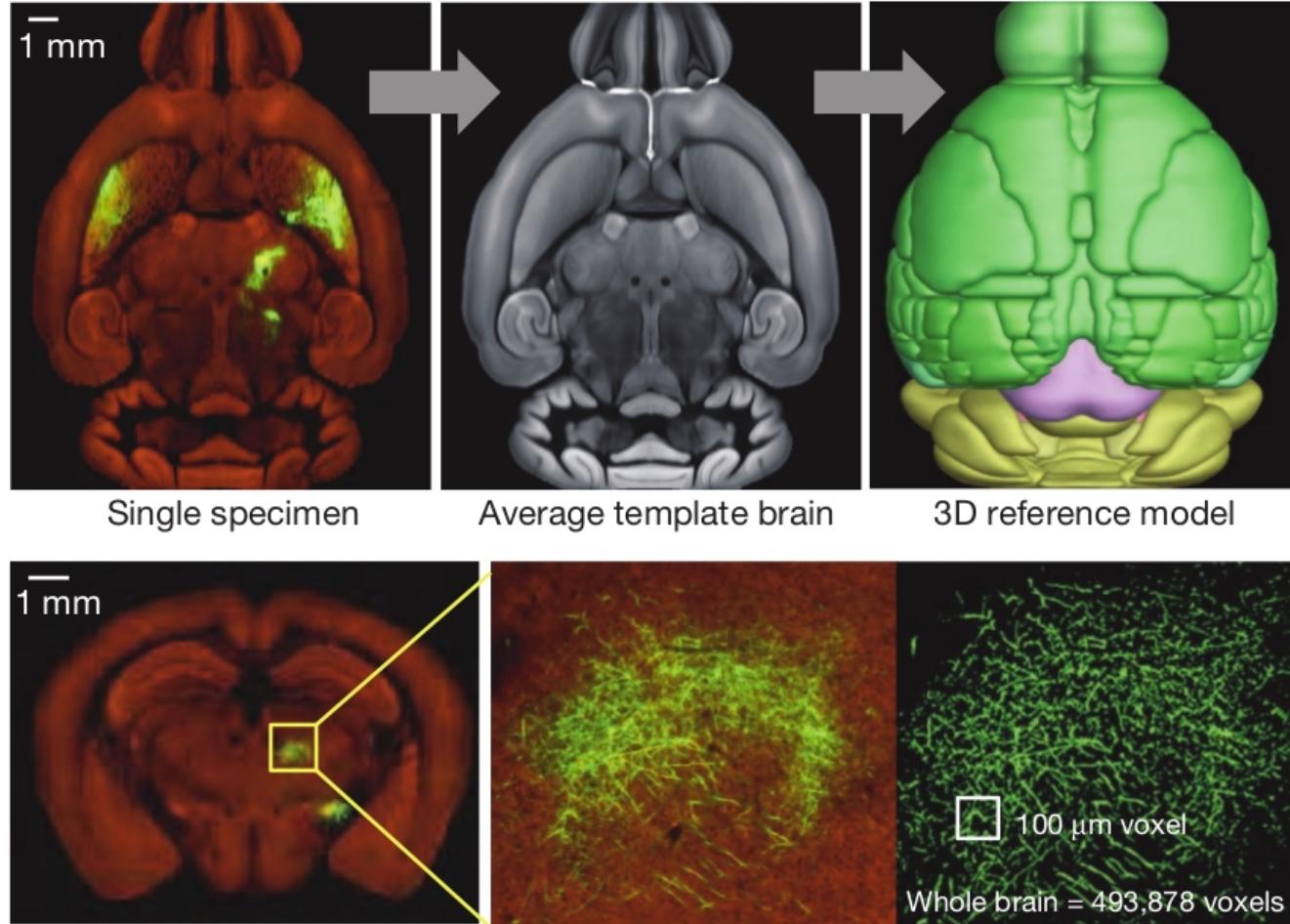
Cell rules
Define here the rules to set the biophysics and morphology of the cells in your network

Synaptic mechanisms
Define here the synaptic mechanisms available in your network

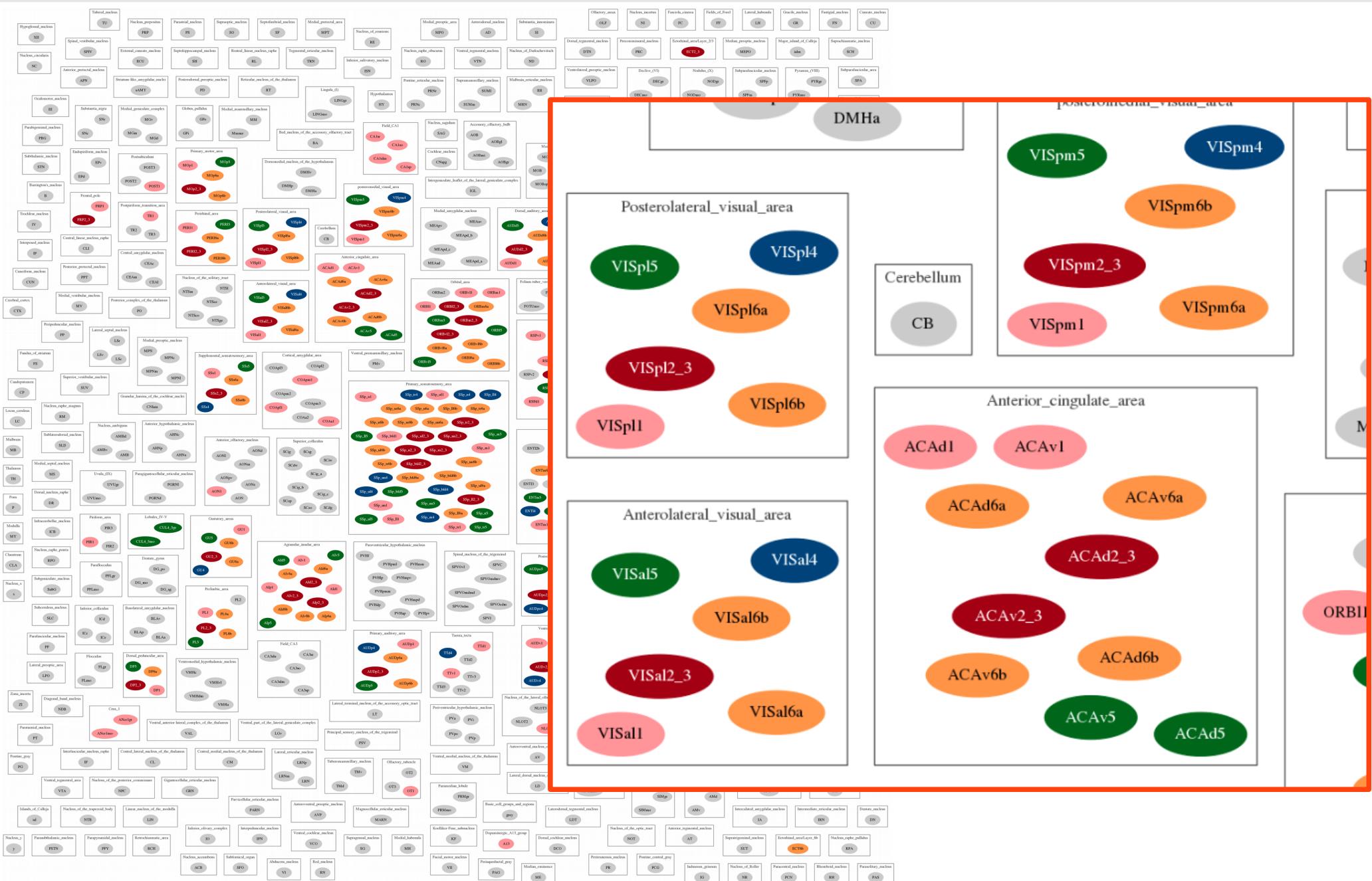
Work in progress: Google Summer of Code



In progress: Allen Institute mesoscale connectome



In progress: Allen Institute mesoscale connectome



INCF SIG on Standardised Representations of Network Structures

This SIG deals with the various tools and formats for creating and sharing representations of biological neuronal networks, and will work towards ensuring these are as interoperable and usable as possible for computational neuroscientists.

Contact info

Email: p.gleeson@uc.ac.uk

Current members

- Anton Arkhipov, Allen Institute, USA
- Tom Close, Monash University, Australia
- Sharon Crook, Arizona State University, USA
- Kael Dai, Allen Institute, USA
- Andrew Davison, UNIC, CNRS, France
- Lia Domide, Codemart, Romania & Aix-Marseille Université, France
- Salvador Durá-Bernal, SUNY Downstate Medical Center, USA

Formats for simulation setup (dt, duration, recording etc.)

Formats for low level (lists of positions/ connections, etc) specifications

Formats for high level declarative specifications of networks

Packages for procedural generation of networks

Formats for expressing (raw) experimental data

NeuroMLlite Simulation

NetPyNE simConfig

Sonata/BMTK

NeuroML (XML & H5)

Sonata

NetPyNE data model

NeuroMLlite JSON

PyNN

NeuroMLlite API

libNeuroML

NetPyNE API

BMTK

Brain connectivity formats -TVB?

SWC

Rate/
population
based

I&F/abstract
neuron models

Single
compartment
HH based

Multi-
compartmental