

# **Standards and Tools in Neuroscience**

A summary of the Open Source Brain workshop,  
September 2019

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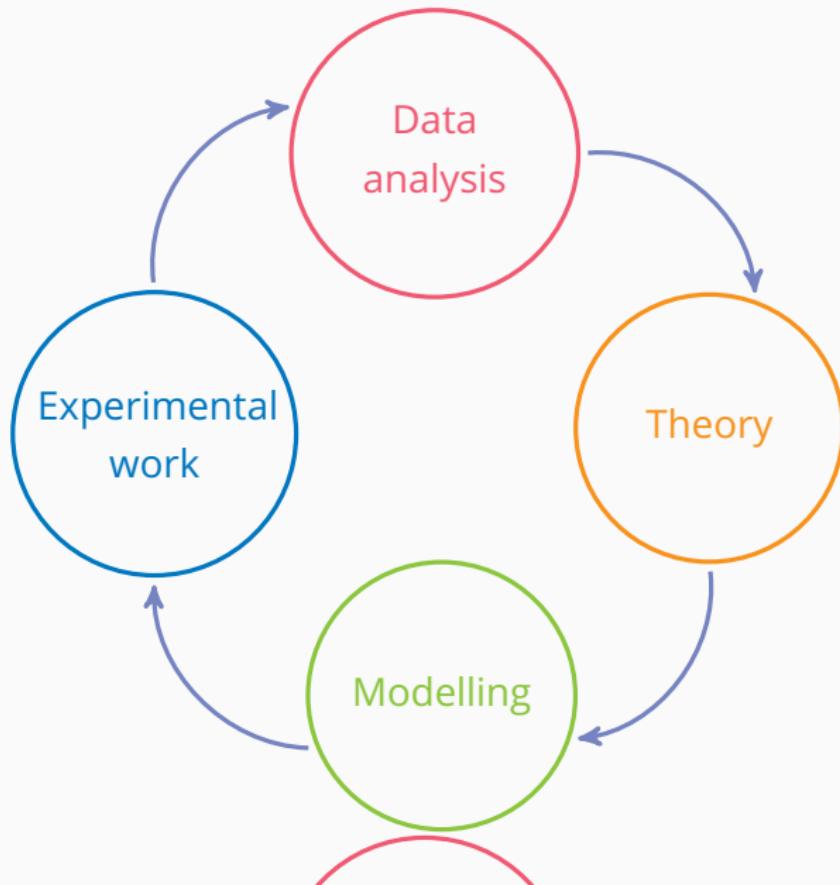
Ankur Sinha

Ph.D. candidate: UH Biocomputation Group, UK,  
Volunteer: Fedora Project.

## The problem statement

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# Neuroscience is complex, and massive



Free/Open science:

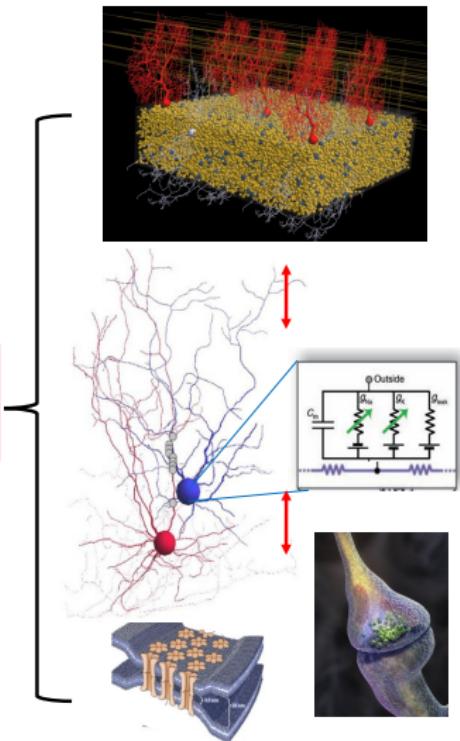
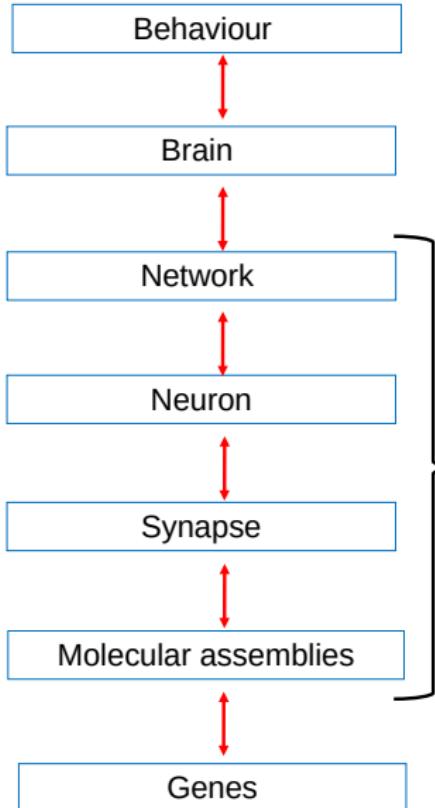
Scientific material should be easily, openly **accessible to all**.

# Experimental neuroscience data is heterogeneous, multiscale and analysis is complex

Anatomy	Electrophysiology	Functional imaging	Behaviour
Receptor Immunohistochemistry	Single/ensemble channel recordings	Synaptic imaging	Restricted task
Neuronal morphologies	Whole cell patch-clamp recordings	Single cell imaging	Freely moving
Brain mapping & Connectomes	Multielectrode array	Population imaging	Natural environment

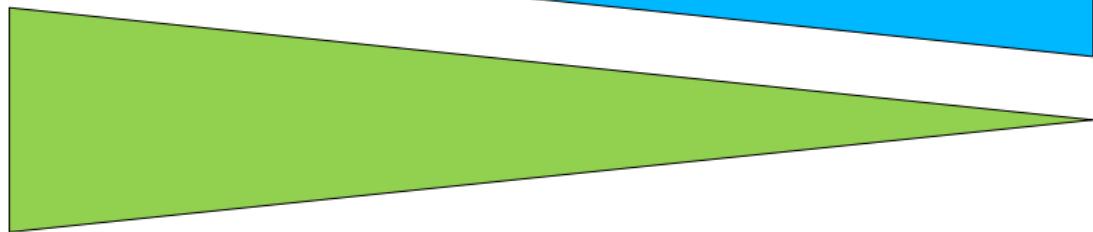
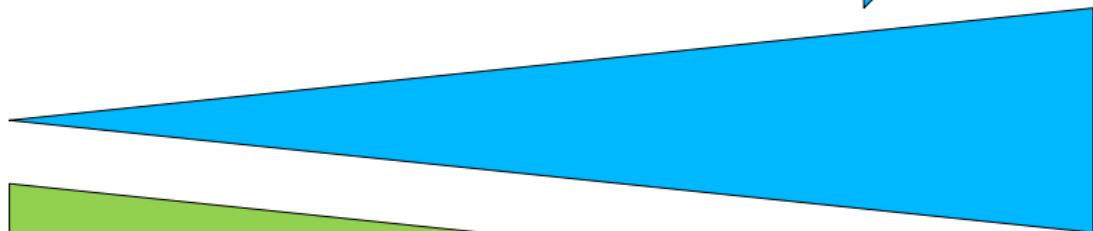
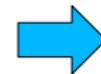
How can we structure neuroscience data to facilitate reuse?

# Models of brain function span multiple spatial scales



# A scaling problem

Model complexity



Transparency, accessibility, reproducibility,  
reuse.....and utility as a scientific tool

## Standards: the common tongue

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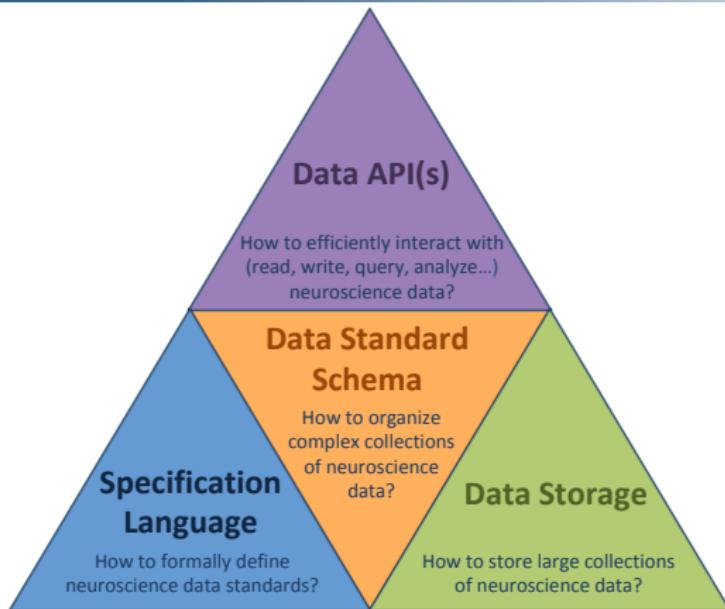
# NWB:N 2.0: An Ecosystem for Neurophysiology Data Standardization

Oliver Rübel

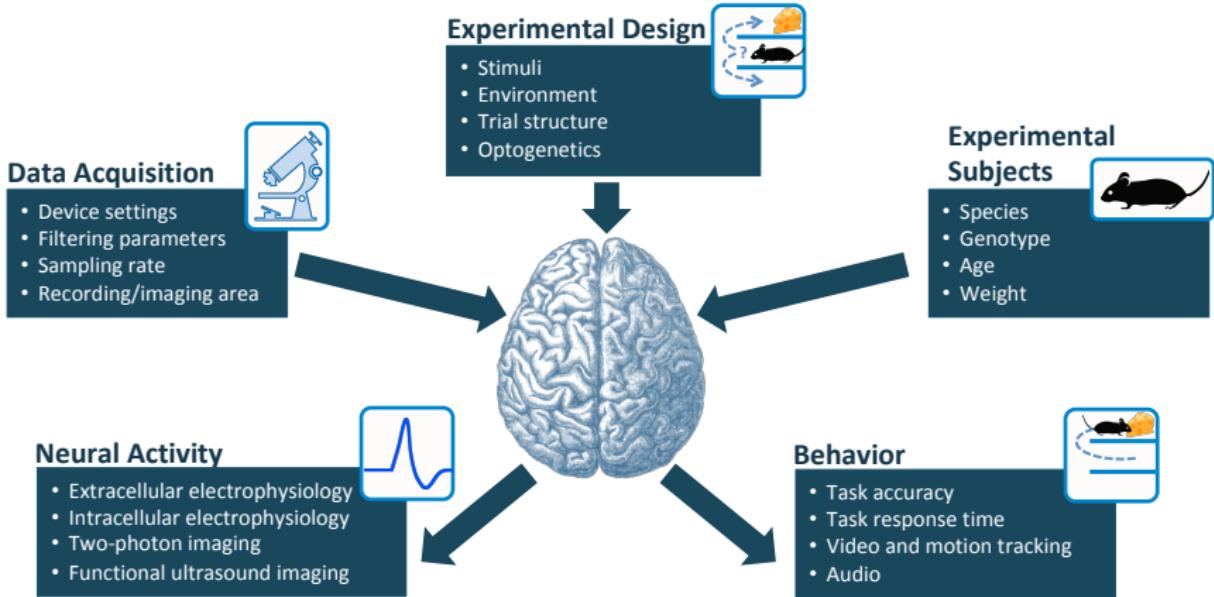
Computational Research Division, Lawrence Berkeley National Laboratory

Open Source Brain Workshop  
Alghero, Sardinia  
September 10, 2019

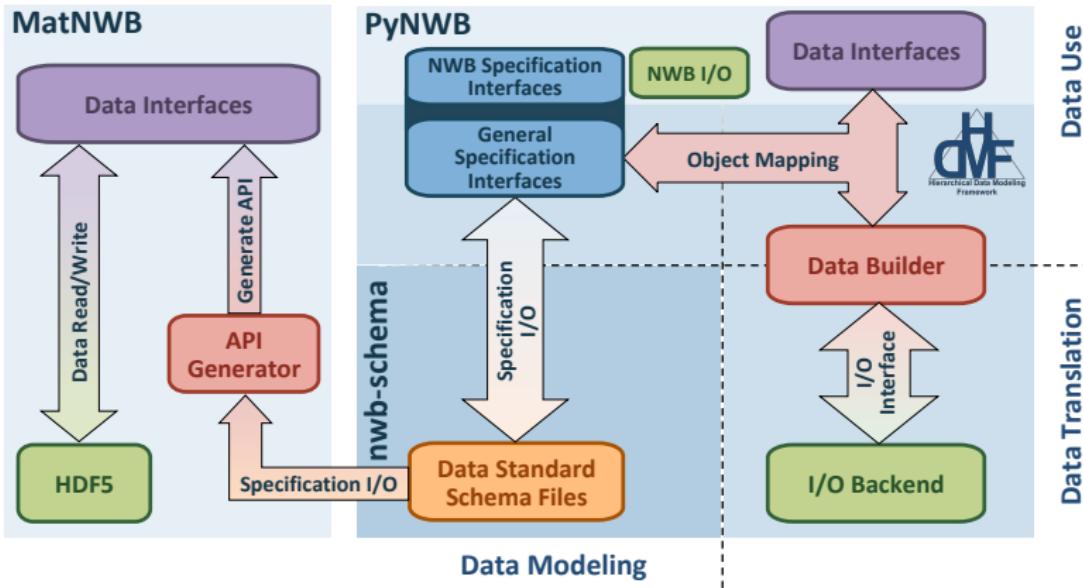
# Main components of the NWB:N ecosystem



# NWB:N supports complex collections of data required for understanding the brain

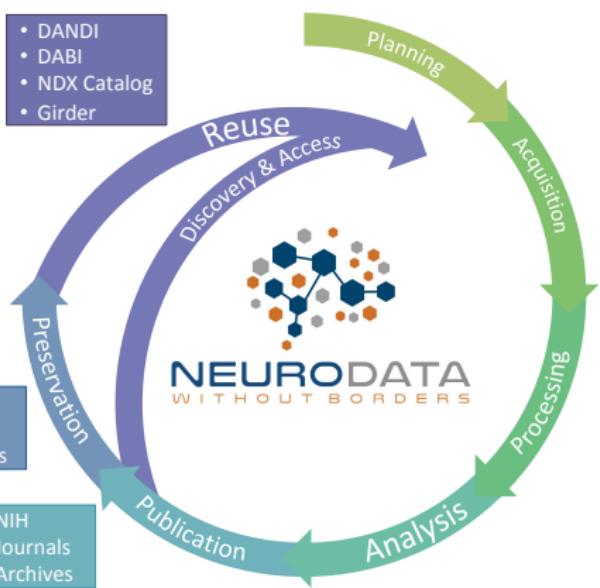


# Advanced software architecture for data standardization



# Neurophysiology Tools

NWB:N technologies at the heart of the neurodata lifecycle and applications



Electrophysiology	Optical Physiology
DataJoint, NWB Tutorials	MiniScope ScanImage
OpenEphys, Plexon, Neuralynx, Intan, TDT, SpikeGadgets, SpikeGLX	
PyNWB, MatNWB, HDMF, HDF5 tools/libs	
SpikeInterfaces MountainSort, KiloSort, npzsorting	NoRMCorre CNMF-E CELLMax EXTRACT
BrainStorm WaveClust, UltraMegaSort2000, KiloSort Kluster	
NWB-Explorer (OpenSourceBrain) NWB-JupyterWidgets	
BrainStorm, RAVE, Neo, SpikeWidgets, EcogVis, ephys-viz, ...	CalmAn

Reference herein to any specific product, process, or service does not constitute or imply its endorsement, recommendation, or favoring by NWB or LBNL.



# MetaCell

SOFTWARE FOR NEUROSCIENCE

## NWB Explorer

Open Source Brain Meeting

Alghero, Italy

10th September 2019



OPEN SOURCE BRAIN



OpenWorm



wellcome

NWB Explorer

Not Secure nwbeplorer.opensourcebrain.org/user/fdb1ef05-eaa3-486a-810f-eb483b310e6c/groppo

# Welcome to NWB Explorer<sup>beta</sup>

Visualise and understand your neurophysiology data

What file do you wish to load?

Paste a URL pointing to an NWB file

Load NWB file

Don't have a file to load?

Pick a sample and get started!

Simple time series

Ferguson et al. 2016 2 3 4 5

Triplett et al. 2018

Lantyer et al. 2018

Brought to you by OPEN SOURCE BRAIN MetaCell

Supported by



# NWB EXPLORER

DEMO

Try it out at

<https://nwbexplorer.opensourcebrain.org>



# **Creating cortical models across scales in NeuroML**

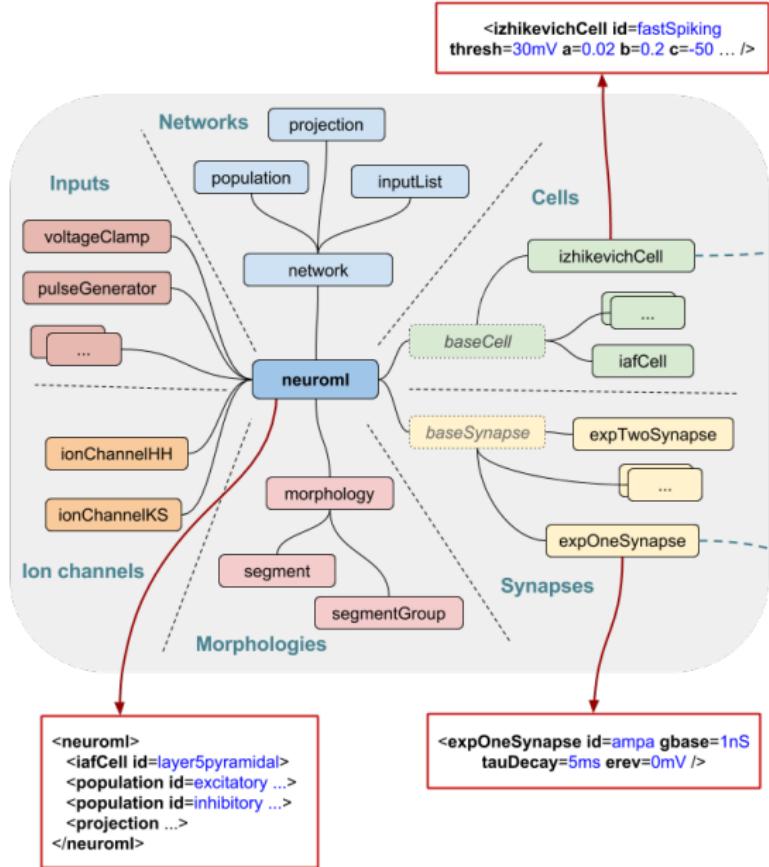


**Open Source Brain workshop 2019**

11th Sept 2019

Padraig Gleeson  
[p.gleeson@ucl.ac.uk](mailto:p.gleeson@ucl.ac.uk)  
University College London

## NeuroML 2



## LEMS

### Standard NeuroML 2 ComponentType definitions

#### Cells.xml

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

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

#### Synapses.xml

ComponentType: **expOneSynapse**  
Parameters: **gbase, tauDecay, erev**

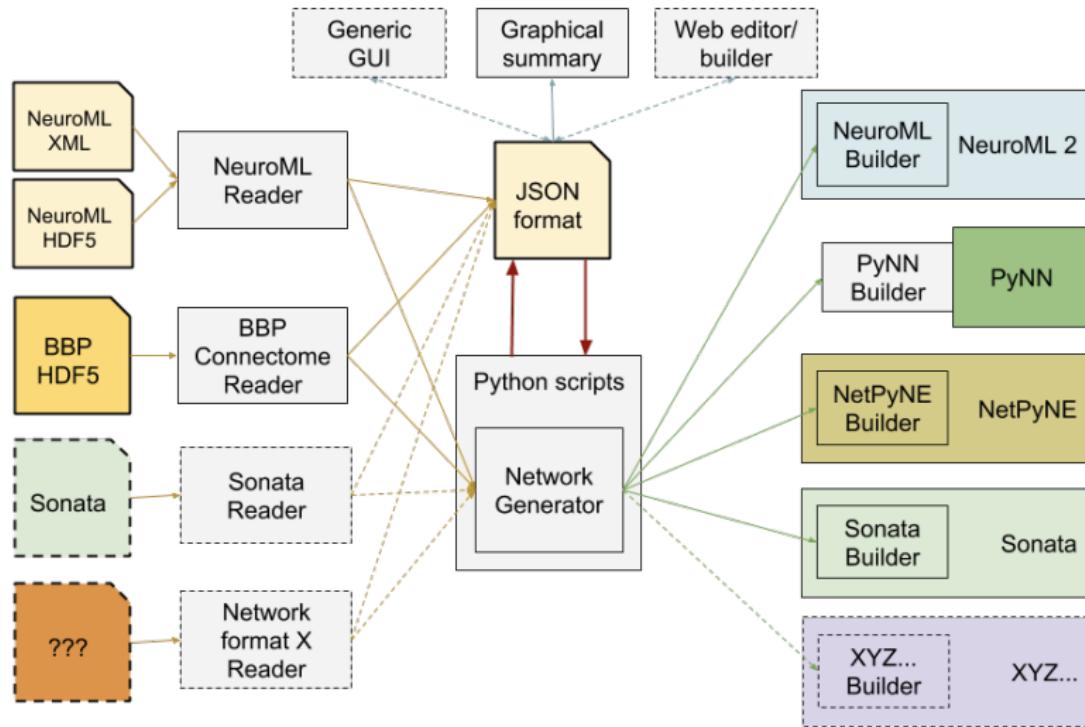
**Dynamics**  
StateVariables: **g**  
TimeDerivatives:  
 $dg/dt = -g / \tau_{decay}$   
DerivedVariables:  
 $i = g * (erev - v)$   
OnEvents:  
 $g = g + gbase$

#### Networks.xml

#### Inputs.xml

...

...

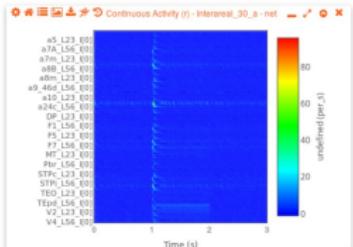
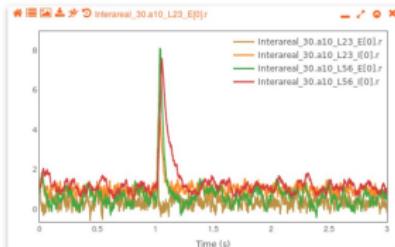
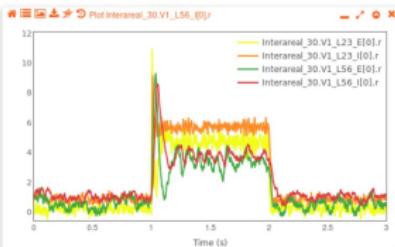
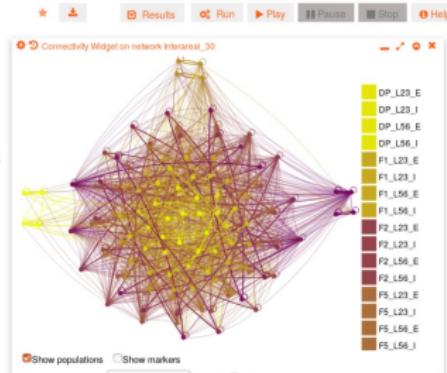
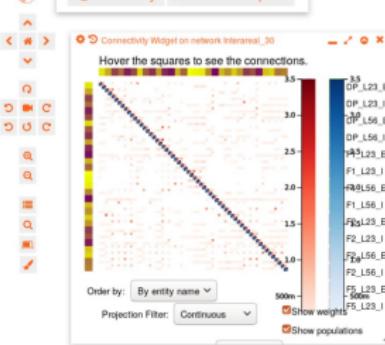


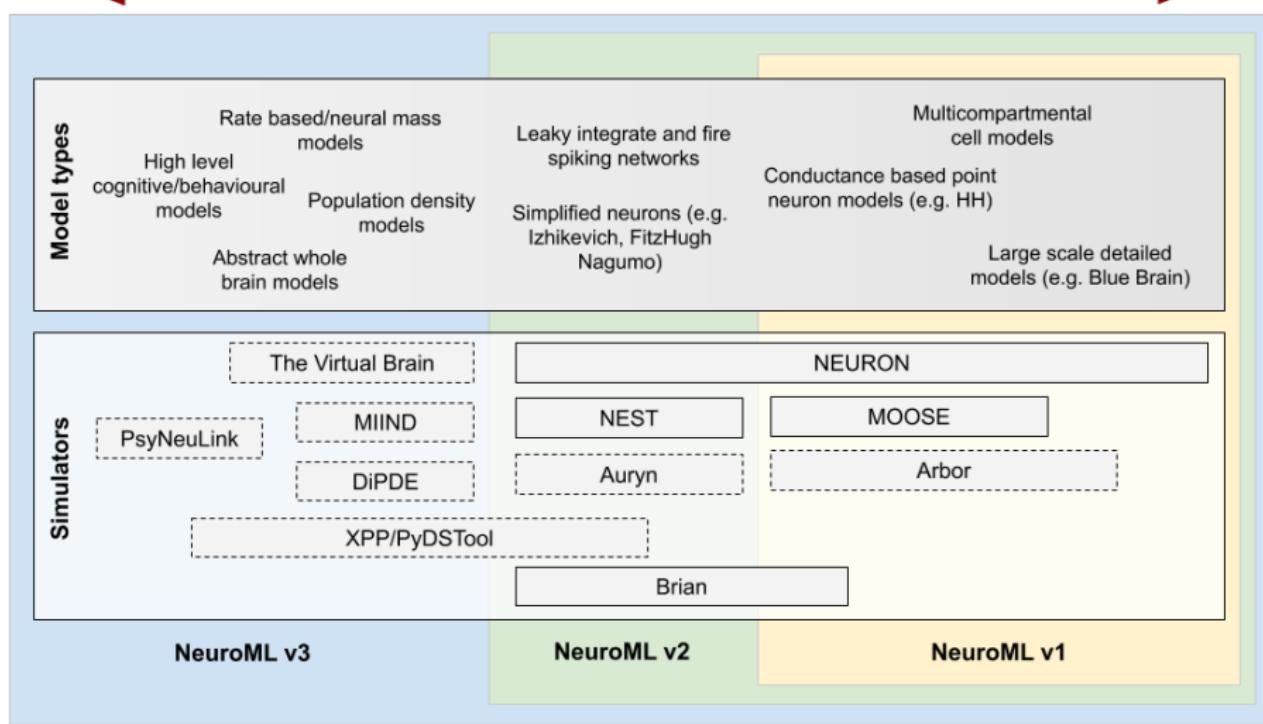
## Large scale laminar cortical network Mejias et al. 2016

Return to project



Connectivity Model Description





# 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:** [p.gleeson@uc.ac.uk](mailto:p.gleeson@uc.ac.uk)

## 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

Viktor Jirsa, Aix-Marseille Université, France

Padraig Gleeson, University College London, UK

Sascha von Albeda, Würzburg Research Centre, Germany

# Converting simulator specific formats to NeuroML2

Open Source Brain Meeting 2019



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Boris Marin

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Universidade Federal do ABC

# Converting NMODL to NeuroML

The Simple™, OSB sponsored way of converting models to NeuroML2



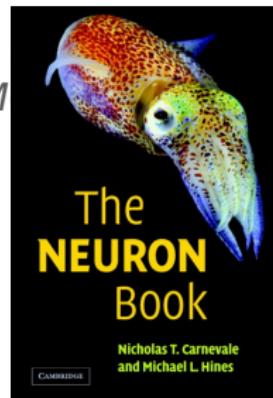
<mailto:p.gleeson@ucl.ac.uk>

# The *NEURON* simulator

## Defining models in *NEURON*

<https://www.neuron.yale.edu/neuron/>

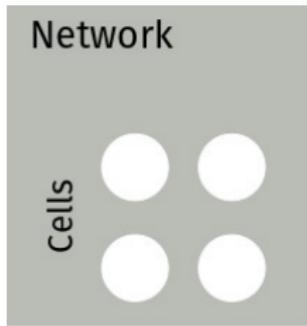
- Cells, Networks: *hoc* language (accessible from Python)
  - morphologies
  - synaptic connections
  - *.hoc* files
- Ion Channels (membrane mechanisms): *NM*
  - *.mod* files



# What is NeuroML, and why should I care?

Why can OSB process any NeuroML2 file?

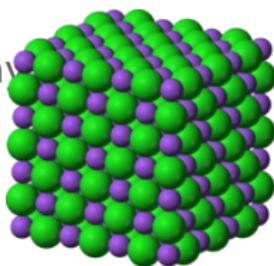
- NML is *structured* (not unlike a *Type System*)



# It is all about **Structure**

## Structure in NeuroML / NMODL

- A *Type System* (composability rules) is what grants NML its superpowers
- nmodl is also powerful, but can be used as a general purpose language
  - VERBATIM blocks
  - many different ways of achieving same goal
  - prone to *unstructuredness*
- OSB could in theory treat nmodl the same way NML...
  - .... if only people stuck to "good practices"!



# Levels of Abstraction

## NeuroML2

```
<ionChannelHH id="kChan" conductance="10pS" species="k">

    <gateHHrates id="n" instances="4">
        <forwardRate type="HHExpLinearRate" rate="0.1per_ms" midpoint="-55mV" scale="10mV"/>
        <reverseRate type="HHExpRate" rate="0.125per_ms" midpoint="-65mV" scale="-80mV"/>
    </gateHHrates>

</ionChannelHH>
```

## NMODL

```
BREAKPOINT {
    SOLVE states METHOD cnexp
    gk = gkbar * n ^ 4
    ik = gk * (v-ek)
}
INITIAL{
    n = alpha(v) / (alpha(v) + beta(v))
}
DERIVATIVE states{
    n' = (1 - n) * alpha(v) - n * beta(v)
}
```

```
FUNCTION alpha(Vm(mV))/(ms){
    LOCAL x
    UNITSOFF
    x = (Vm + 55) / 10
    if(fabs(x) > 1e-6){
        alpha=0.1*x/(1-exp(-x))
    }else{
        alpha=0.1/(1-0.5*x)
    }
    UNITSON
}
```

# Levels of Abstraction

## Declarative vs Imperative

- NeuroML2 operates (at least syntactically) closer to the level of abstraction employed by electrophysiologists
- The gory details exist, but elsewhere: *LEMS*
  - i.e. what to do with  $\alpha$ ,  $\beta$ ; the definition of an *ExpRate*; how all of that is converted to conductances/currents...
- But we seldom need (want!) to interact with that level  
(look under the hood)

```
<Network ...>
  <Cell ...>
    <Channel ...>
      <Gate ...>
        <Rate ...>
```

```
SOLVE{...} METHOD euler
...
DERIVATIVE {...}
...
FUNCTION trap(v){...}
```

# Levels of Abstraction

## NetPyNE: structured network specification

i) 

```
popParams['EXC_L2'] = {
    'cellType': 'PYR',
    'cellModel': 'simple',
    'yRange': [100, 400],
    'numCells': 50}
```

ii) 

```
popParams['EXC_L5'] = {
    'cellType': 'PYR',
    'cellModel': 'complex',
    'yRange': [700, 1000],
    'density': 80e3}
```

iii) 

```
cellParams['PYR_simple'] = {
    'conds': {'cellType': 'PYR',
              'cellModel': 'simple'},
    'secs': {'soma': {'geom': ('diam': 18, 'L': 18),
                      'mechs': {'hh': {'gnabar': 0.12,
                                      'gkbar': 0.036,
                                      'gI': 0.003,
                                      'el': -70)}},
              ...}}
```

iv) 

```
importCellParams(
label = 'PYR_complex',
conds = {'cellType': 'PYR',
          'cellModel': 'complex'},
fileName = 'L5_pyr_full.hoc',
cellName = 'PYR_L5')
```

vi) 

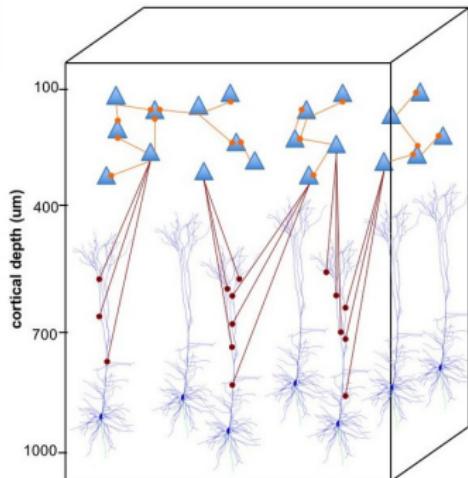
```
synMechParams['AMPA'] = {
    'mod': 'Exp2Syn',
    'taul': 0.8,
    'tau2': 5.3,
    'e': 0}
```

vii) 

```
connParams['L2->E2'] = {
    'preConds': {'y': [100, 400]},
    'postConds': {'pop': 'EXC_L2'},
    'probability': '1*exp(-dist_3D/200)',
    'weight': 0.4,
    'delay': 5,
    'synMech': 'AMPA'}
```

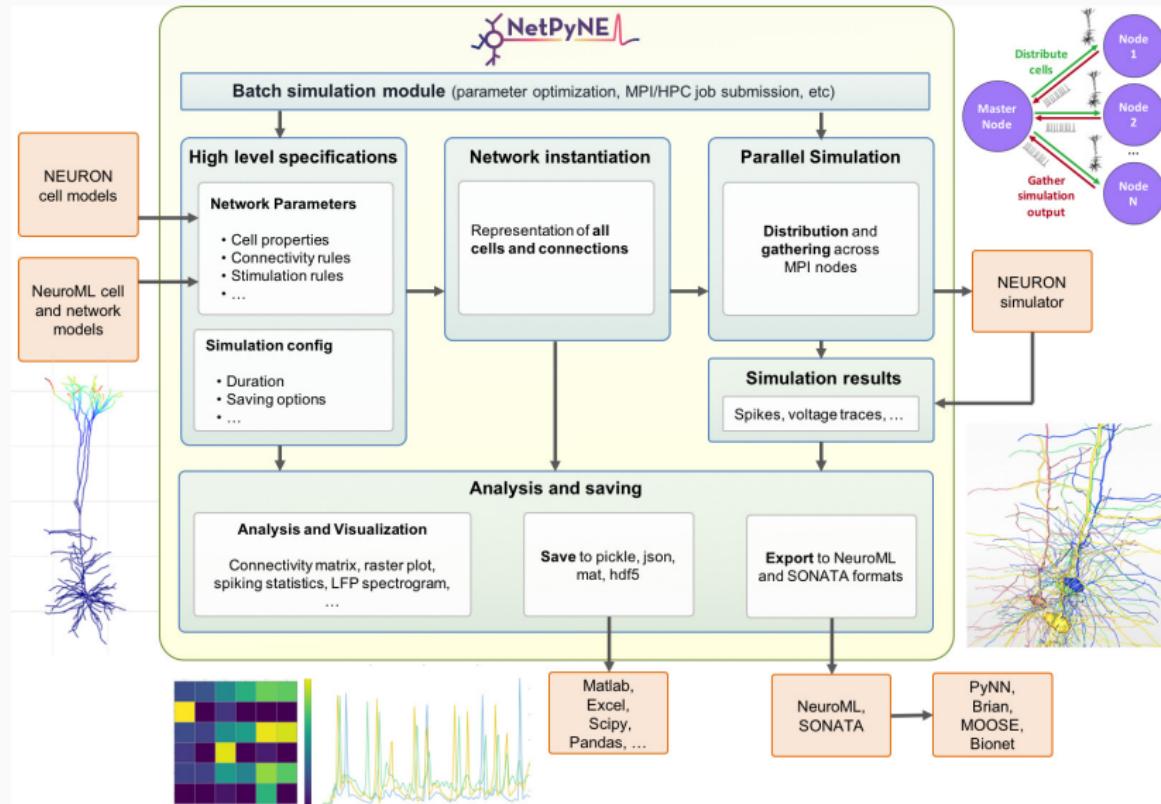
viii) 

```
connParams['E2->L5'] = {
    'preConds': {'pop': 'EXC_L2'},
    'postConds': {'y': [700,1100],
                  'cellModel': 'complex'},
    'convergence': 25,
    'weight': '0.001 * post_ynorm',
    'delay': 'dist_3D/propVelocity',
    'sec': 'allbend',
    'synMech': 'AMPA',
    'synsPerConn': 3}
```

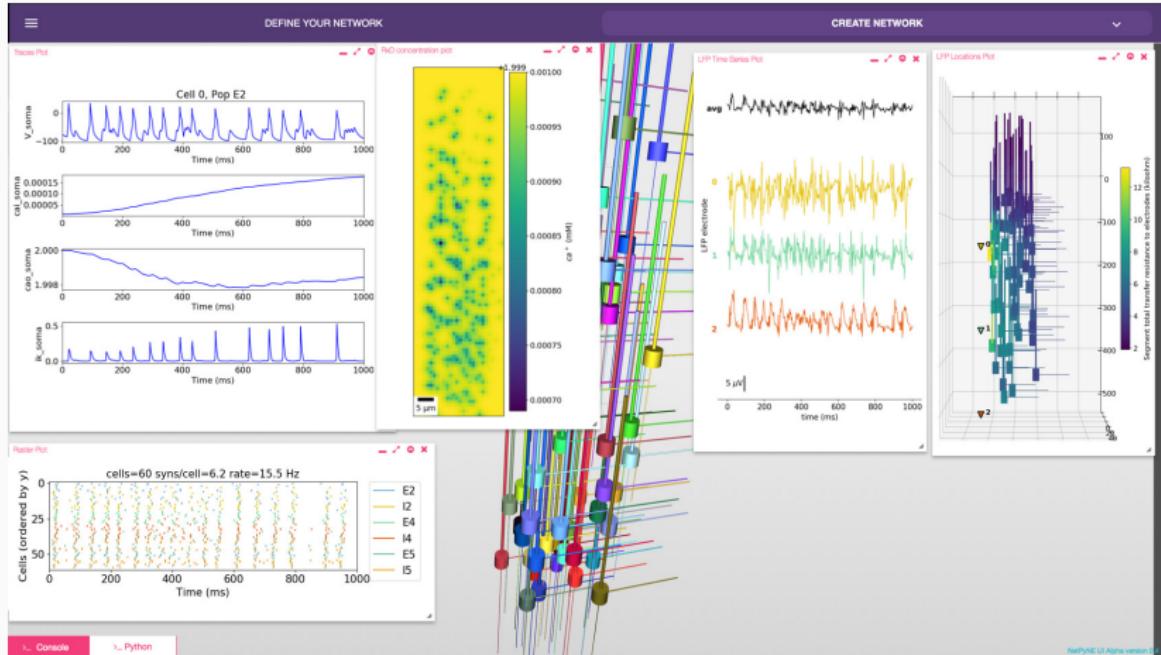


Dura-Bernal, Salvador, et al. "NetPyNE, a tool for data-driven multiscale modeling of brain circuits." Elife 8

# Netpyne workflow



# Netpyne GUI

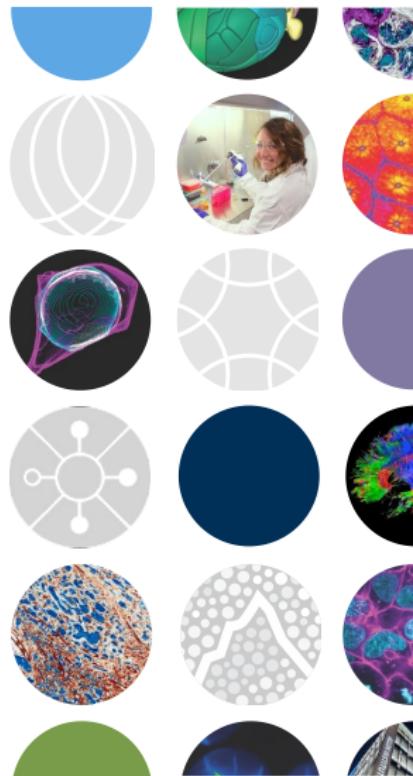




## Large-scale Datasets and Modeling Tools from the Allen Institute for Brain Science

**Yazan N. Billeh**

yazanb@alleninstitute.org





ALLEN INSTITUTE for  
BRAIN SCIENCE



ALLEN INSTITUTE for  
CELL SCIENCE



ALLEN INSTITUTE for  
IMMUNOLOGY



THE PAUL G. ALLEN  
FRONTIERS GROUP



- Established 2003 by Paul G. Allen
- South Lake Union, Seattle, WA
- 500 employees++

hard problems  
complexity  
foundational biology



big science  
team science  
  
open science



data  
knowledge  
tools



# CORE PRINCIPLES

## Team Science

Interdisciplinary teams working towards common goal



## Big Science

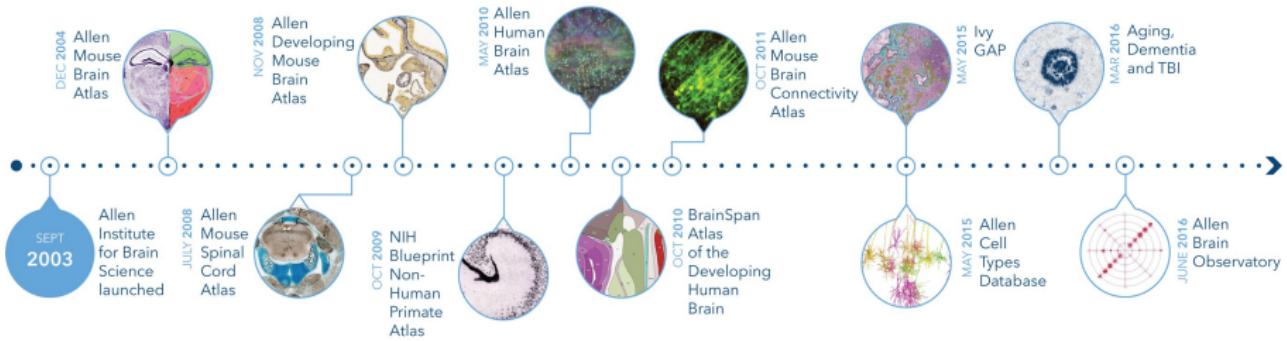
Large-scale projects with robust, massive data

## Open Science

All resources available online at  
[brain-map.org](http://brain-map.org) or [allencell.org](http://allencell.org)

# Allen Institute - Online Public Resources

[www.brain-map.org](http://www.brain-map.org)

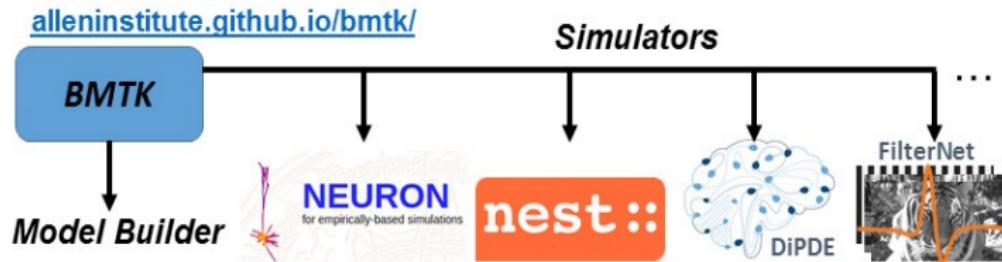


## All data are:

- publicly accessible via API as soon as they pass QC
- freely available without any commercial restrictions

# Our Models and Modeling Software Are Freely Available to the Community

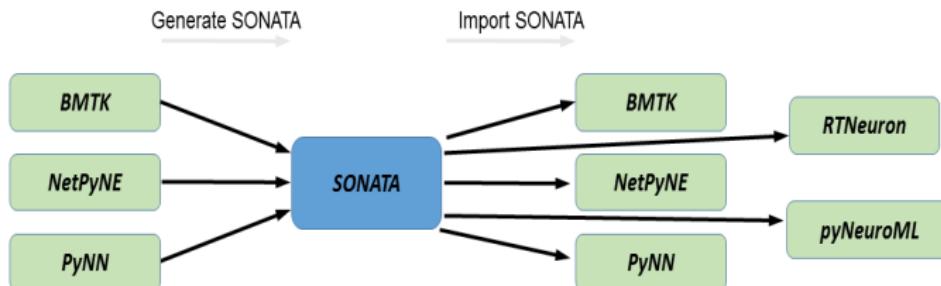
Brain Modeling ToolKit (BMTK): <https://alleninstitute.github.io/bmtk/>



# Our Models and Modeling Software Are Freely Available to the Community

**Scalable Open Network Architecture TemplAte (SONATA):**  
<https://github.com/AllenInstitute/sonata>

An interface between SONATA and the NWB format has been developed as well





# *How model standardization enables new tools and applications in neuroscientific research*

*Insights from the HBP*

Yann Zerlaut

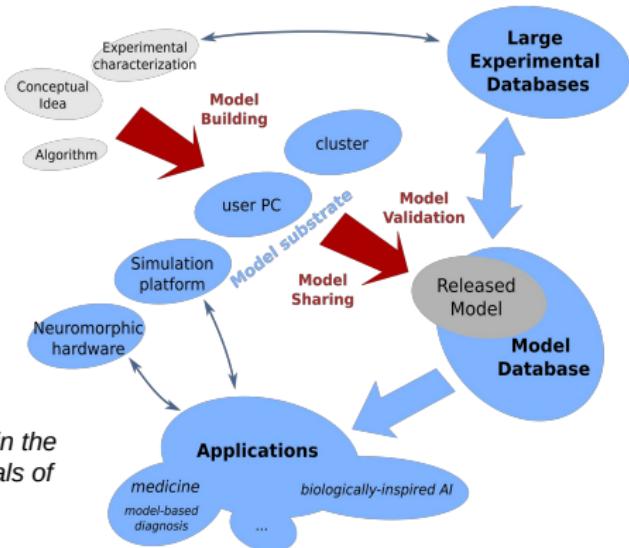
Neuroinformatics team / group of A. Davison  
Centre National de la Recherche Scientifique, France



*Open Source Brain Meeting 2019, Alghero*



# Motivation





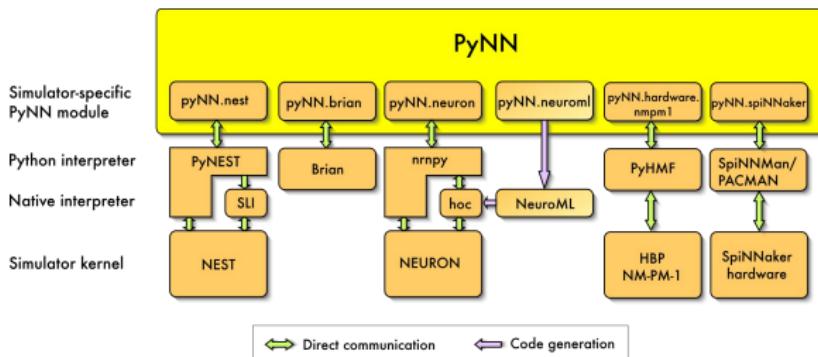
## A unified interface for neuronal network simulators

### Simulator-independent environments for developing neuroscience models:

- keep the advantages of having multiple simulators or hardware devices
- but remove the translation barrier.

Three (complementary) approaches:

- GUI (e.g. neuroConstruct)
- XML-based language (e.g. NeuroML, NineML)
- interpreted language (e.g. Python)



# Sonata (pyNN support)

Large-scale simulation of biophysically-detailed neuronal circuits  
→ sets specific constraints

the SONATA Data Format emerges as the standard  
optimized for performance for simulation, analysis and  
visualization of large-scale circuits  
(joint initiative of Blue Brain Project and the  
Allen Institute for Brain Science)

## Export to Sonata format

```
from pyNN.network import Network
from pyNN.serialization import export_to_sonata

sim.setup()
...
# create populations, projections, etc.
...

# add populations and projections to a Network
net = Network(pop1, pop2, ..., prj1, prj2, ...)

export_to_sonata(net, "sonata_output_dir")
```

## Import from Sonata format

```
from pyNN.serialization import import_from_sonata, load_sonata_simulation_plan
import pyNN.neuron as sim

simulation_plan = load_sonata_simulation_plan("simulation_config.json")
simulation_plan.setup(sim)
net = import_from_sonata("circuit_config.json", sim)
simulation_plan.execute(net)
```

**Include a validation framework in model development**✓ **What is SciUnit?**

A *Test*-driven framework for formally validating scientific models against data.

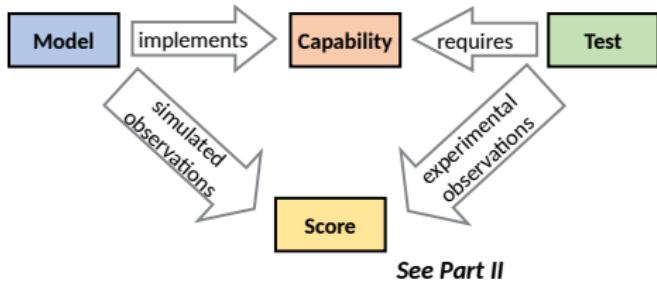
It employs the concept of **Capabilities**.

✓ **What are Tests?**

A procedure intended to establish the quality, performance, or reliability of a model

✓ **What are Capabilities?**

- interfaces through which the model and the validation framework communicate
- implemented as methods (functions) within the model



Requires the participation of modellers:

- ✓ support to wrap your models for SciUnit
- ✓ add/request new tests to the library
- ✓ critique existing tests
- ✓ suggest new features

# Test Packages

The overall test suite has been divided into a number of components, some containing validation tests specific to particular brain regions, others more generic. All validation tests are written in Python, using the SciUnit framework. Some of these are listed below:

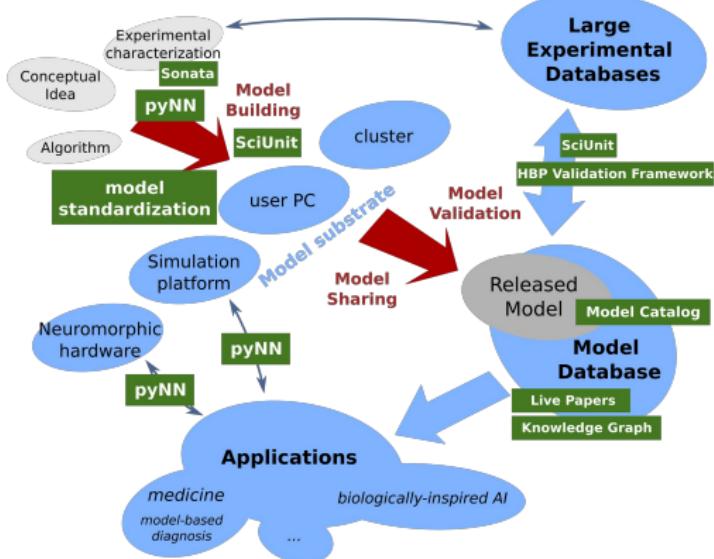
## Test suites for specific brain regions

- ❑ **HippoUnit:** <https://github.com/KaliLab/hippounit>
- ❑ **HippoNetworkUnit:** <https://github.com/pedroernesto/HippoNetworkUnit>
- ❑ **CerebUnit:** <https://github.com/lungsi/cerebellum-unit>
- ❑ **BasalUnit:** <https://github.com/appukuttan-shailesh/basalunit>

## Test suites for model features, independent of cell type or brain region

- ❑ **MorphoUnit:** <https://github.com/appukuttan-shailesh/morphounit>
- ❑ **NetworkUnit:** [https://github.com/mvonpapen/simrest\\_validation](https://github.com/mvonpapen/simrest_validation)
- ❑ **eFELUnit:** <https://github.com/appukuttan-shailesh/eFELunit>

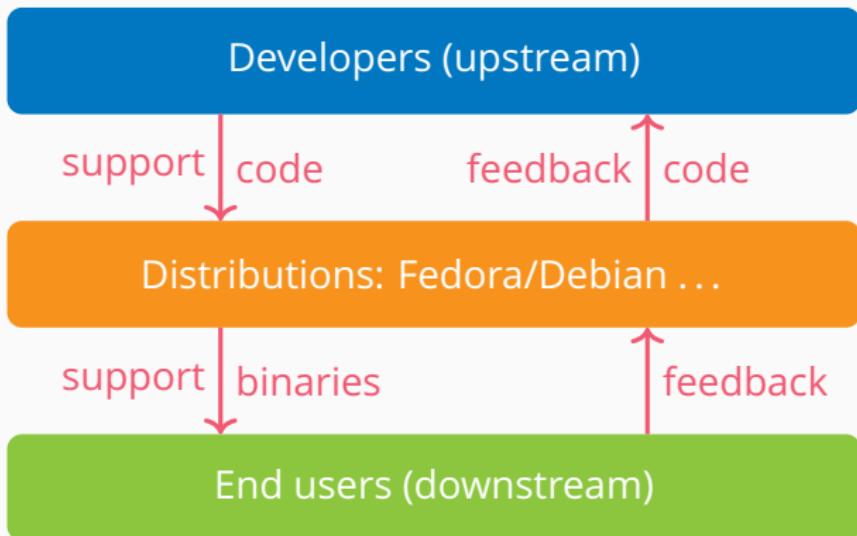
# Summary



## NeuroFedora: marketing pitch

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# Liaison between developers and users



## Search: “NeuroFedora”



“Live” ISO now ready to download (demo)

Mailing list: [neuro-sig@lists.fedoraproject.org](mailto:neuro-sig@lists.fedoraproject.org)

IRC: #fedora-neuro on Freenode

Telegram: [t.me/NeuroFedora](https://t.me/NeuroFedora)

Documentation [neuro.fedoraproject.org](http://neuro.fedoraproject.org)

Blog: [neuroblog.fedoraproject.org](http://neuroblog.fedoraproject.org)

Pagure.io (FOSS Git forge): [neuro-sig/NeuroFedora](https://pagure.io/neuro-sig/NeuroFedora)

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