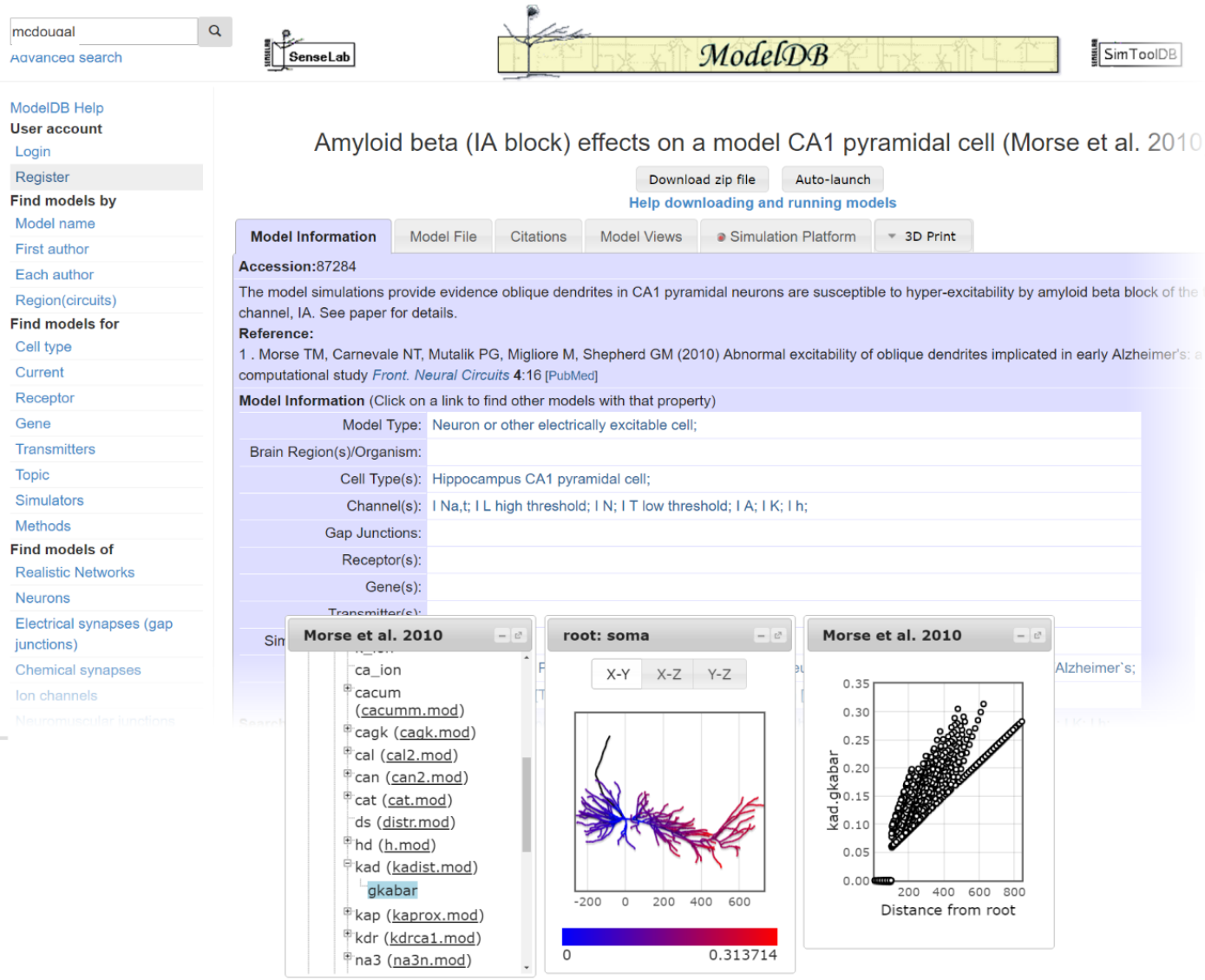
ModelDB

http://modeldb.yale.edu

ModelDB promotes discoverability and reproducibility of computational neuroscience research by serving as a platform for curated sharing and visualization of published models.




```
from neuron import h, rxd
import neuron.rxd.node as node
from matplotlib import pyplot
import time


h.load_file('stdrun.hoc')

soma = h.Section()
soma.L = 10
soma.diam = 10
soma.nseg = 11
dend = h.Section()
dend.connect(soma)
dend.L = 50
dend.diam = 2
dend.nseg = 51

def print_nodes():
    print ', '.join(str(v) for v in node._states)

print 'defining rxd'
region = rxd.Region(h.allsec(), nrn_region='i')
ca = rxd.Species(region, name='ca', d=1, charge=2, initial=
reaction = rxd.Rate(ca, -ca * (1 - ca) * (0.3 - ca))

print 'initializing'
h.finitialize()

print 'before:'
print_nodes()
print
```

Morse TM, Carnevale NT, Mutalik PG, Migliore M, Shepherd GM (2010) Abnormal excitability of oblique dendrites implicated in early Alzheimer's: a computational study *Front. Neural Circuits* **4**:16[PubMed]

References and models cited by this paper

Acker CD, White JA (2007) Roles of I(A) and morphology in action potential propagation in CA1 pyramidal cell dendrites. *J Comput Neurosci* **23(2)**:201-16 [Journal] [PubMed]

- **Roles of I(A) and morphology in AP prop. in CA1 pyramidal cell dendrites (Acker and White 2007) [Model]**

Anderton BH, Callahan L, Coleman P, Davies P, Flood D, Jicha GA, Ohm T, Weaver C (1998) Dendritic changes in Alzheimer's disease and factors that may underlie these changes. *Prog Neurobiol* **55**:595-609 [PubMed]

Andrasfalvy BK, Makara JK, Johnston D, Magee JC (2008) Altered synaptic and non-synaptic properties of

References and models that cite this paper

Culmone V, Migliore M (2012) Progressive effect of beta amyloid peptides accumulation on CA1 pyramidal neurons: a model study suggesting possible treatments *Front Comput Neurosci* **6**:52 [Journal] [PubMed]

- **CA1 pyramidal neurons: effects of Alzheimer (Culmone and Migliore 2012) [Model]**

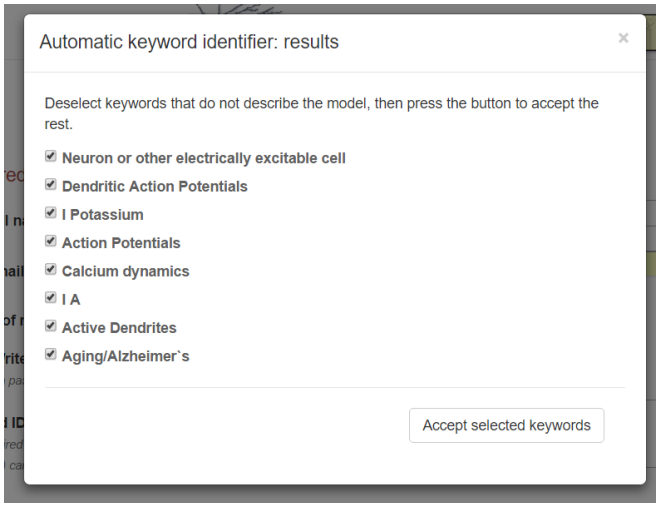
McDougal RA, Morse TM, Hines ML, Shepherd GM (2015) ModelView for ModelDB: online presentation of model structure *Neuroinformatics* **13(4)**:459-70 [Journal] [PubMed]

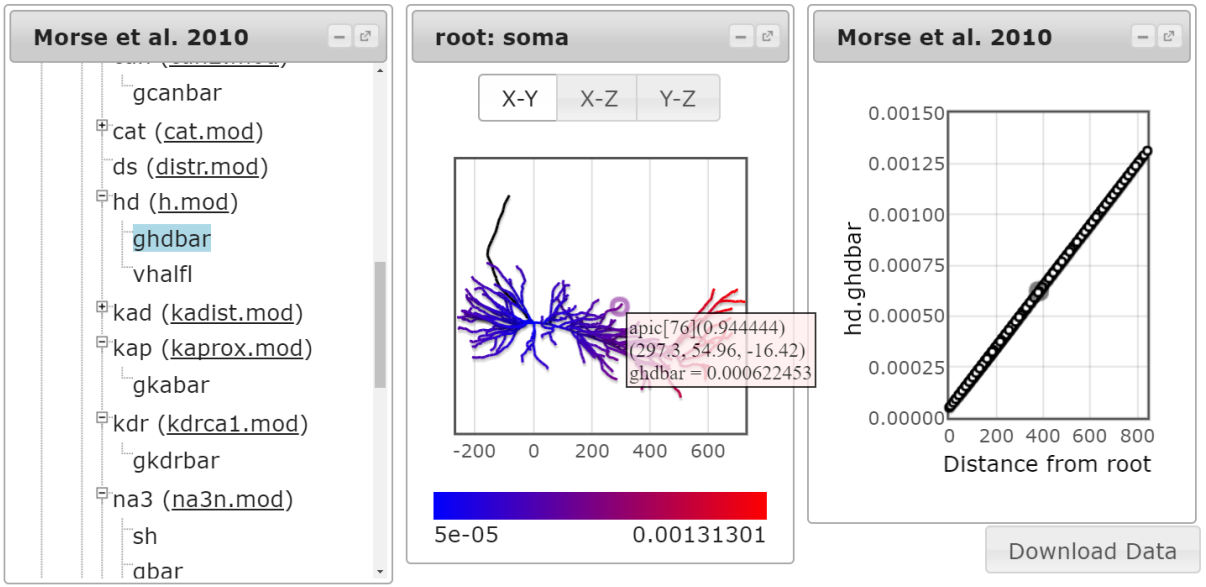
- **ModelView: online structural analysis of computational models (McDougal et al. 2015) [Model]**

Over 1200 models · 76 simulation environments · 178 cell types · 145 topics (Alzheimer's, STDP, etc) · 16+ species · 54 ion channels, pumps, etc · 24+ mammalian brain regions

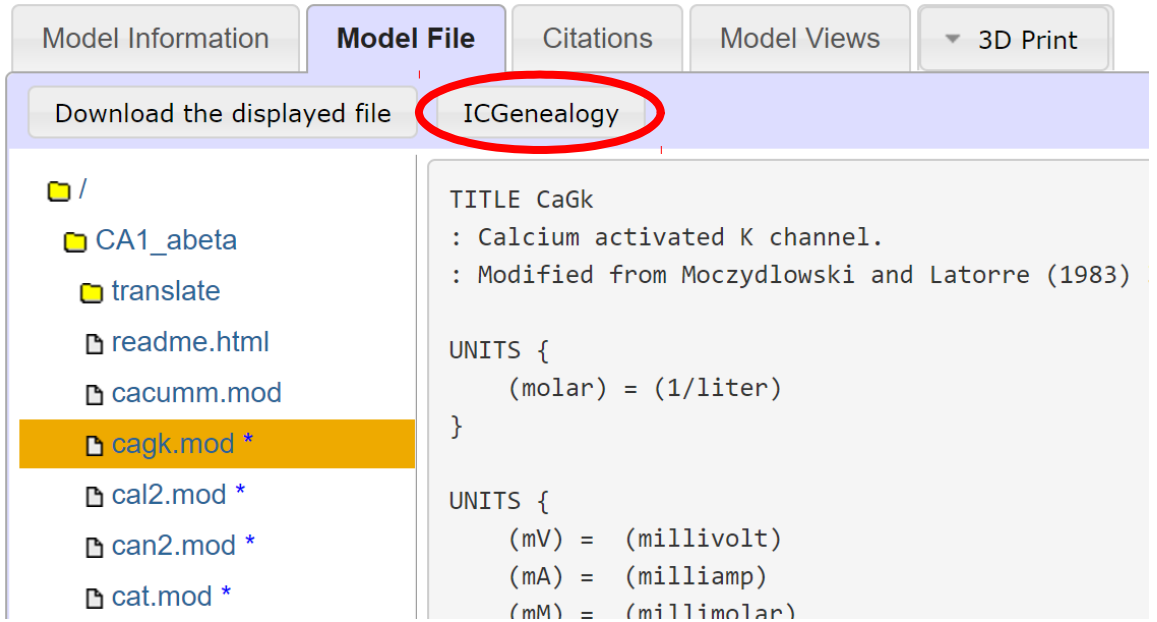
Ongoing ModelDB projects

Improving quantity and quality of model entries *by actively identifying new modelling literature and providing NLP tools to assist entry of descriptive metadata.*





Model visualization tools *make models more accessible by allowing insight into the model structure without reading code.*



General data

- **ICG id:** 2464
- **ModelDB id:** 87284
- **Reference:** *Morse TM, Carnevale NT, Mutalik PG, Migliore M, Shepherd GM (2010)*:
  Abnormal Excitability of Oblique Dendrites Implicated in Early Alzheimer's: A Computational Study.

Metadata classes

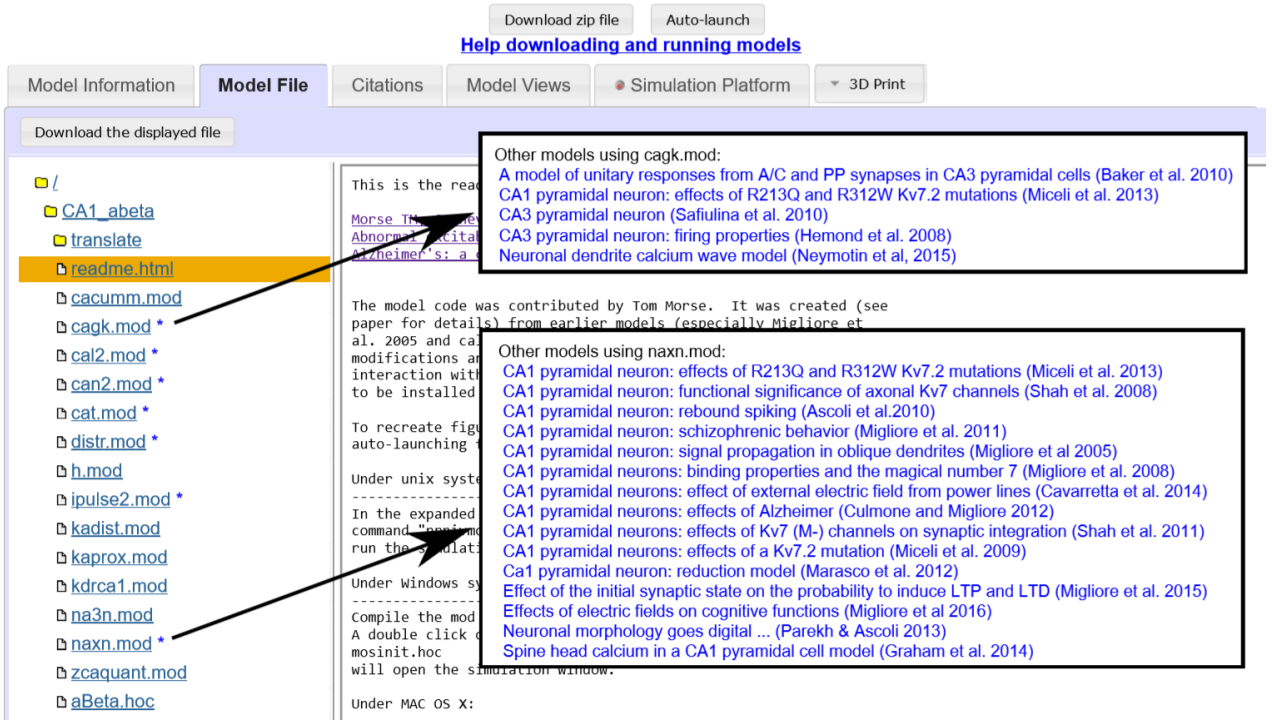
- **Animal Model:** rat
- **Brain Area:** hippocampus, CA1
- **Neuron Region:** unspecified
- **Neuron Type:** pyramidal cell
- **Runtime Q:** Q4 (slow)
- **Subtype:** not specified

Metadata generic

- **Age:** 7-14 weeks old.
- **Authors:** M Migliore.
- **Comments:** Calcium activated k channel, modified from moczydlowski and latorre (1983). From hemond et al. (2008), model no. 101629, with no changes (identical mod file). Animal model taken from chen (2005) which is used to constrain model. Channel kinetics from previous study on hippocampal pyramidal neuron (hemond et al. 2008)

Better model context *through partnerships with external neuroinformatics resources like the Ion Channel Genealogy (above) and through identifying repeated patterns within ModelDB itself (right).*

Amyloid beta (IA block) effects on a model CA1 pyramidal cell (Morse et al. 2010)



Open Source Brain

http://www.opensourcebrain.org

Open Source Brain is…

One slide giving an overview of the resource, example datasets, etc.

One slide discussing current work/future plans

Optional 3rd slide…

General requests:

- Please favour graphical content over text where possible

- Please don't use animation (use multiple slides if required)

- Try to keep to font Arial

- Save slides as .pptx (Powerpoint 2007-2013); slides will be concatenated into a single PDF presentation

NeuroML

http://www.neuroml.org

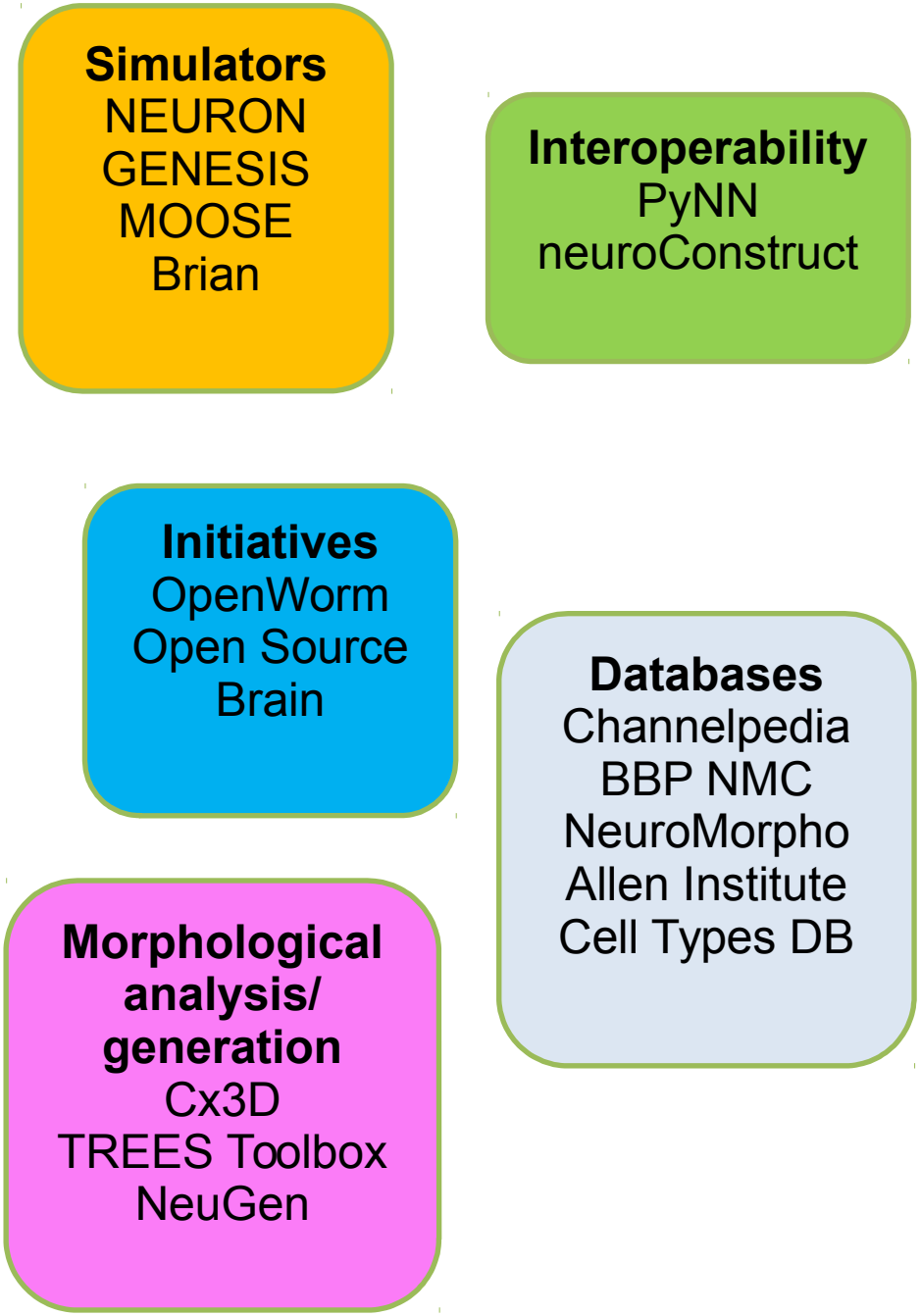
NeuroML is a language for expressing models in computational neuroscience in a simulator independent, standardised format. It can express models from integrate and fire cells to complex networks of multicompartmental neurons.

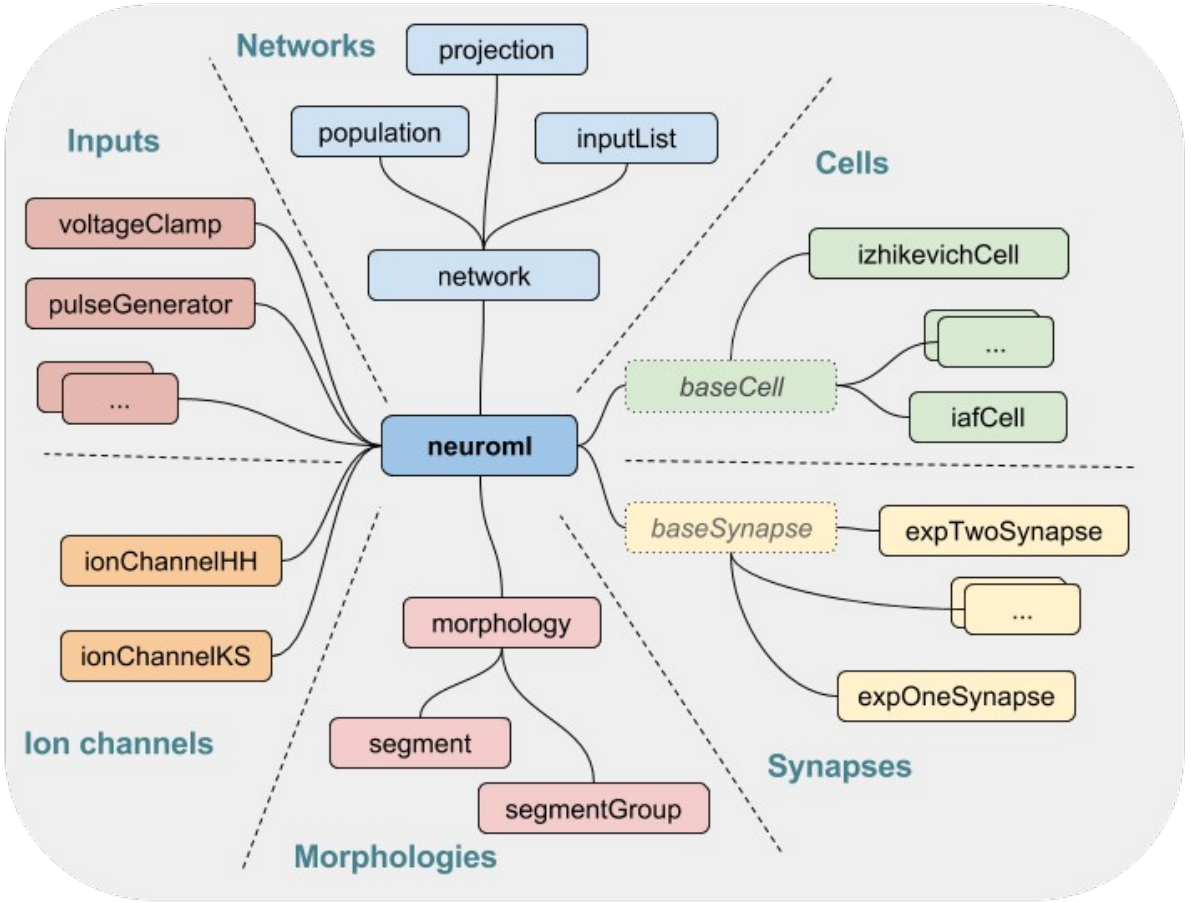
Standardised XML language for computational neuroscience

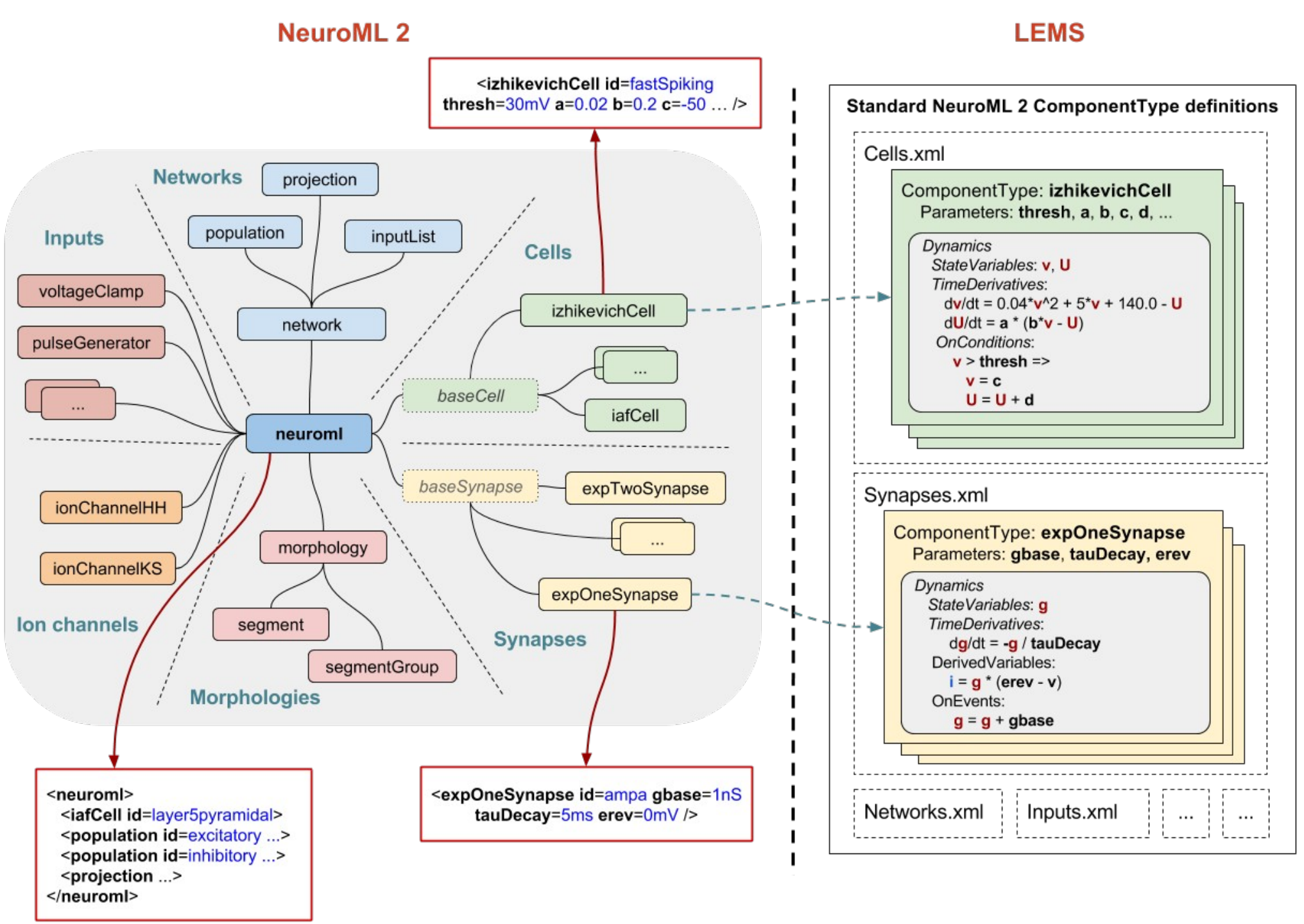
Version 1.x allowed specification of:

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

30+ simulators/applications/ databases/libraries support NeuroML




Networks
projection
population
inputList
network
Inputs
voltageClamp
pulseGenerator
...
ionChannelHH
ionChannelKS
Ion channels
neuroml
Cells
izhikevichCell
baseCell
...
iafCell
baseSynapse
expTwoSynapse
...
expOneSynapse
Synapses
morphology
segment
segmentGroup
Morphologies


NeuroML 2
LEMS
<izhikevichCell id=fastSpiking thresh=30mV a=0.02 b=0.2 c=-50 … />
Networks
projection
population
inputList
Inputs
Cells
voltageClamp
network
izhikevichCell
pulseGenerator
...
baseCell
...
iafCell
...
neuroml
baseSynapse
expTwoSynapse
ionChannelHH
...
morphology
ionChannelKS
expOneSynapse
Ion channels
segment
Synapses
segmentGroup
Morphologies
<neuroml>
<iafCell id=layer5pyramidal>
<population id=excitatory ...>
<population id=inhibitory ...>
<projection ...>
</neuroml>
<expOneSynapse id=ampa gbase=1nS tauDecay=5ms erev=0mV />
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 * (b*v - U)
OnConditions:
v > thresh =>
v = c
U = U + d
Synapses.xml
ComponentType: expOneSynapse
Parameters: gbase, tauDecay, erev
Dynamics
StateVariables: g
TimeDerivatives:
dg/dt = -g / tauDecay
DerivedVariables:
i = g * (erev - v)
OnEvents:
g = g + gbase
Networks.xml
Inputs.xml
...
...

Geppetto

http://www.geppetto.org

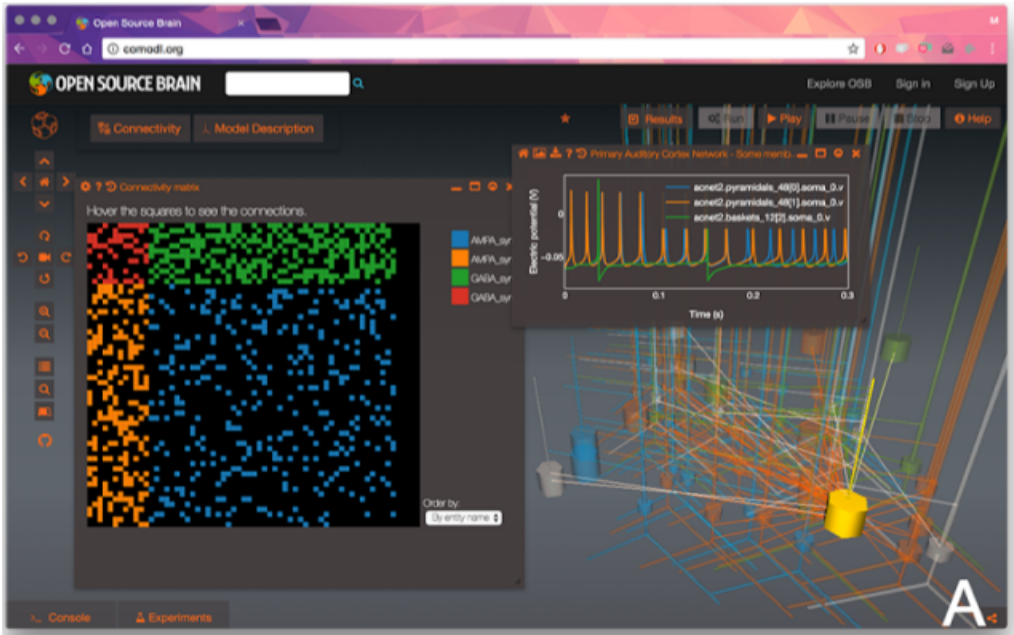
Geppetto is a web-based visualisation and simulation platform engineered to explore complex biological systems. In use by a number of neuroinformatics resources including Open Source Brain and Virtual Fly Brain, Geppetto facilitates integration of diverse data and models, and can support different standard formats for both experimental and computational data.

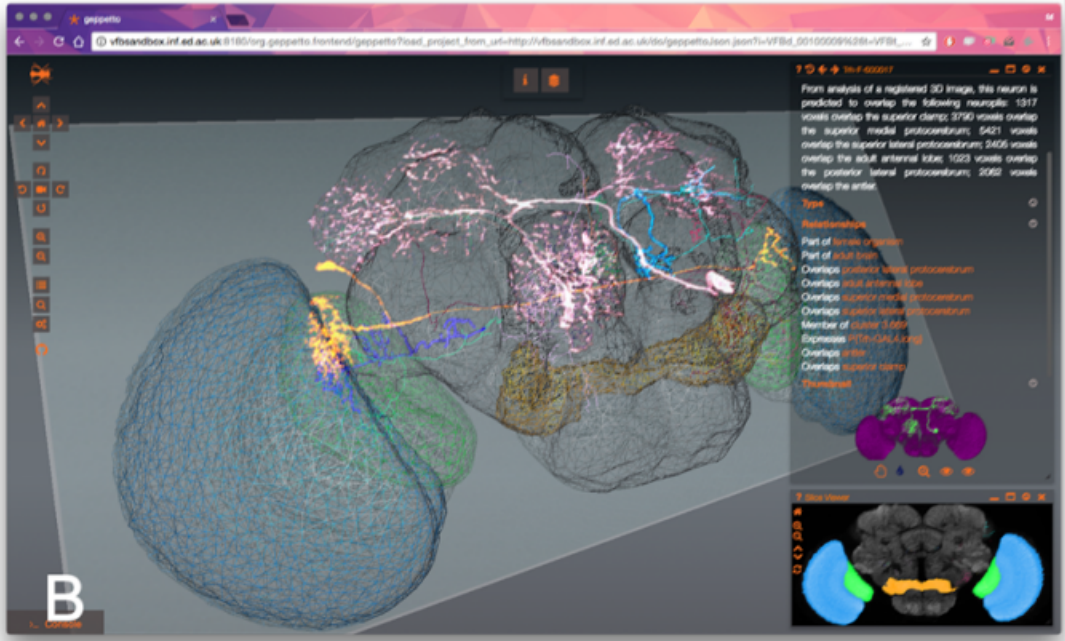

geppetto
Geppetto is an open source web platform to **explore** and **simulate** **neuroscience** models and data in a **web** browser

What can Geppetto do?

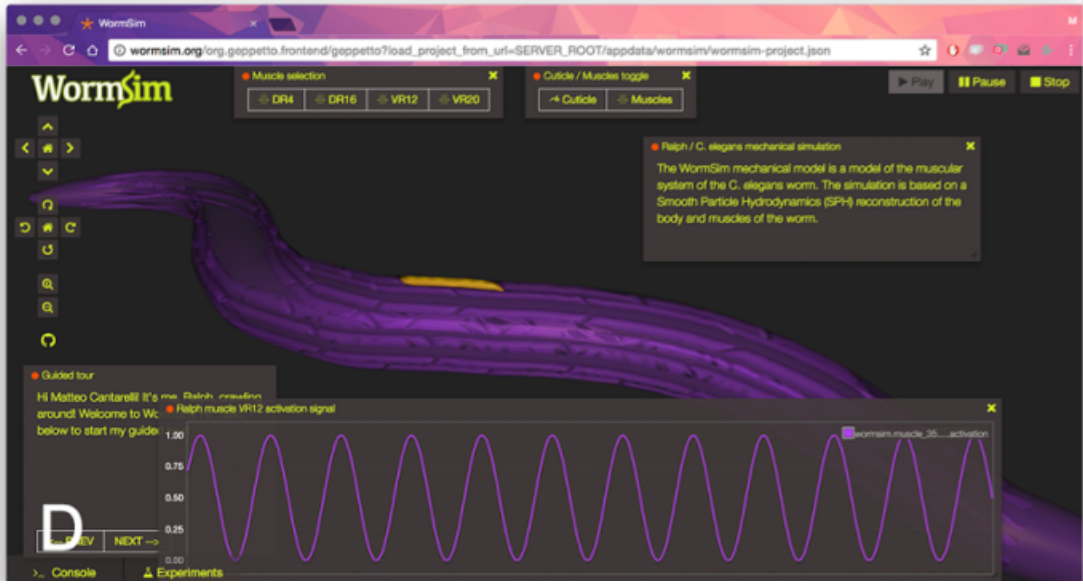
- Visualize **neuroscience data** in the browser
  - Computational Neuroscience Models (NeuroML, NEURON)
  - Morphology reconstructions (SWC, OBJ, Collada)
  - Electrophisiology recordings (NWB, HDF5)
  - Medical data (MRI, Electromicroscopy via DICOM, NIFTI, DZI)
- **Record variables, set parameters, an run simulations** from the browser
  - Simulation can run in the same server where Geppetto is running or in a remote one (e.g. San Diego Supercomputer center)
- Connect to Jupyter Notebook
- Seamless **exploration** of data and models in the browser
- Facilitates **reproducibility** of workflows
  - The entire user interface works on top of an API layer. Every user action corresponds to an API command easy to inspect and reproduce.

geppetto


Open Source Brain
OPEN SOURCE BRAIN
Explore OSB
Sign in
Sign Up
Connectivity
Model Description
Hover the squares to see the connections.
Console
Experiments
A


geppetto
B


geppetto
11.1750ms
Console
Experiments
Python
C


WormSim
wormsim.org/org.geppetto.frontend/geppetto?load_project_from_url=SERVER_ROOT/appdata/wormsim/wormsim-project.json
WormSim
Muscle selection
DR4
DR16
VR12
VR20
Cuticle / Muscles toggle
Cuticle
Muscles
Play
Pause
Stop
Ralph / C. elegans mechanical simulation
The WormSim mechanical model is a model of the muscular system of the C. elegans worm. The simulation is based on a Smooth Particle Hydrodynamics (SPH) reconstruction of the body and muscles of the worm.
Guided tour
Ralph muscle VR12 activation signal
Console
Experiments
D

ReScience

http://rescience.github.io

Reproducible Science is good, Replicated Science is Better.

ReScience is a scientific journal dedicated to the publication of replication in computational sciences.

Journal Philosophy

ReScience is a peer-reviewed journal that targets computational research and encourages the explicit replication of already published research, promoting new and open-source implementations in order to ensure that the original research is reproducible.

To achieve this goal, the whole publishing chain is radically different from other traditional scientific journals. ReScience lives on GitHub where each new implementation of a computational study is made available together with comments, explanations and tests. Each submission takes the form of a pull request that is publicly reviewed and tested in order to guarantee that any researcher can re-use it.

If you ever replicated computational results from the literature in your research, ReScience is the perfect place to publish your new implementation.

Publishing fees

None. Zero. Nada. 0$. 0€.

Criteria for Publication

To be considered for publication in ReScience, any given submission must satisfy the following criteria:

- Replicability
- Rigorous methodology
- Original source code
- Substantial evidence for replication of the original results

Furthermore, you cannot submit the replication of your own research, nor the research of your close collaborators. We believe such restrictions will favor the cross-fertilization of research and the spread of knowledge.

Open Access

ReScience

Reproducible science is good. Replicated science is better.