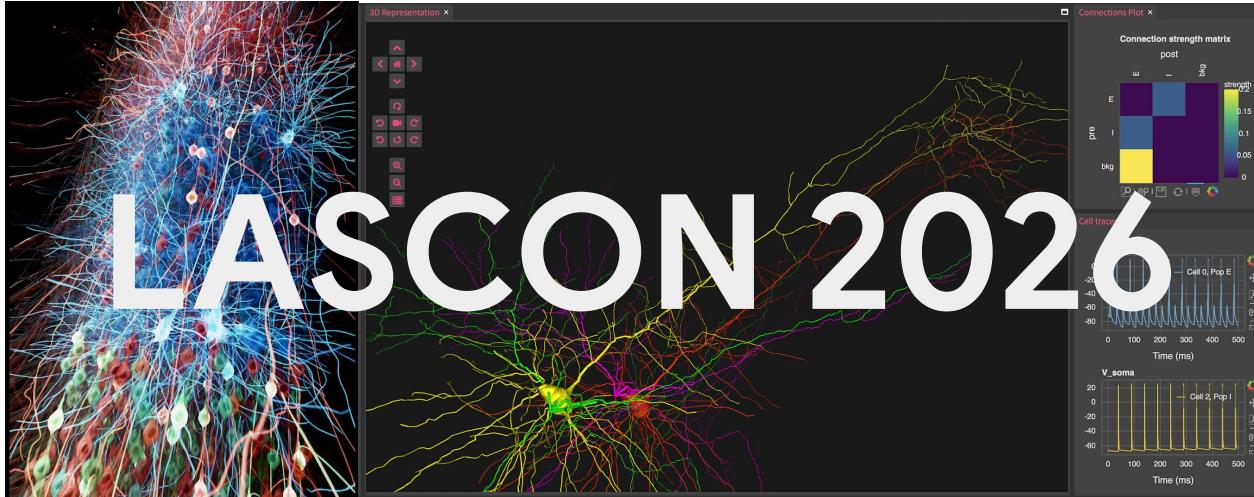


Network Modelling with

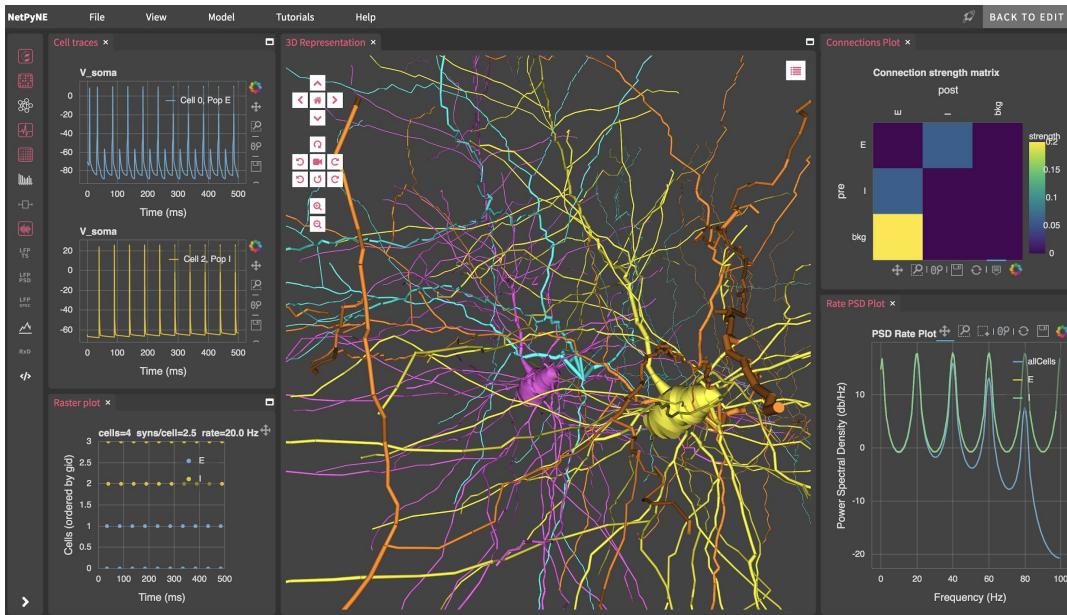


Valery Bragin, State University of New York (SUNY) Downstate vbragin19@gmail.com
PI: Salvador Dura-Bernal, PhD
Assistant Professor, State University of New York (SUNY) Downstate

Lab web: dura-bernal.org



A python package to facilitate the development, parallel simulation, optimization and analysis of biological neuronal networks using the NEURON simulator.



Funded by:



National Institutes
of Health

Motivation

Separate model parameters from standardized implementation

Standardize format – easy to read, interpret, edit, share, reproduce, etc

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



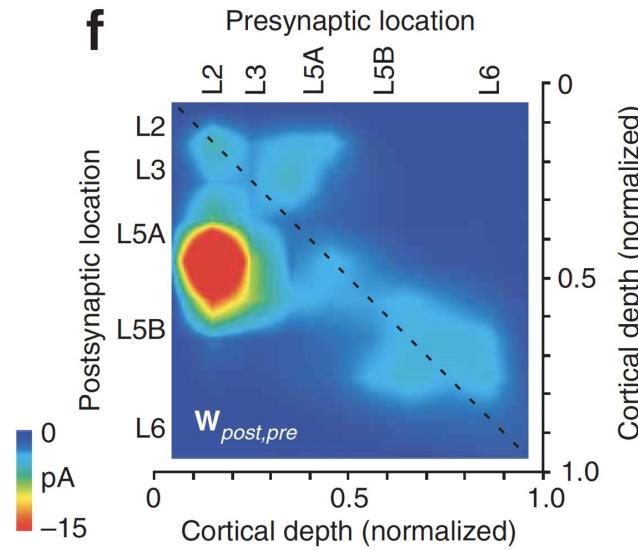
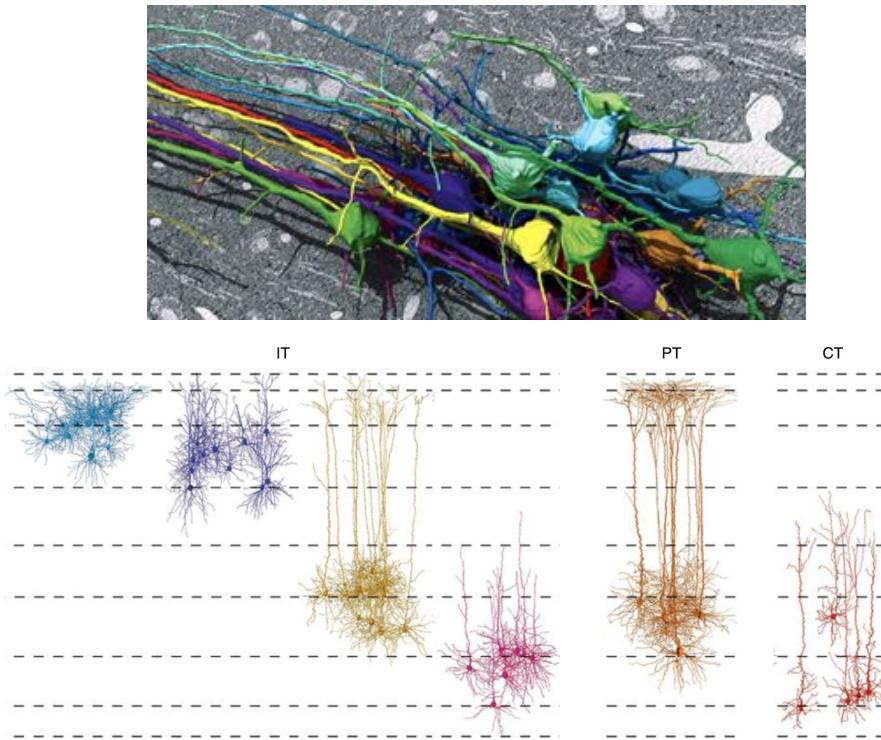
```
for gid in range(pop.numCells):  
    cell = sim.Cell()  
    cell.y = numpy.random(100,400)  
    cell.type = 'PYR'  
    pc.cell(gid, h.NetCon(v_soma, threshold))
```

Standard, efficient and tested
backend implementation

Potentially very different implementations
(arbitrary functions, variables, file names
etc.)

Facilitate incorporation of experimental data at multiple scales

Motivation



NetPyNE High-Level Specifications

NEURON

```
# add exc connection
postSyn1 = h.ExpSyn(postCell.dend(0.5))
postSyn1.tau = 2
postSyn1.e = -90

pre1Con = h.NetCon(preCell1.soma(0.5)._ref_v,
                   postSyn1,
                   sec=preCell1.soma)
pre1Con.delay = 1
pre1Con.weight[0] = 0.001
pre1Con.threshold = 0
```

NetPyNE High-Level Specifications

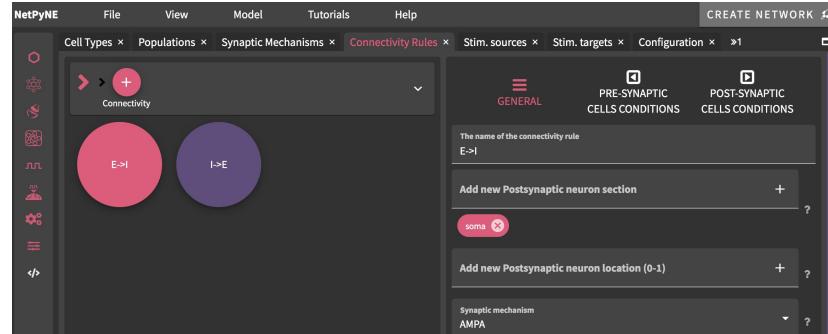
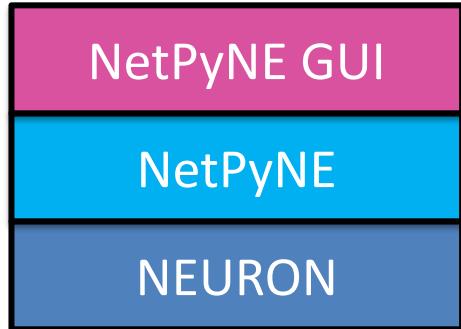
NetPyNE
NEURON

```
## Cell connectivity rules
netParams.connParams['S->M'] = {
    'preConds': {'pop': 'S'},
    'postConds': {'pop': 'M'},
    'probability': 0.5,
    'weight': 0.01,
    'delay': 5,
    'synMech': 'exc'}
```

```
# add exc connection
postSyn1 = h.ExpSyn(postCell.dend(0.5))
postSyn1.tau = 2
postSyn1.e = -90

pre1Con = h.NetCon(preCell1.soma(0.5)._ref_v,
                   postSyn1,
                   sec=preCell1.soma)
pre1Con.delay = 1
pre1Con.weight[0] = 0.001
pre1Con.threshold = 0
```

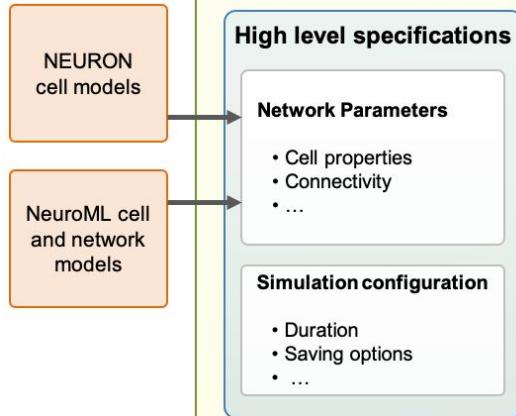
NetPyNE High-Level Specifications

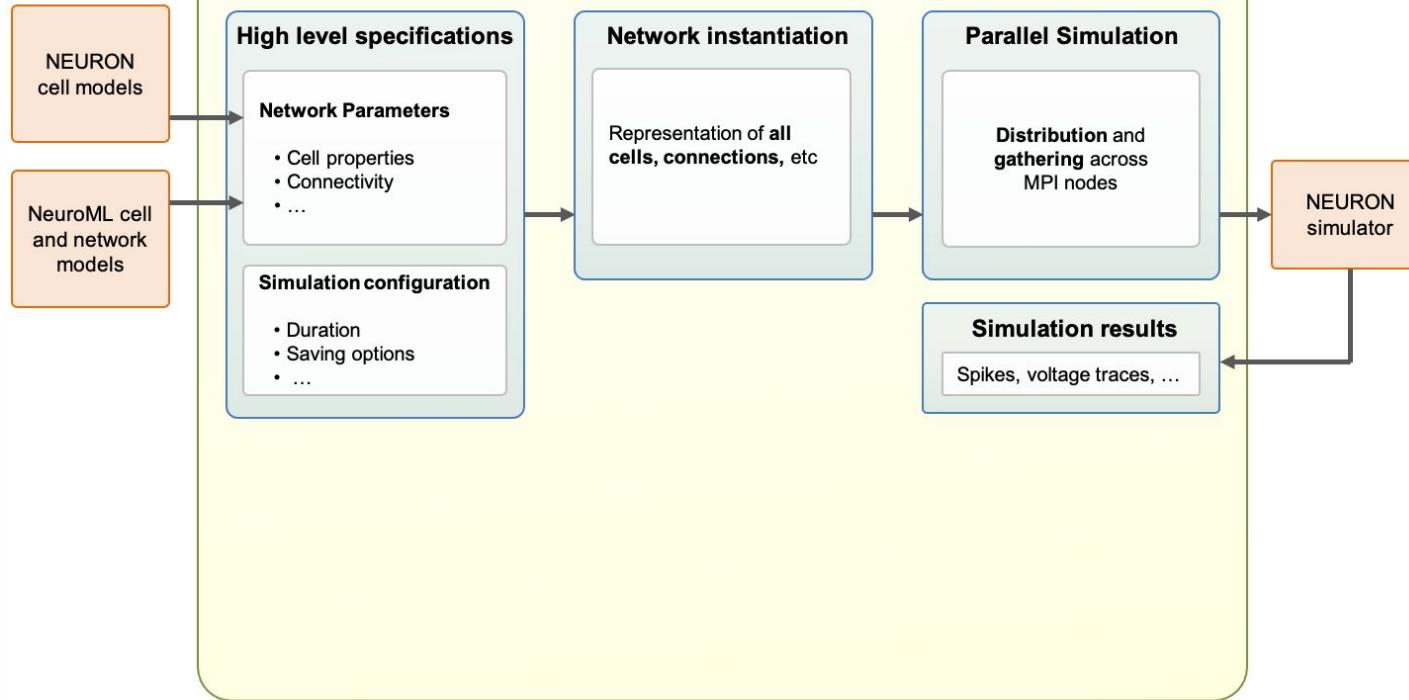


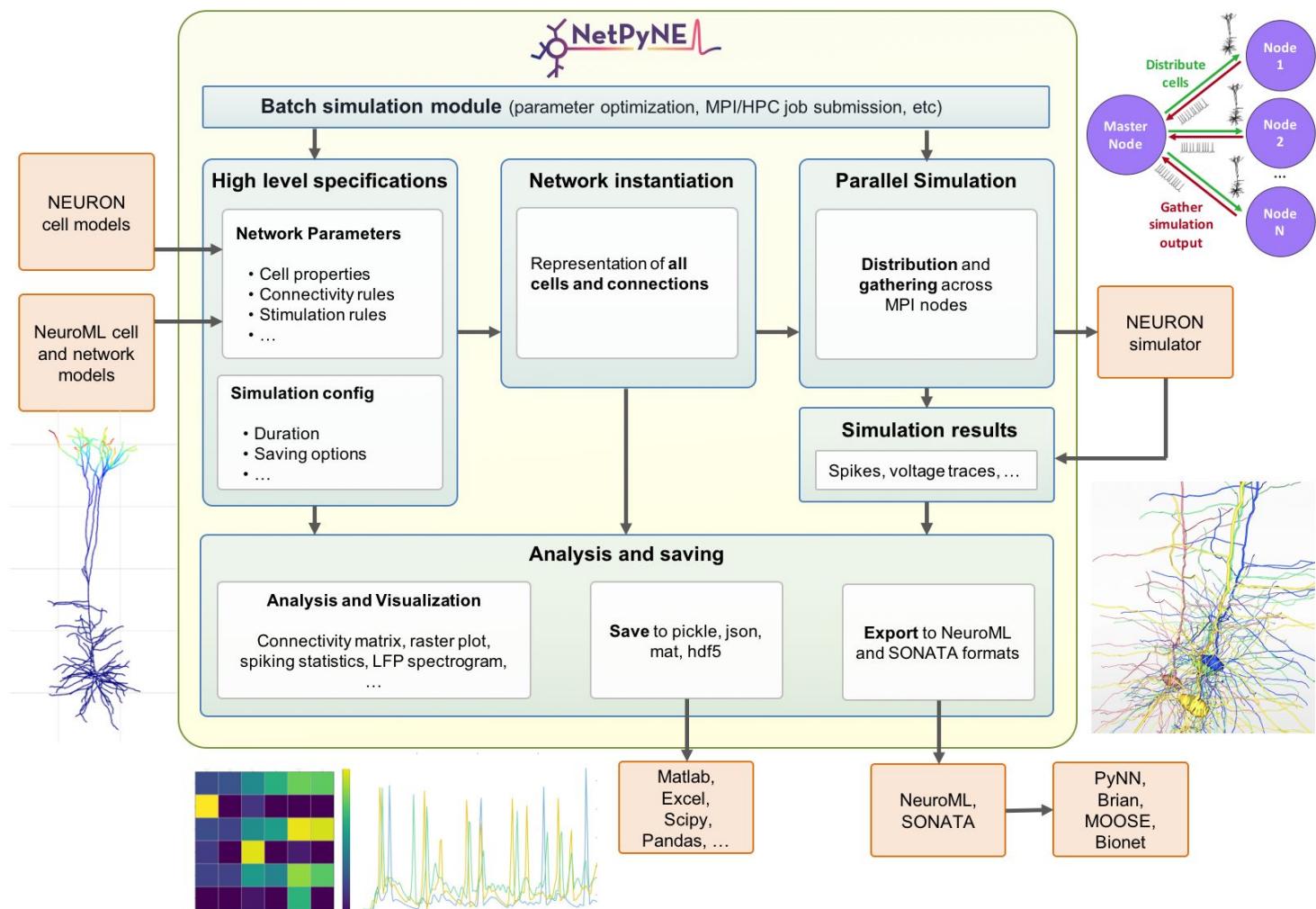
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    'postConds': {'pop': 'M'},
    'probability': 0.5,
    'weight': 0.01,
    'delay': 5,
    'synMech': 'exc'}
```

```
# add exc connection
postSyn1 = h.ExpSyn(postCell.dend(0.5))
postSyn1.tau = 2
postSyn1.e = -90

pre1Con = h.NetCon(preCell1.soma(0.5)._ref_v,
                   postSyn1,
                   sec=preCell1.soma)
pre1Con.delay = 1
pre1Con.weight[0] = 0.001
pre1Con.threshold = 0
```



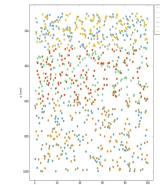




High level specifications

A **standardized, declarative** Python format (JSON-like, lists and dicts) to define:

Populations: cell type, number of neurons or density, spatial extent, ...



Cell properties: Morphology, biophysics, molecular processes ...



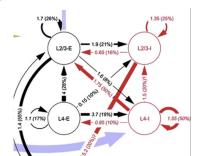
Synaptic mechanisms: Time constants, reversal potential, ...



Stimulation: Spike generators, current clamps, spatiotemporal patterns, ...



Connectivity rules: conditions of pre- and post-synaptic cells, functions, ...



Simulation configuration: duration, saving and analysis, visualization, ...



High level specifications

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,
 'gl': 0.003,
 'el': -70}}}}`

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

v) `rxParams['regions'] = {
 'cyt': {'cells': 'all',
 'secs': 'soma',
 'nrn_region': 'i'}}

rxParams['species'] = {
 'ca': {'regions': 'cyt',
 'charge': 2, 'initial': 1e-4},
 'buf': {'regions': 'cyt', 'initial': 1e-4},
 'cabuf': {'regions': 'cyt', 'initial': 0}}

rxParams['reactions'] = {
 'buffering': {'reactant': '2*ca+buf',
 'product': 'cabuf',
 'rate_f': 1e6, 'rate_b': 1e-2}}

rxParams['rates'] = {
 'degradation': {'species': 'buf',
 'rate': '-1e-3*buf'}}`

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

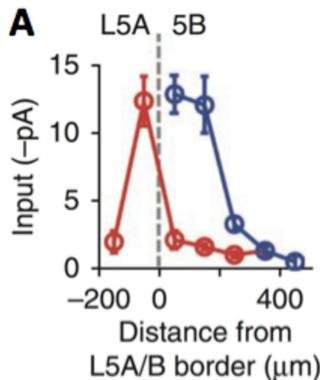
vii) `connParams['L2->E2'] = {
 'preConds': {'y': [100, 400]},
 'postConds': {'pop': 'EXC_L2'},
 'probability': '1*exp(-dist_3D/200)',
 'weight': 0.4, 'delay': 5, 'synMech': 'AMPA'}`

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': 'allDend',
 'synMech': 'AMPA', 'synsPerConn': 3}`

High level specifications

Connectivity

- **Flexible connectivity rules** based on pre- and post-synaptic cell properties (eg, type or location).
- Connectivity **functions** available: probabilistic, convergent, divergent, custom, ...
- Parameters (eg, probability, weight, delay) as a **function of pre/post-synaptic spatial properties**, eg, delays or probability that depend on distance between cells or cortical depth.
- Easily add synapses with **learning** mechanisms (STDP and RL) and **gap junctions**.

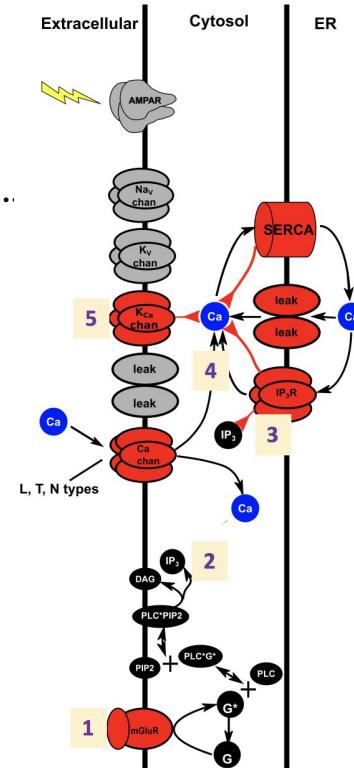
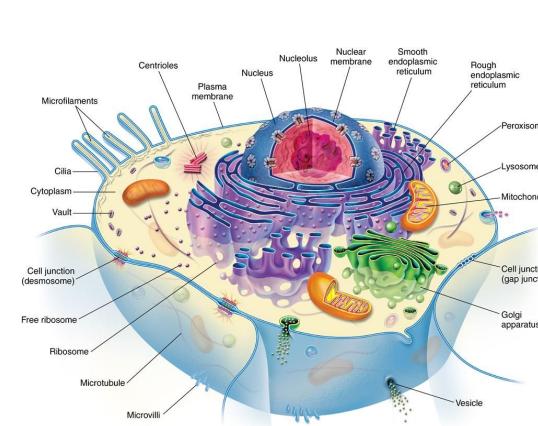
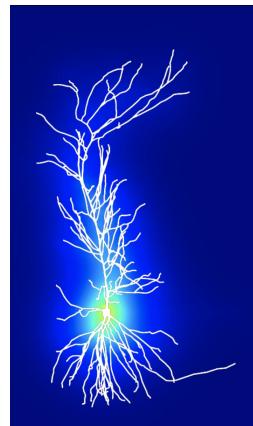
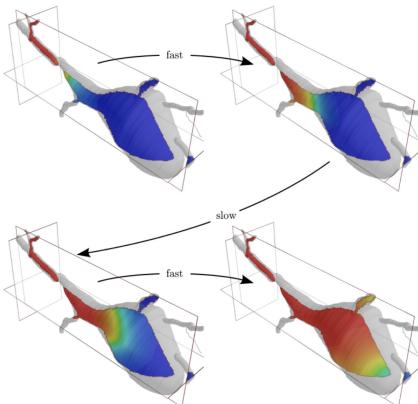


NetPyNE facilitates
building models
based on
experimental data

High level specifications

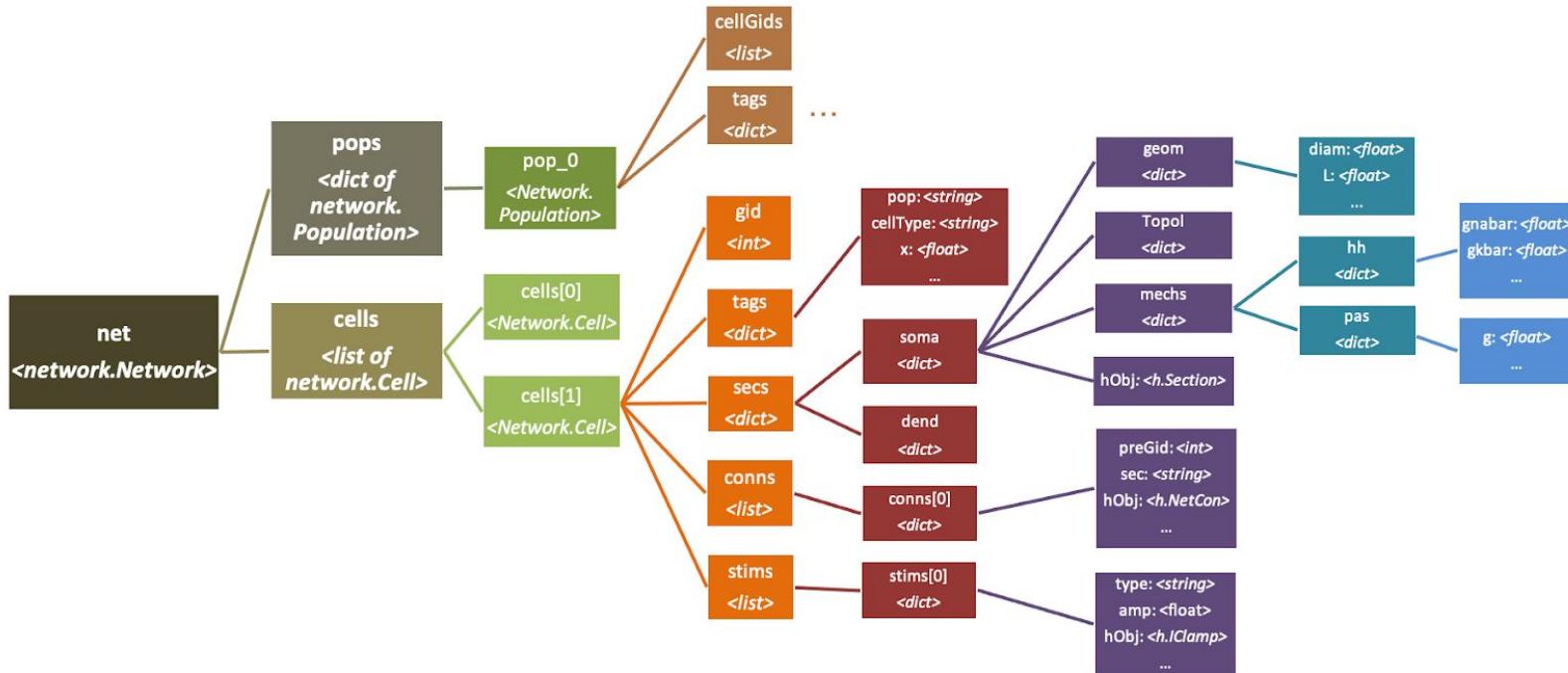
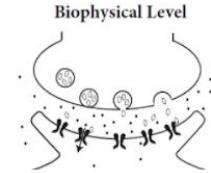
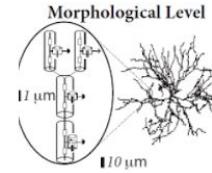
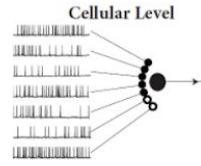
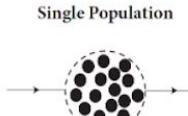
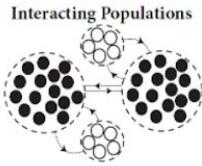
Molecular reaction-diffusion (RxD)

- Intra- and extracellular **diffusion** of ions, proteins (eg, calcium, potassium, IP₃, ...)
- Cell internal structures/**organelles** (eg, endoplasmic reticulum, mitochondria,...)
- Molecular **processes** (eg, phosphorylation, buffering, 2nd messenger cascades,...)
- **Interaction** with cell and network scales (eg, firing, plasticity, ...)



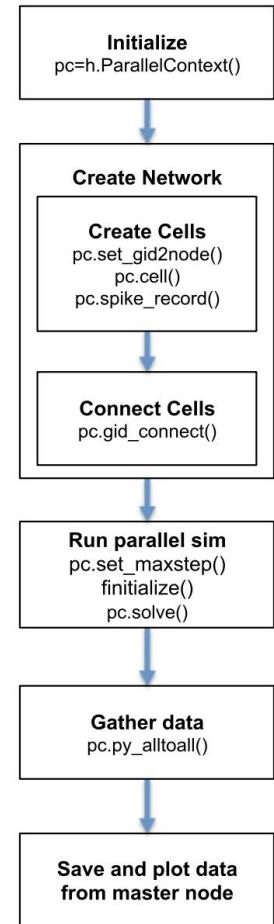
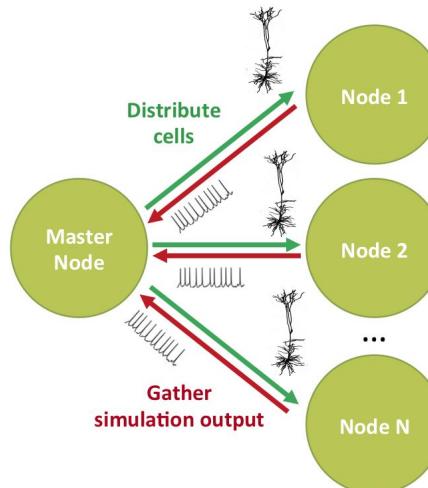
Network instantiation

(sim.net)



Parallel Simulation

- Set up for MPI **parallel simulation** across multiple nodes (via NEURON simulator).
- Takes care of balanced **distribution** of cells and **gathering** of simulation output from nodes.

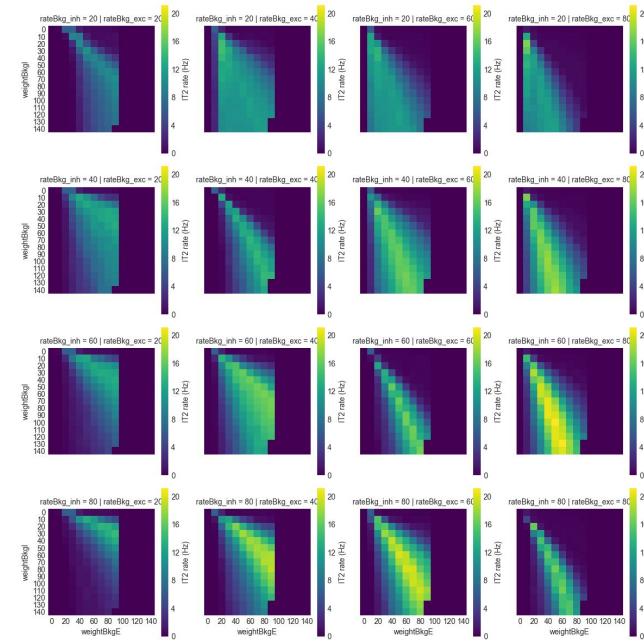


Parallelized parameter exploration

- Easy specification of parameters values to explore in batch simulations (param sweep and evolutionary)
- Pre-defined, configurable setups to automatically submit jobs in multicore machines (Bulletin board) or supercomputers (SLURM or PBS Torque)



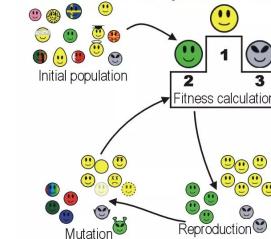
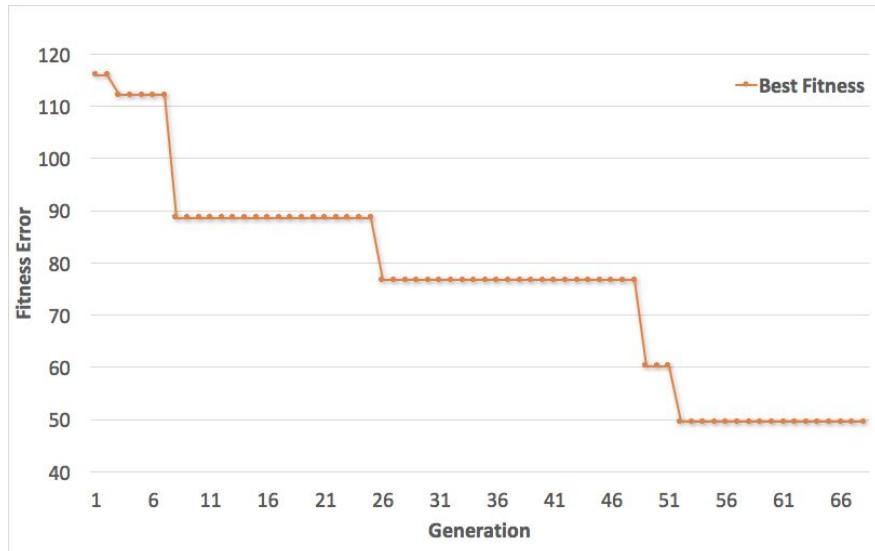
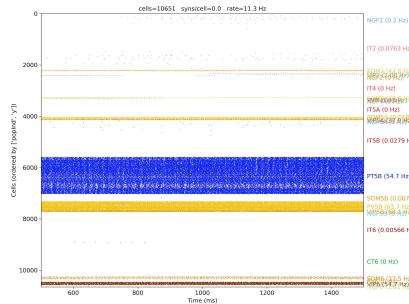
SDSC SAN DIEGO
SUPERCOMPUTER CENTER



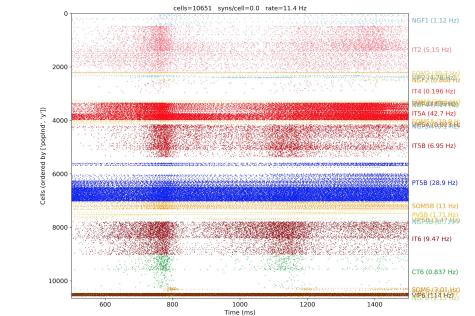
Parallelized parameter exploration

- Evolutionary algorithm optimization (for networks)

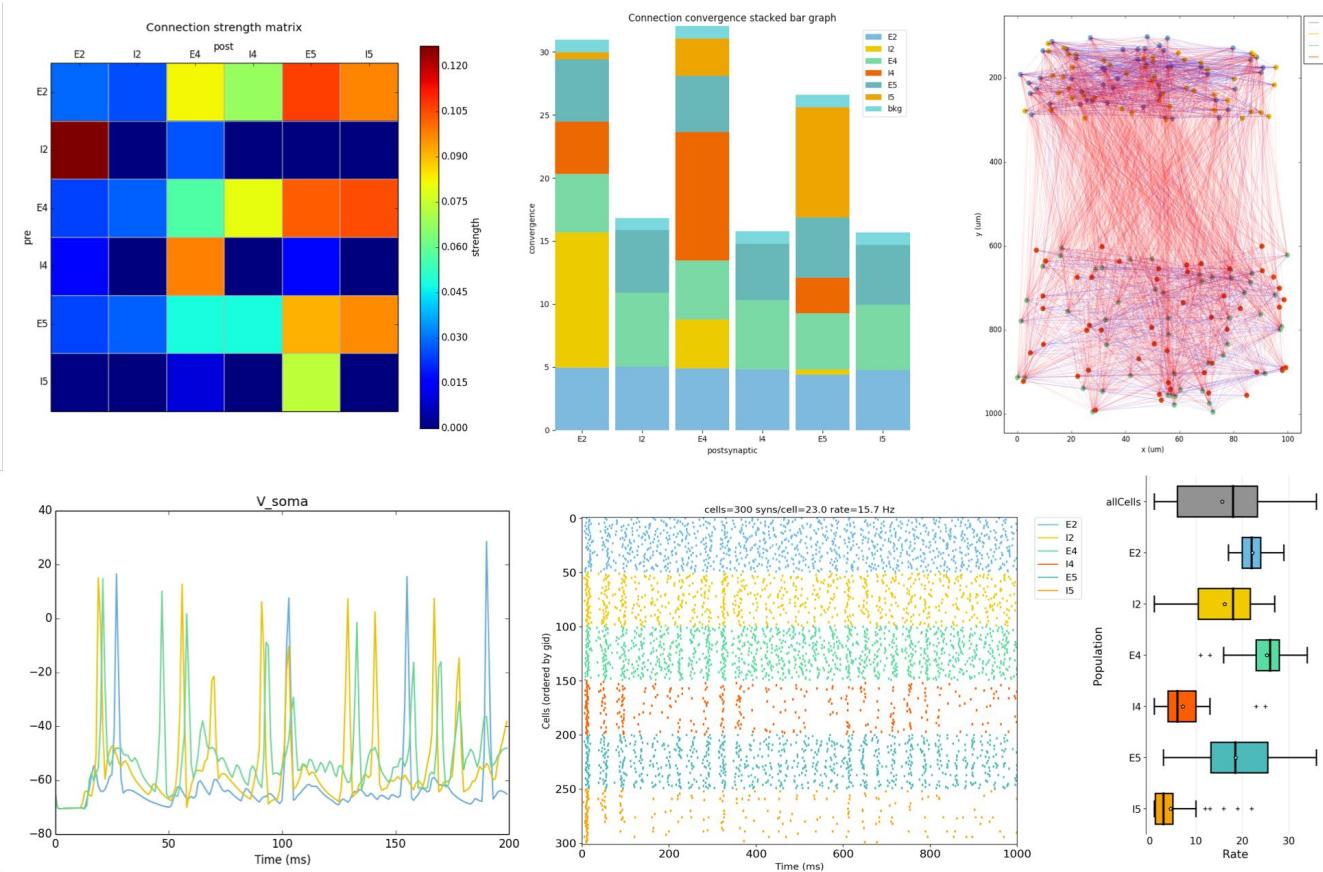
Initial candidate



Final candidate

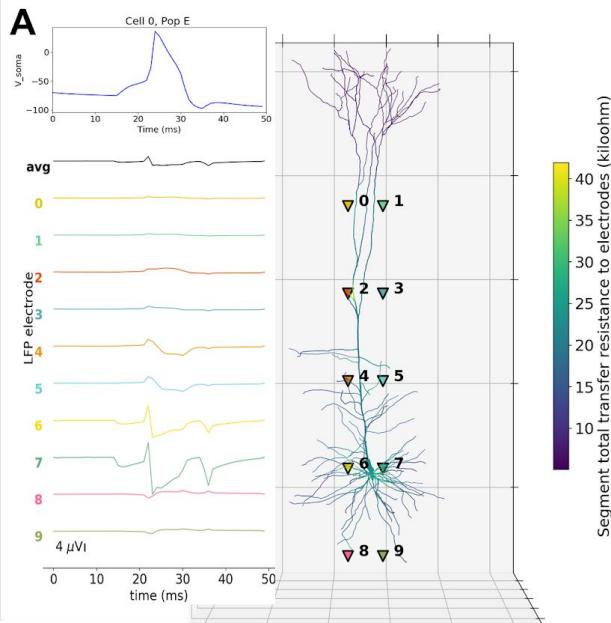


Simulation Analysis

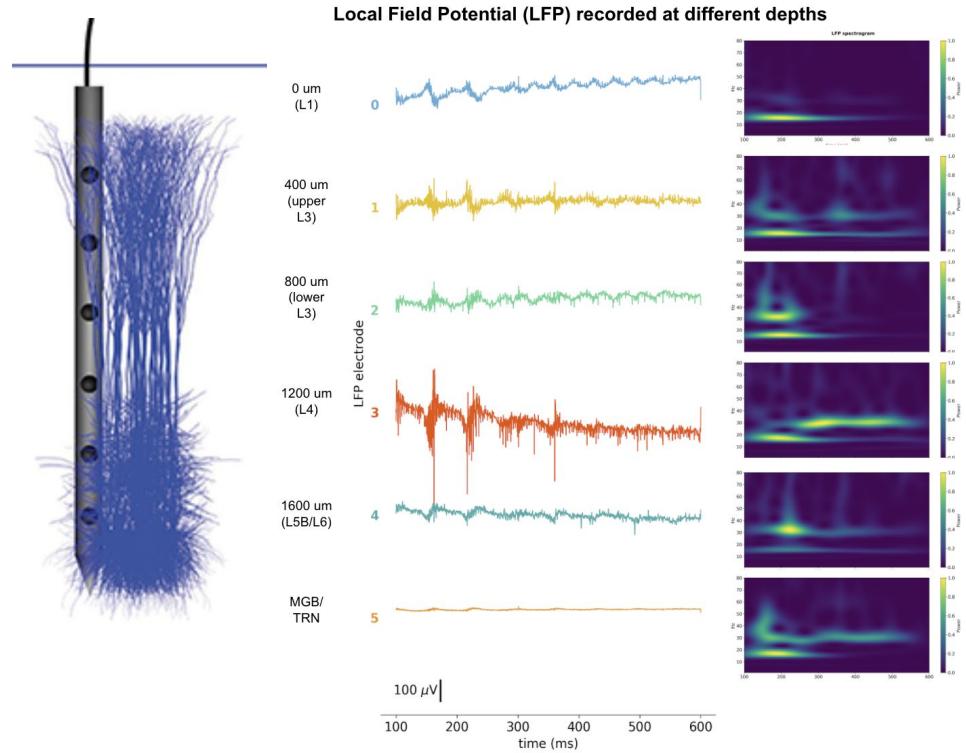


Local Field Potentials

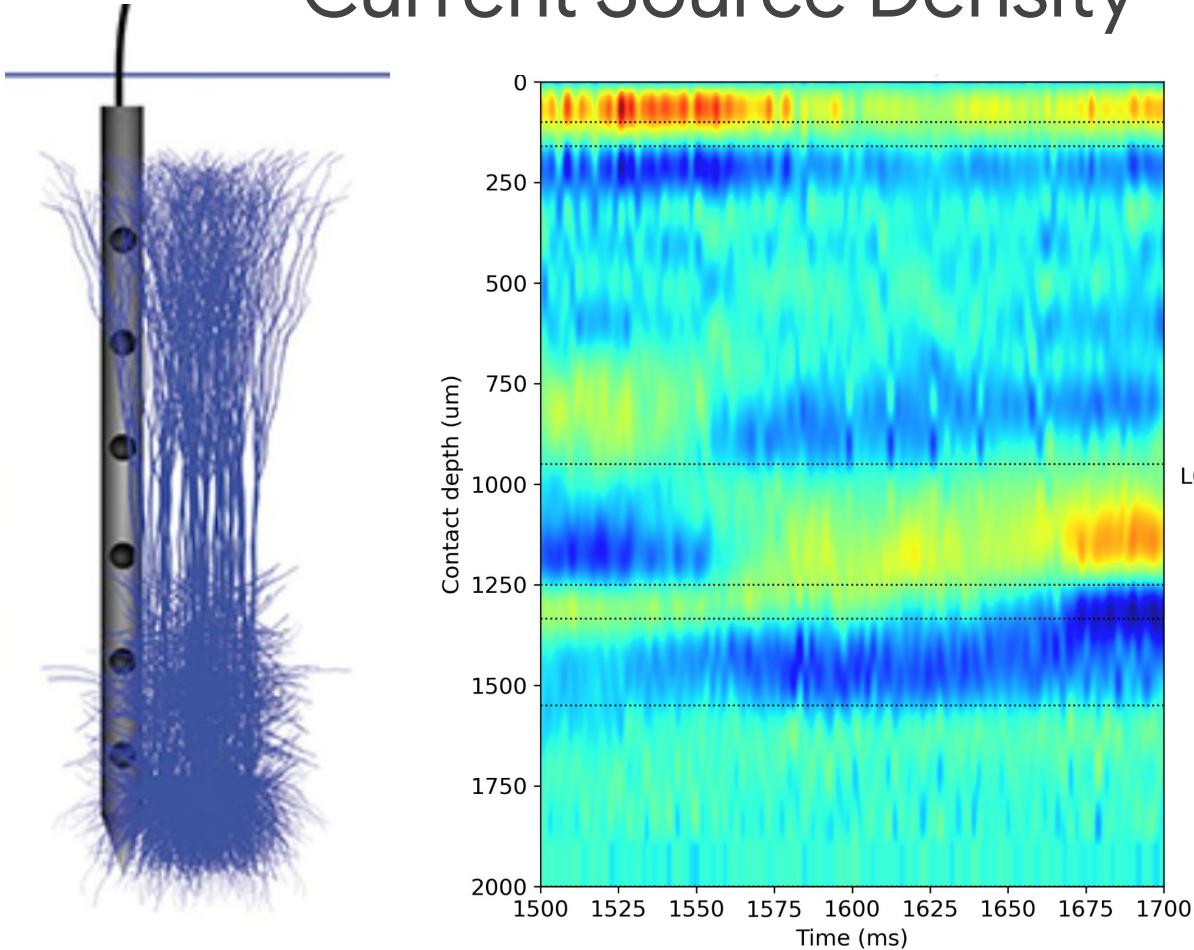
Single cell



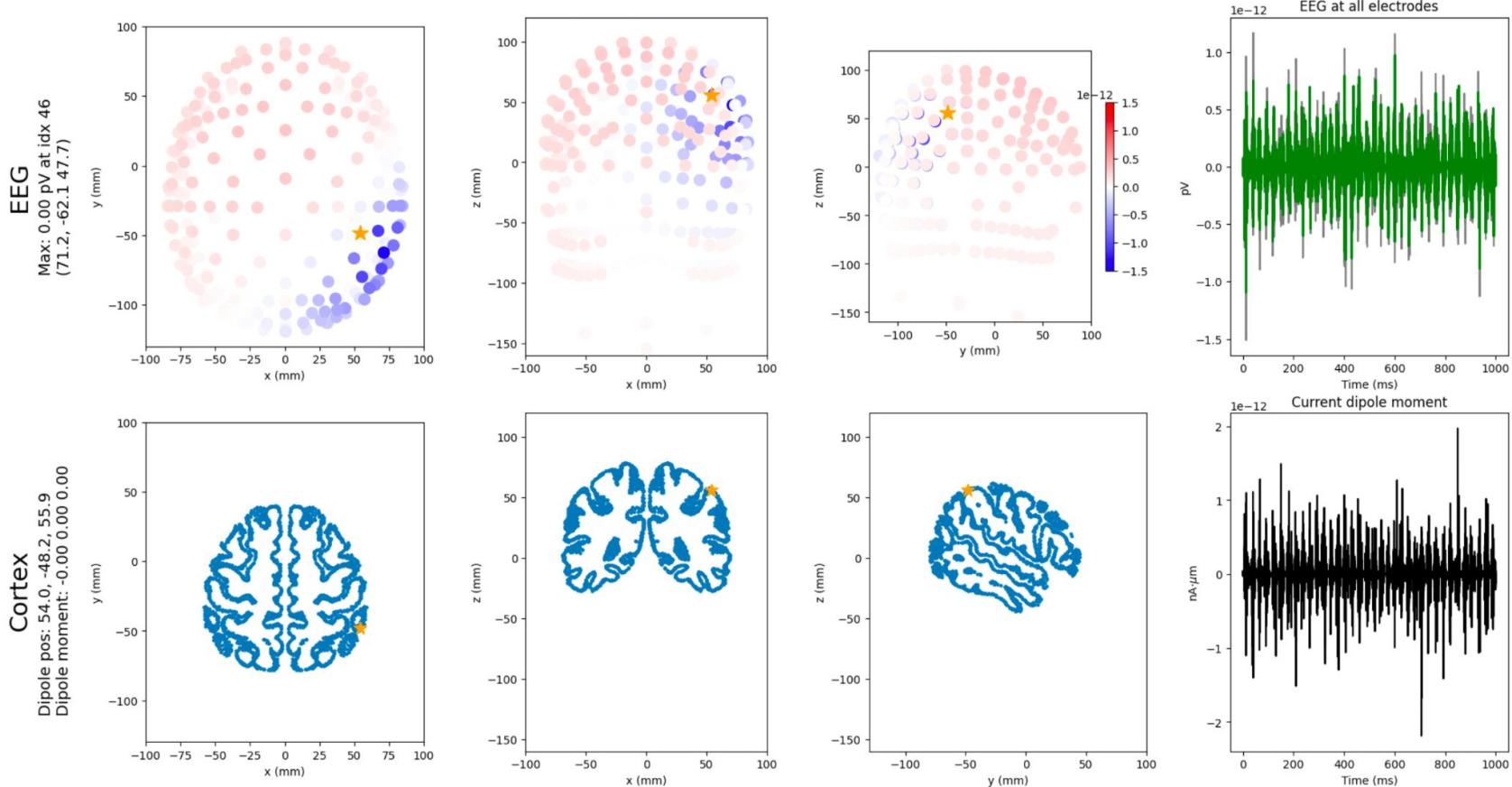
Network



Current Source Density



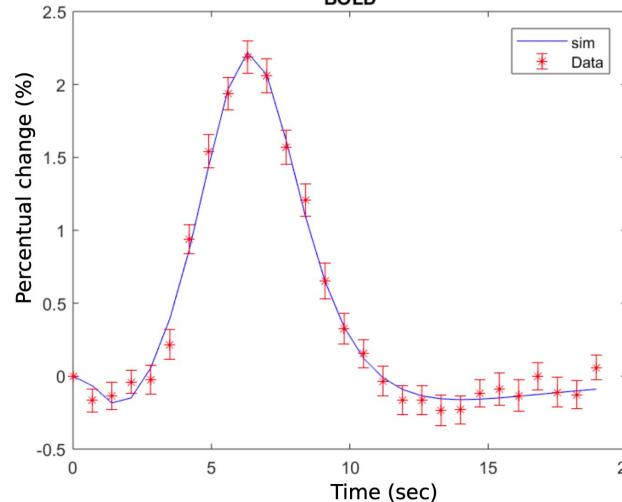
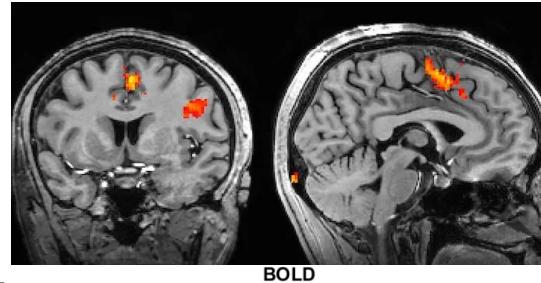
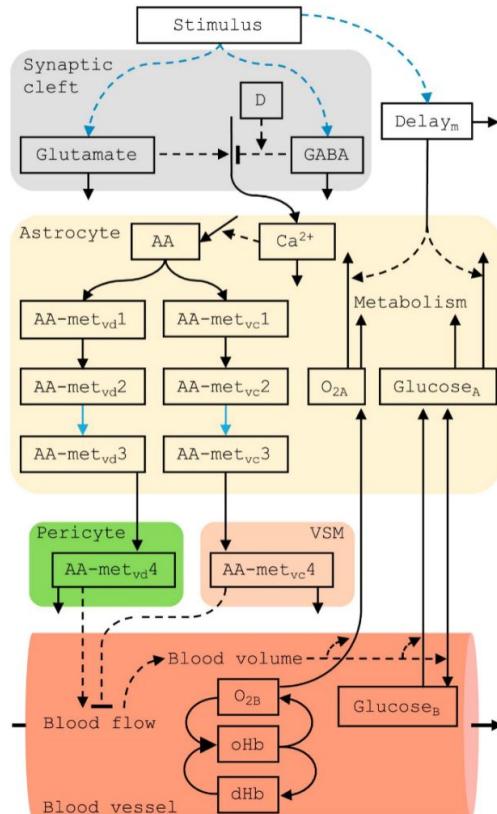
Current dipoles and EEG



Neurovascular coupling model (BOLD / fMRI)

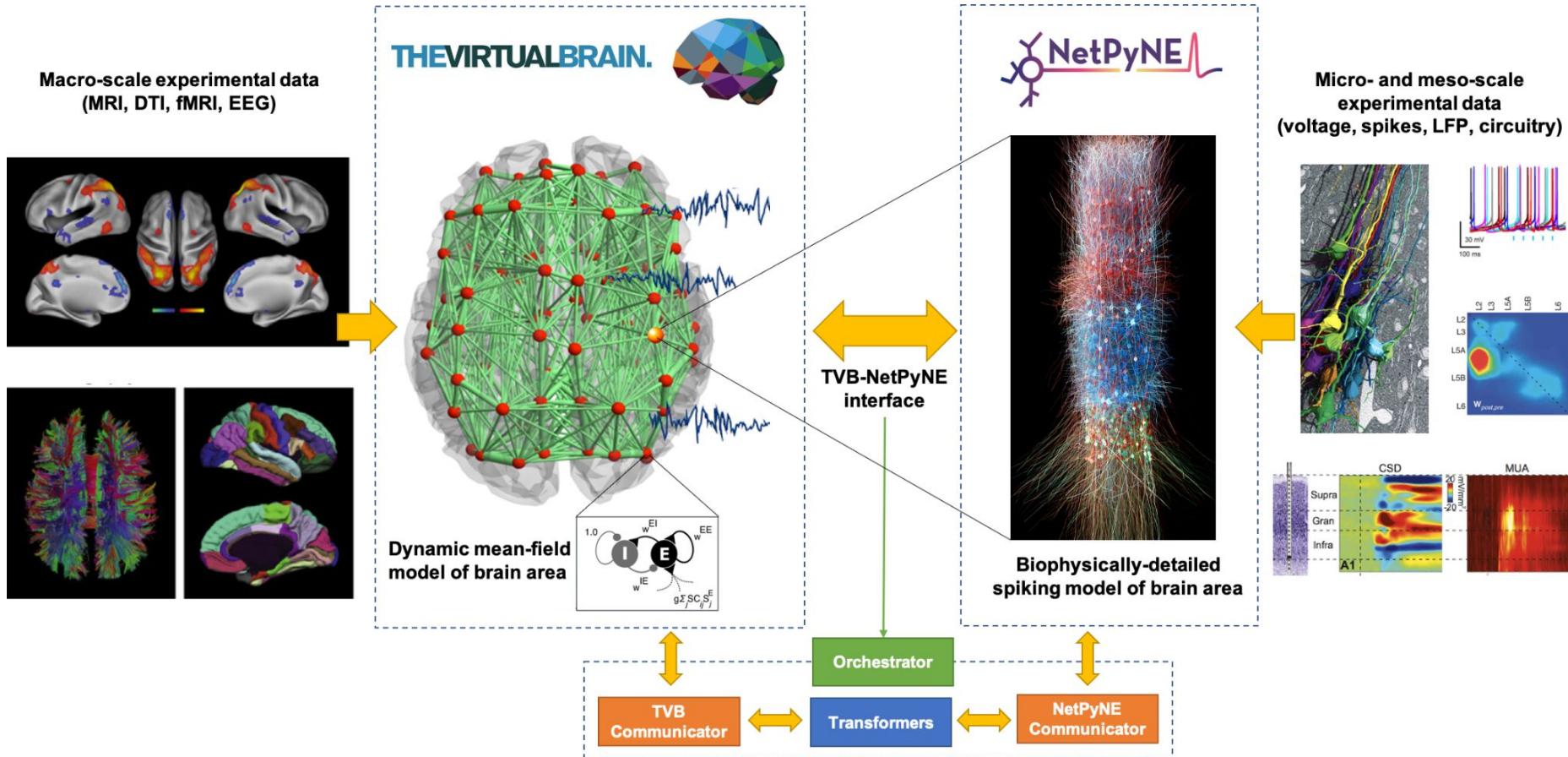
A

Model representation



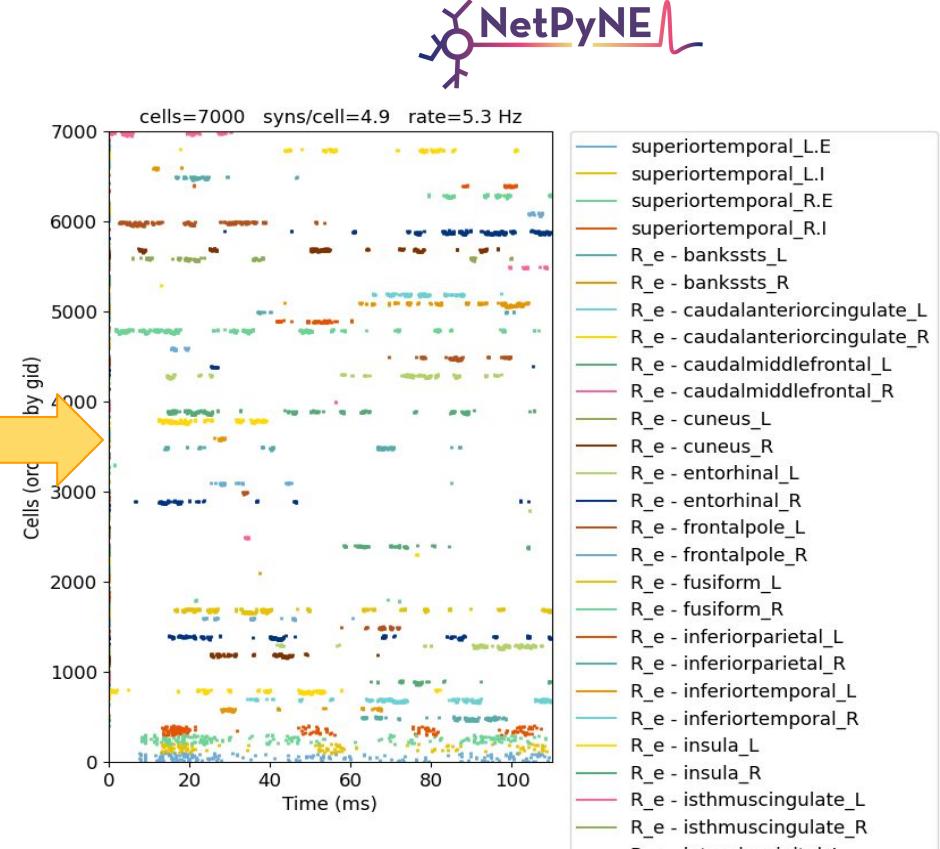
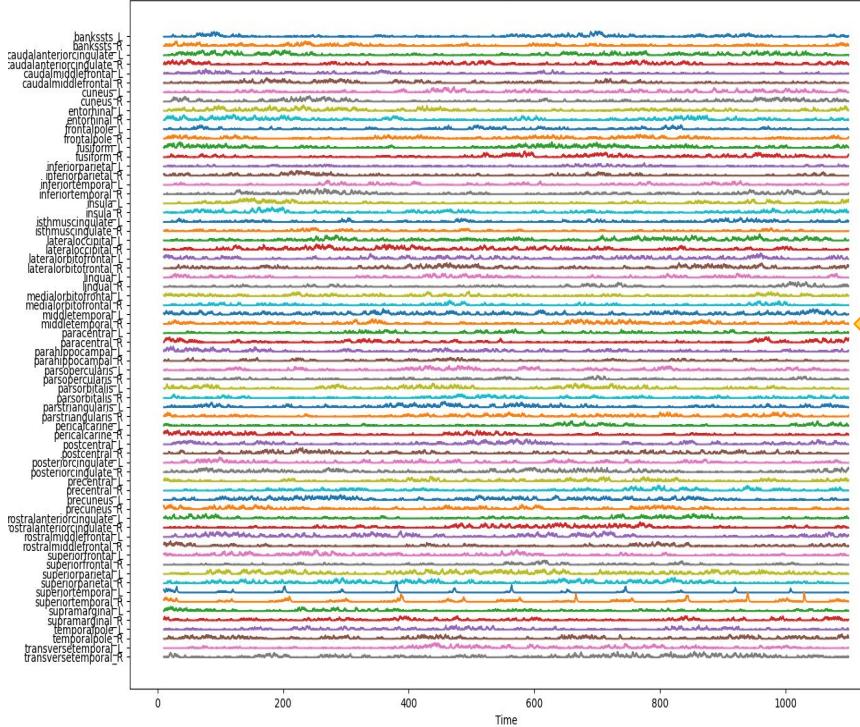
Sten S, et.al. Neural inhibition can explain negative BOLD responses: A mechanistic modelling and fMRI study. Neuroimage. 2017 Sep 1;158:219–31.

TVB-NetPyNE co-simulation

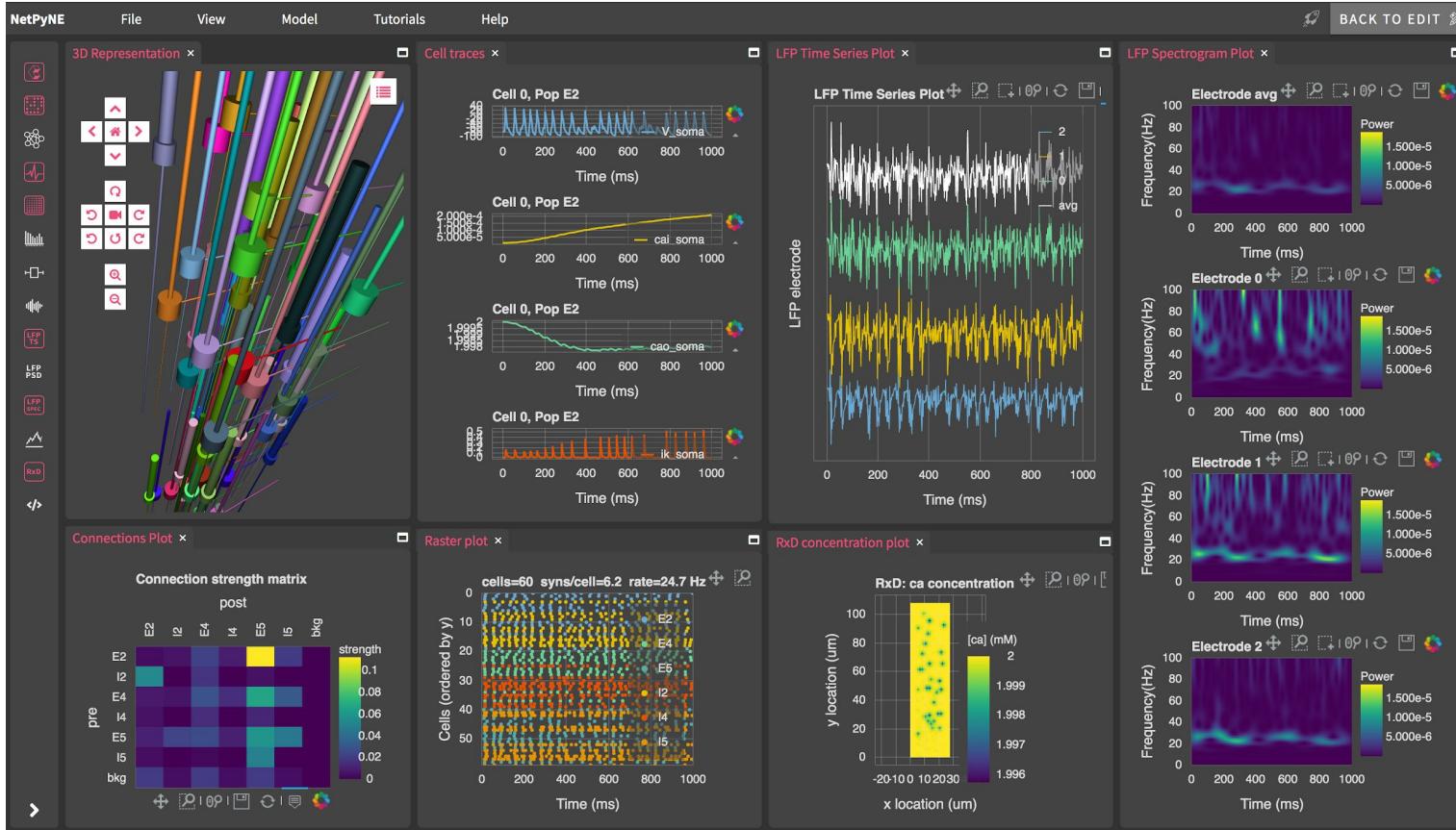


TVB-NetPyNE Example

THE VIRTUAL BRAIN.



GUI for Development, Simulation, Analysis



Useful for

- Students/beginners
- Model prototyping
- Exploring/Visualizing (interactive in sync)

GUI for Development, Simulation, Analysis

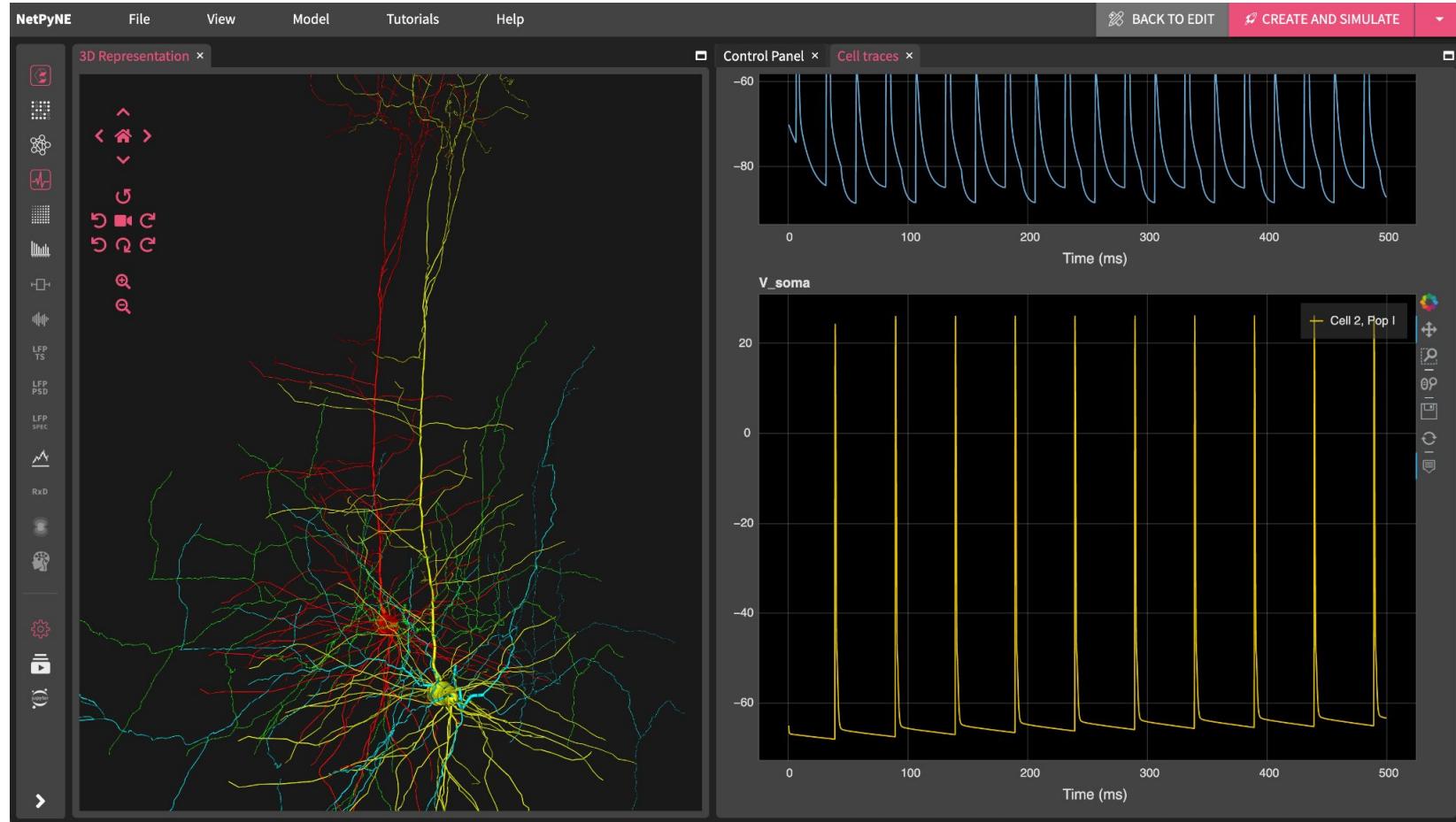
The screenshot shows the NetPyNE graphical user interface. The top navigation bar includes links for File, View, Model, Tutorials, Help, GO TO EXPLORER, CREATE NETWORK, and various configuration tabs like Cell Types, Populations, Synaptic Mechanisms, etc.

The left sidebar contains a 'Model Specification' section with icons for Cell Types, Populations, Synaptic Mechanisms, Connectivity Rules, Stim. sources, Stim. targets, Plot Settings, Rxd Configuration, and Configuration. Below this is a 'Tools' section with Experiment Manager and Python.

The main central area displays the 'Cell Types' panel. It features a breadcrumb navigation bar: Cell > CT > S > Mech. Below this is a grid of synaptic mechanism icons (represented as gears) labeled: kBK, pas, cat, ih, kap, can, cal, nax, and kdr. A detailed configuration panel on the right lists parameters for the selected 'kBK' mechanism:

- gpeak: 0.01529200755489
- caPh: 0.002
- caPk: 1
- caPmax: 1
- caPmin: 0
- caVhh: 0.002
- caVhmax: 155.67
- caVhmin: -2.1899738592999967
- k: 17
- tau: 1

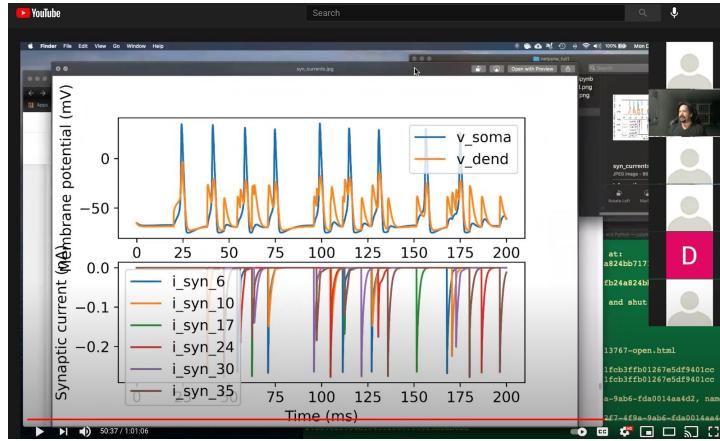
GUI for Development, Simulation, Analysis



Documentation, tutorials and examples

<http://netpyne.org>

- [All learning resources:](#)
 - [Documentation](#)
 - [Jupyter Notebook Tutorials](#)
 - [Video tutorials \(40+ hours\)](#)
 - [Package reference](#)
- [Example models](#)
- [Q&A Forum](#)
- [Mailing List](#)



★ NetPyNE Q&A forum 66 members

NetPyNE (www.netpyne.org) is a high-level python interface to NEURON that facilitates the development, parallel simulation, and enables users and developers to post questions, answers and comments about the tool.
Our previous Q&A forum with many posts can be found here: <https://www.neuron.yale.edu/phpBB/viewforum.php?f=45>

	zirui.w...@gmail.com	LFP signal baseline offset, fluctuate below baseline 0 – Hello, I am usi...
	maliha....@gm..., vbra...@gma... 2	Specify colours in rasterplot – Hi Maliha, You can use `popColors` para...
	zirui.w...@gma..., Eugenio Urda... 2	how to reset kernel in netpyne – Hi Zirui, to get different results you sho...
	bh...@rice.e..., ... Gin Estrella Cr... 4	Problem with importing cells – I'm somewhat glad to hear that I'm not t...

NetPyNE tool: Publication in eLife

The image shows the header of the eLife website. It features the eLife logo on the left, followed by a horizontal navigation bar with links for 'ABOUT', 'COMMUNITY', 'SUBMIT MY RESEARCH' (in a blue box), and a user icon. Below this is a secondary navigation bar with 'HOME', 'MAGAZINE', and 'INNOVATION' links, along with a search icon.

Accepted manuscript, PDF only. Full online edition to follow.



COMPUTATIONAL AND SYSTEMS BIOLOGY, NEUROSCIENCE



NetPyNE, a tool for data-driven multiscale modeling of brain circuits



Salvador Dura-Bernal , Benjamin A Suter, Padraig Gleeson, Matteo Cantarelli, Adrian Quintana, Facundo Rodriguez, David J Kedziora, George L Chadderdon, Cliff C Kerr, Samuel A Neymotin, Robert A McDougal, Michael Hines, Gordon M G Shepherd, William W Lytton
[« see less](#)

State University of New York Downstate Medical Center, United States; Northwestern University, United States; University College London, United Kingdom; Metacell LLC, United States; EyeSeeTea Ltd, United Kingdom; University of Sydney, Australia; Yale University, United States

TOOLS AND RESOURCES Apr 26, 2019

CITED 0 VIEWS 272 ANNOTATIONS

CITE AS: eLife 2019;8:e44494 DOI: 10.7554/eLife.44494

NetPyNE-based papers

<http://netpyne.org/about.html#publications>

nature > schizophrenia

Article | Open Access | Published: 28 April 2022

The effect of alterations of schizophrenia-associated genes on gamma band oscillations

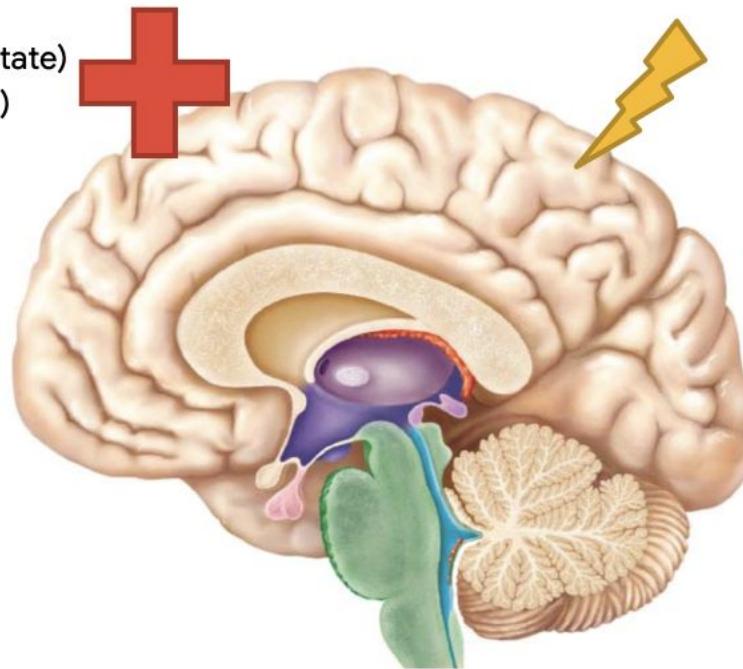
Christoph Metzner , Tuomo Mäki-Marttunen, Gili Karni, Hana McMahon-Cole & Volker Steuber

Schizophrenia 8, Article number: 46 (2022) | [Cite this article](#)

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Growing community (>80 models, >40 Labs)

- Schizophrenia (TU Berlin, Brown)
- Ischemic stroke (Yale, Downstate)
- Epilepsy (Cincinnati, Brown, Downstate)
- Chronic Pain (Okinawa, Downstate)
- Depression (Brown)
- Parkinson's (Edinburgh)



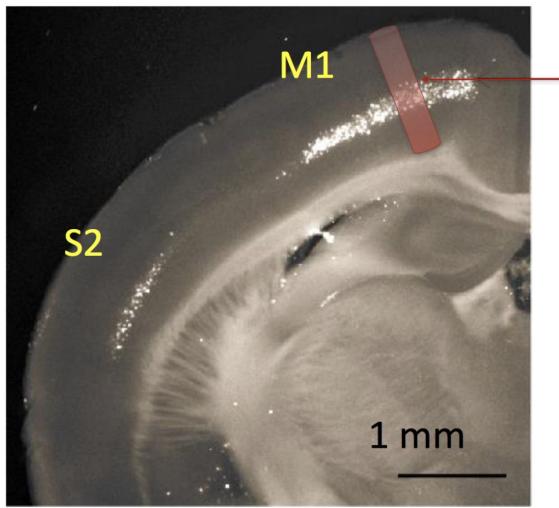
- PFC (Sao Paulo)
- Thalamus (UCL, Missouri)
- Olfactory Bulb (Palermo)
- Striatum (Dublin)
- Amygdala (Princeton)
- Hippocampus (Sao Paulo)
- Cardiac circuits (Jefferson, Downstate, Pavia)



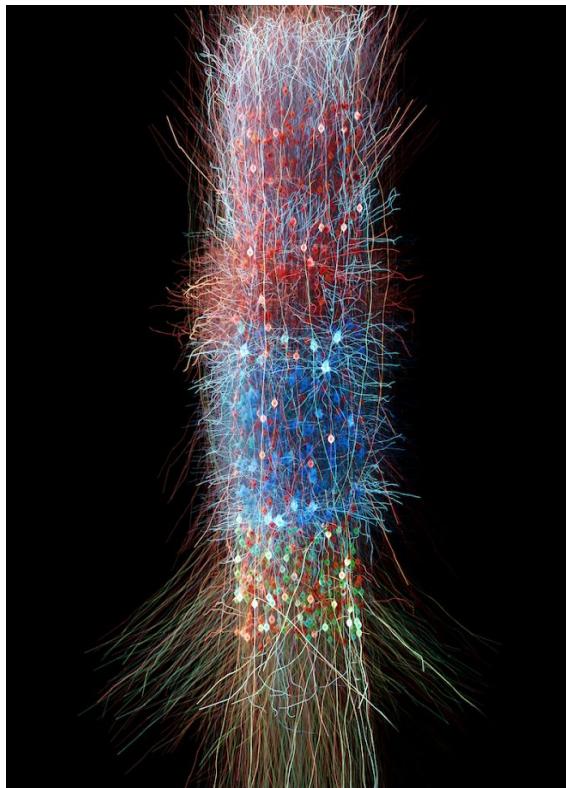
- TMS / tDCS / tACS (Duke, Toronto)
- Optogenetics (Sydney)
- Electrical stimulation (Downstate)
- Ketamine (Brown)
- EEG/MEG (Puerto Rico, Brown, Rice)
- fMRI (Linkopig)
- M1 and S1 (Downstate)
- A1 (NKI)
- V1 (Queensland, Sao Paulo)
- Claustrum (Singapore)
- Cerebellum (Sao Paulo)
- Spinal Cord (Northeastern)
- Enteric / gastrointestinal circuits (Melbourne)

Data-driven model of motor cortex (M1) circuits

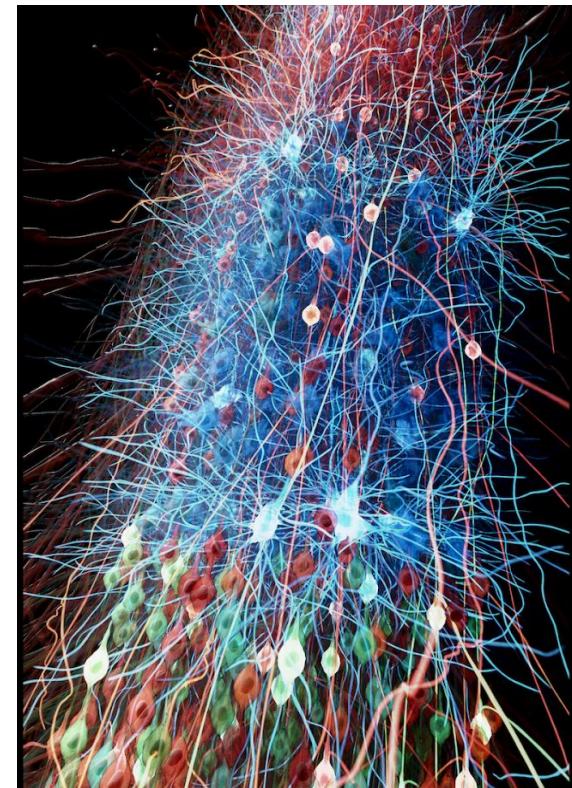
300 um diameter column



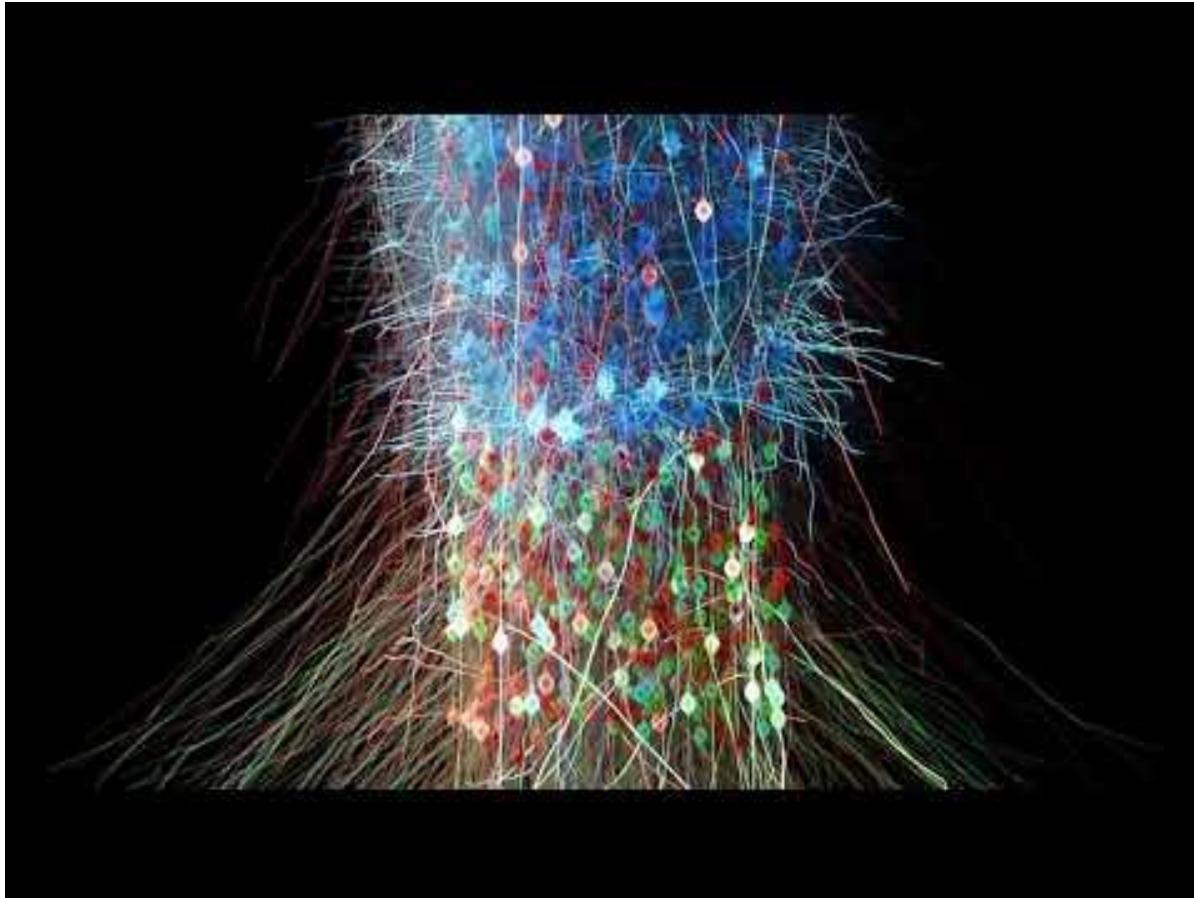
10,000 neurons



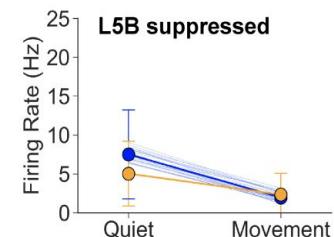
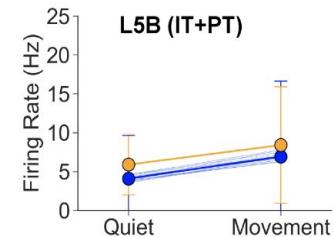
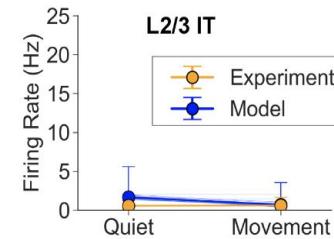
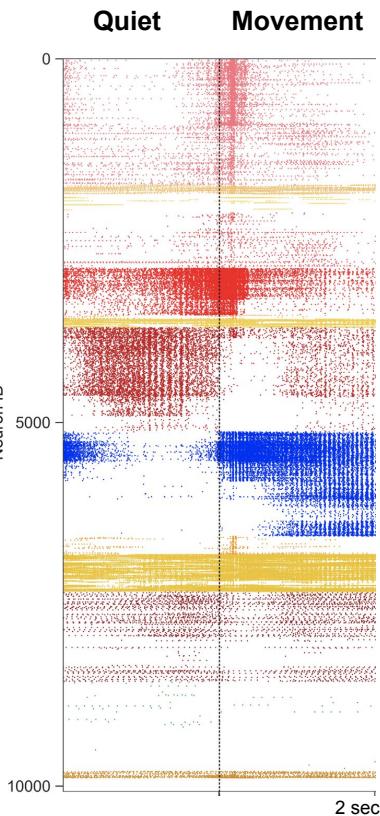
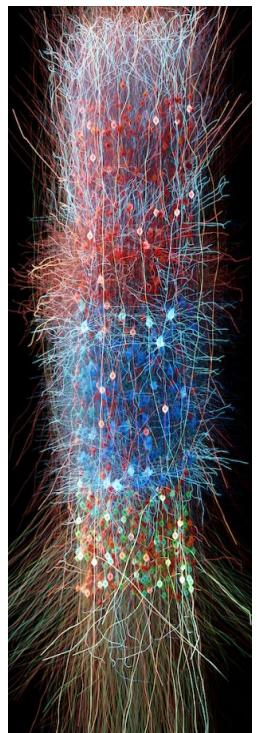
30 million connections



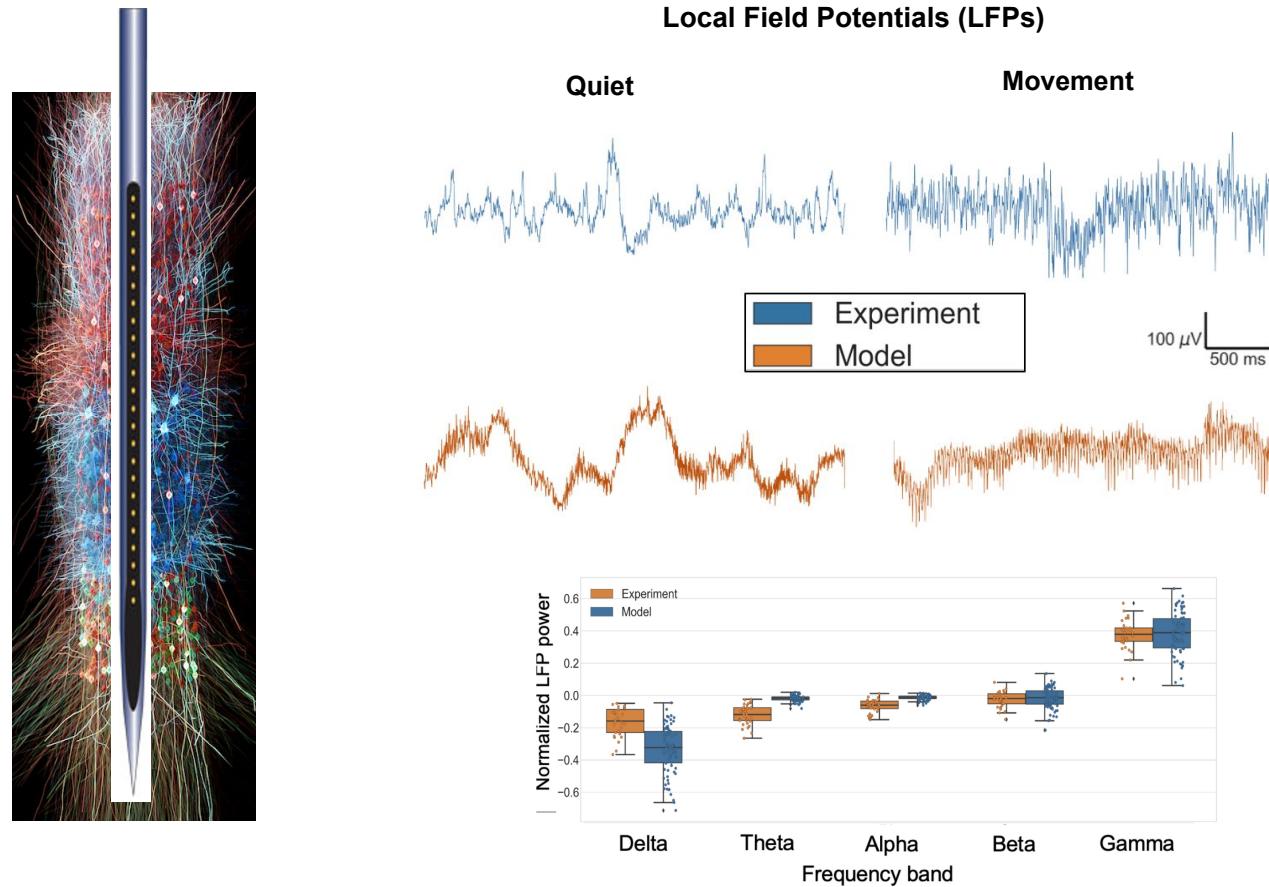
Data-driven model of motor cortex (M1) circuits



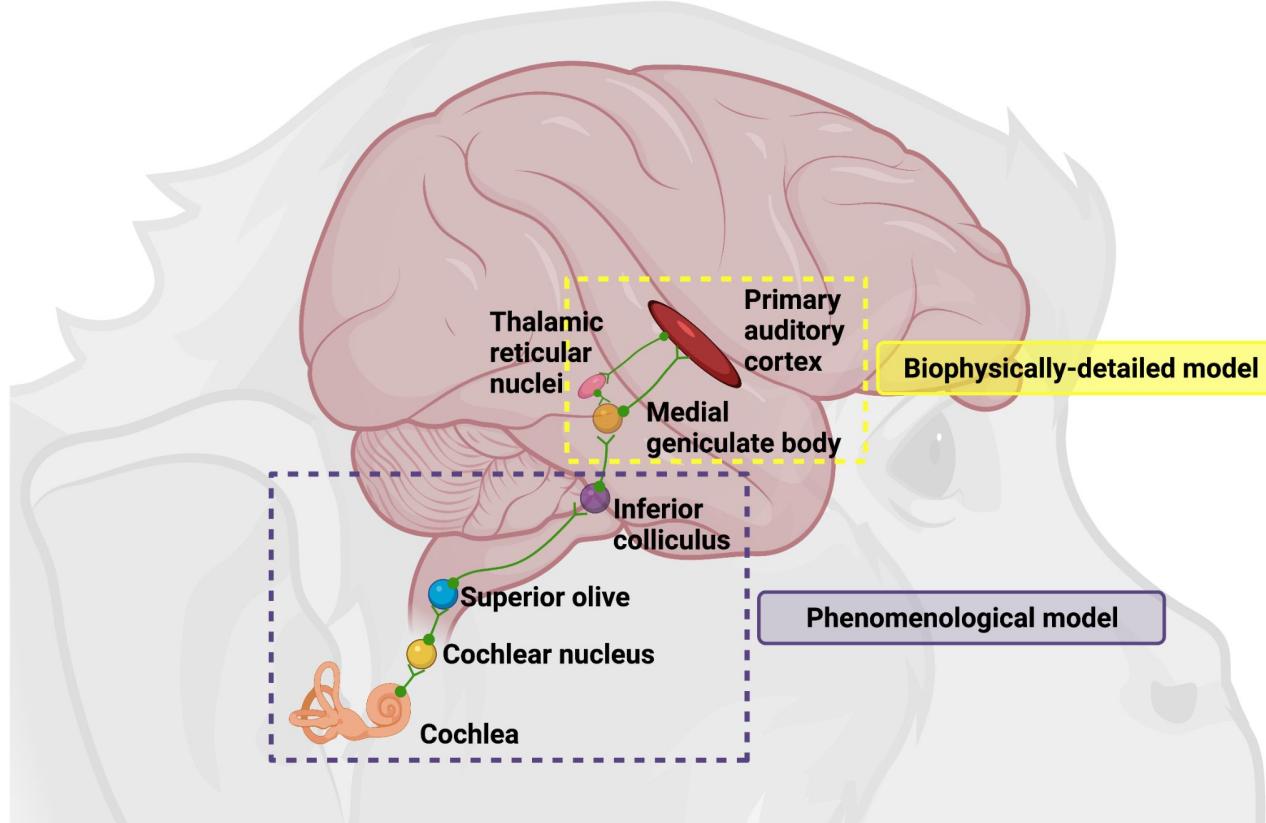
M1 model validated against in vivo data



M1 model validated against in vivo data

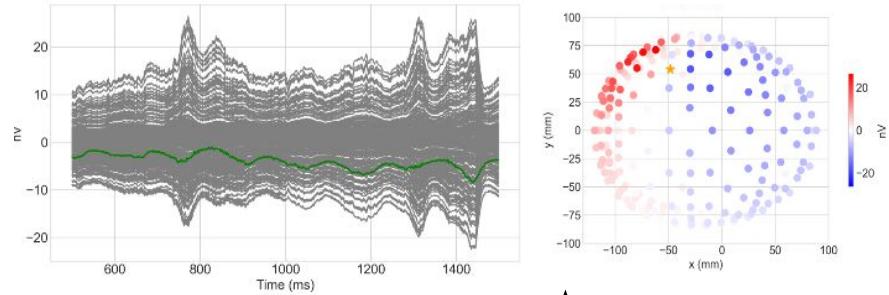


Macaque auditory thalamocortical model

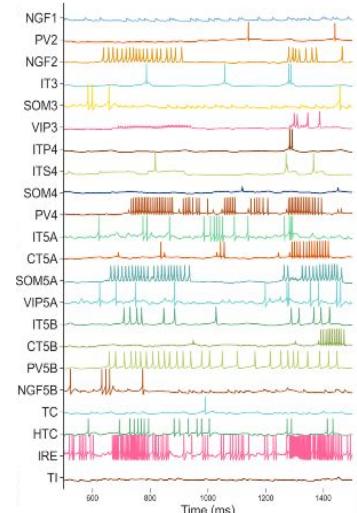


A1 model recordings at multiple scales/modalities

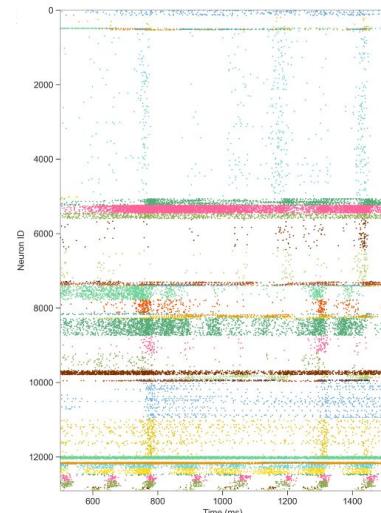
EEG



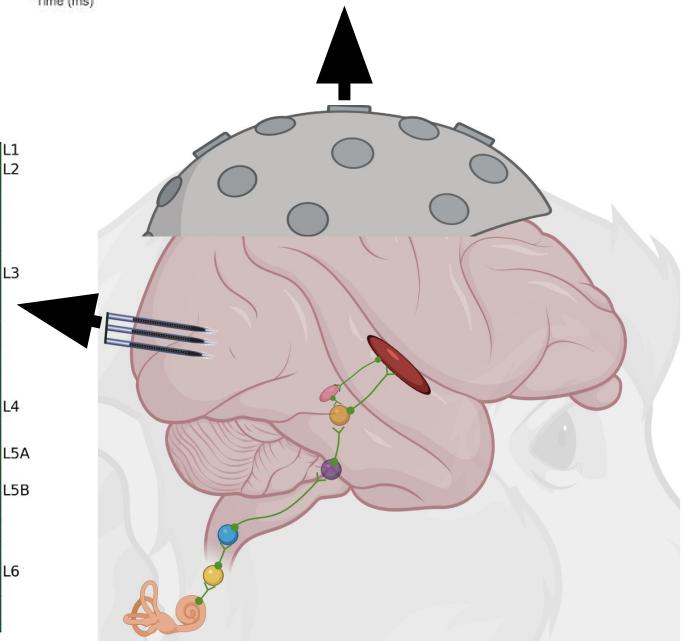
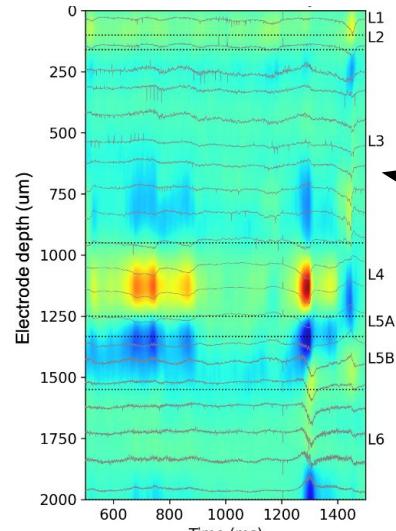
Membrane Voltage



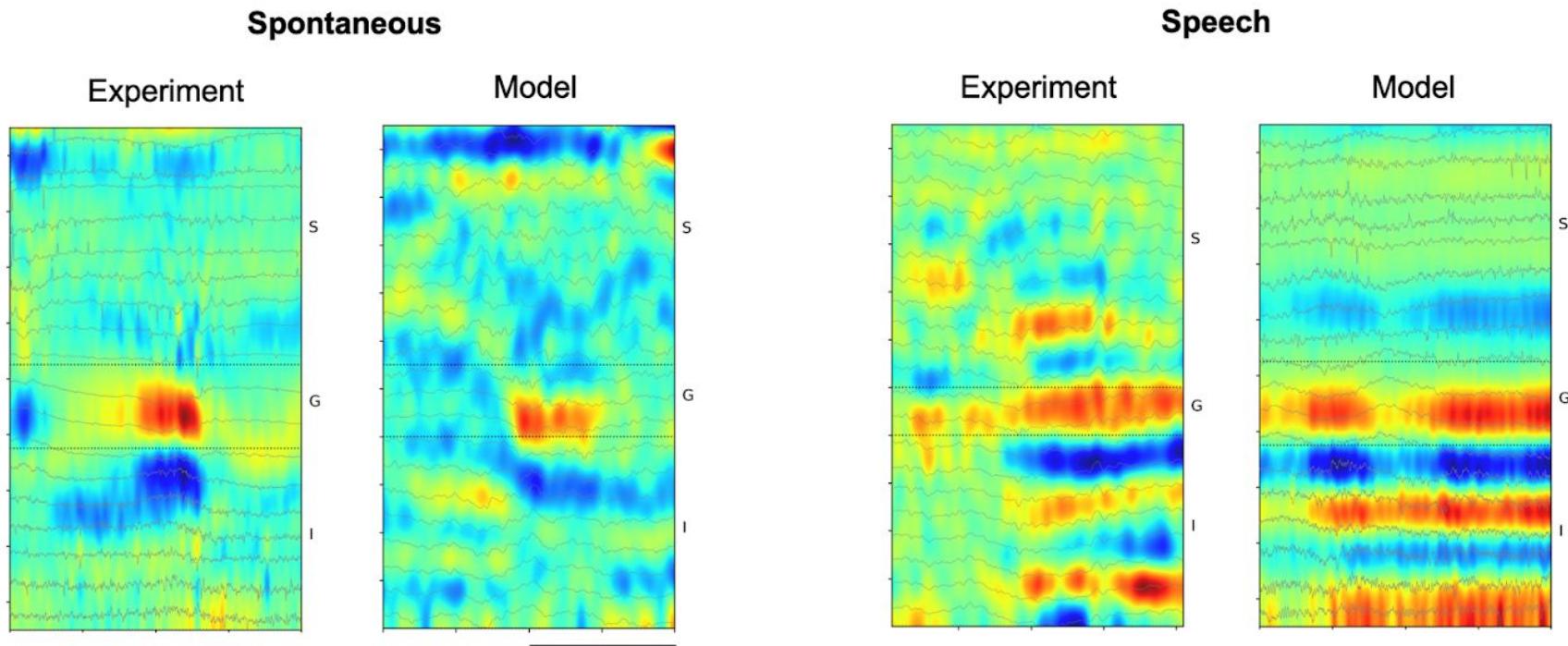
Spikes



LFP / CSD

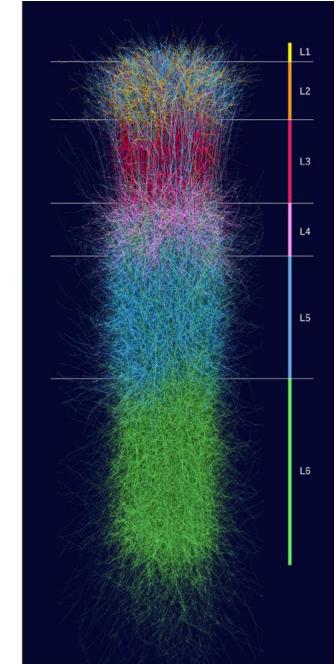
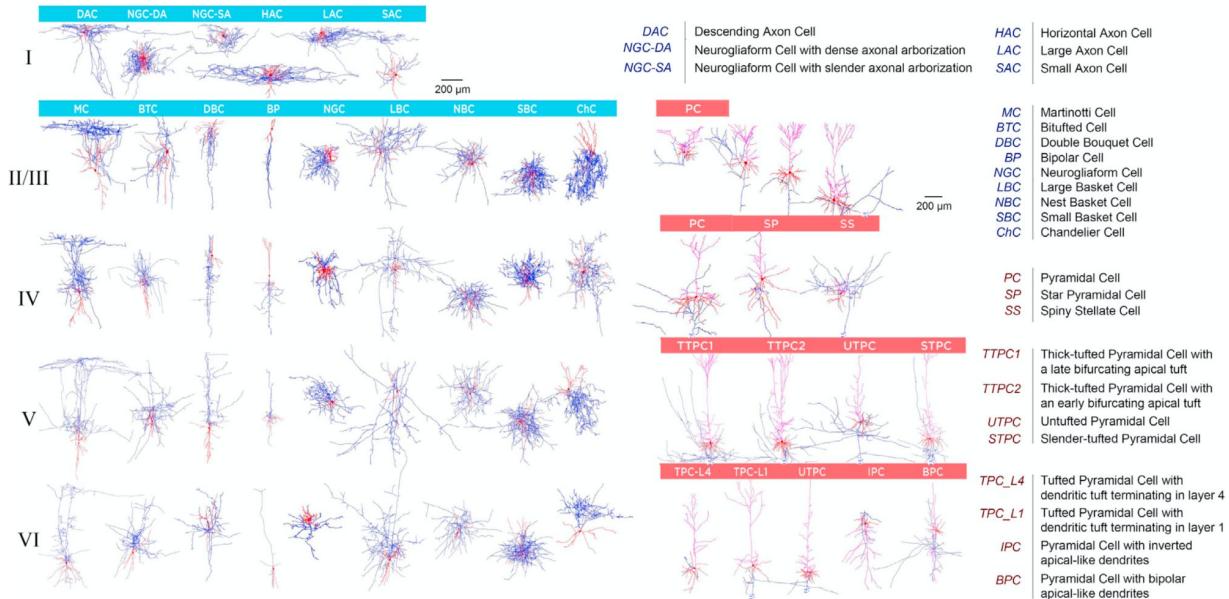


A1 model validated against in vivo data



Somatosensory thalamocortical circuits

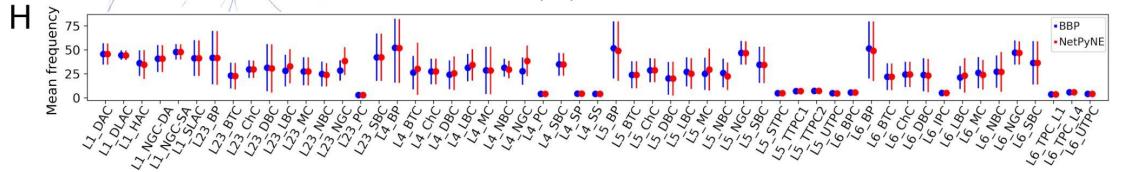
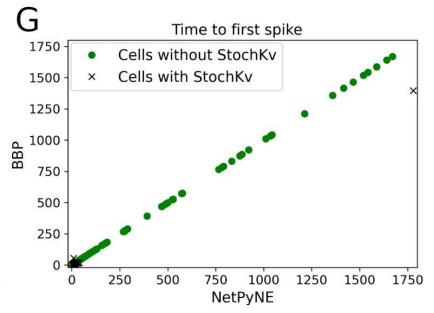
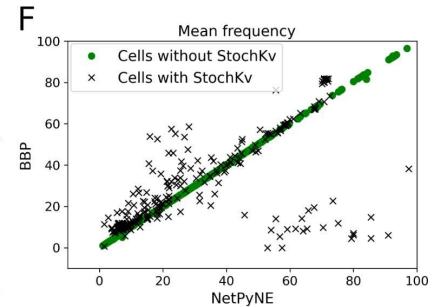
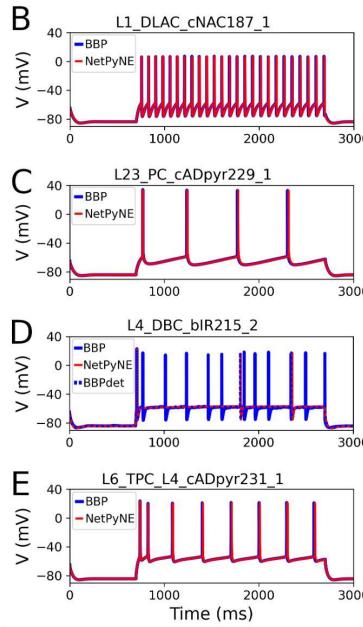
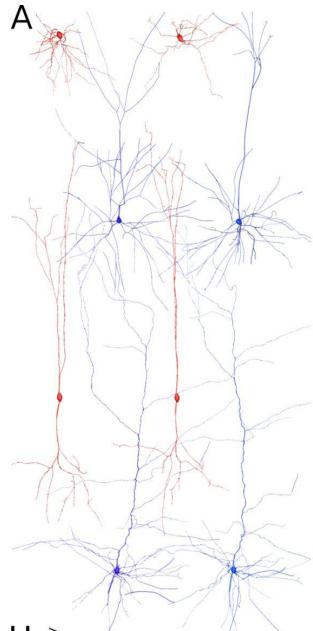
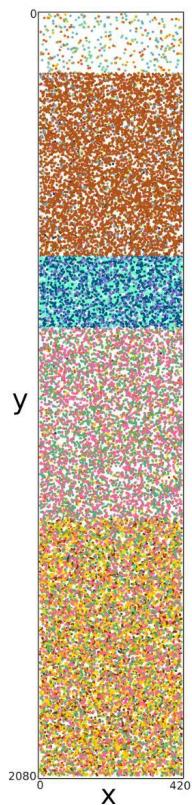
- Highly detailed model: 31k cells, 37M synapses, 207 cell types, 1941 pathways
- Original model by EPFL Blue Brain Project



Markram et al, 2015

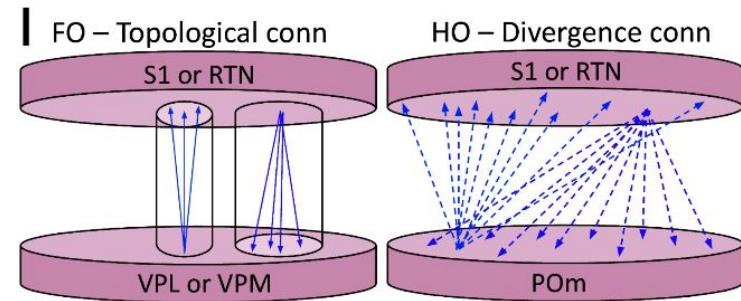
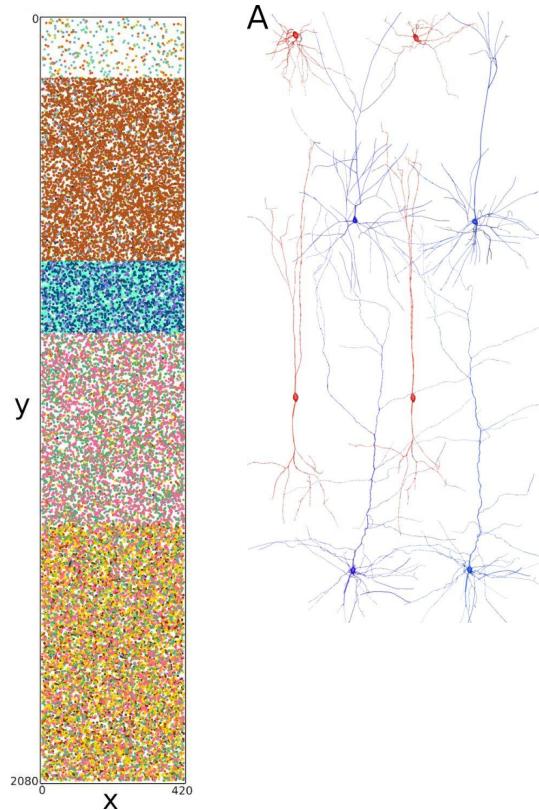
Somatosensory thalamocortical circuits

- Reimplemented
in NetPyNE

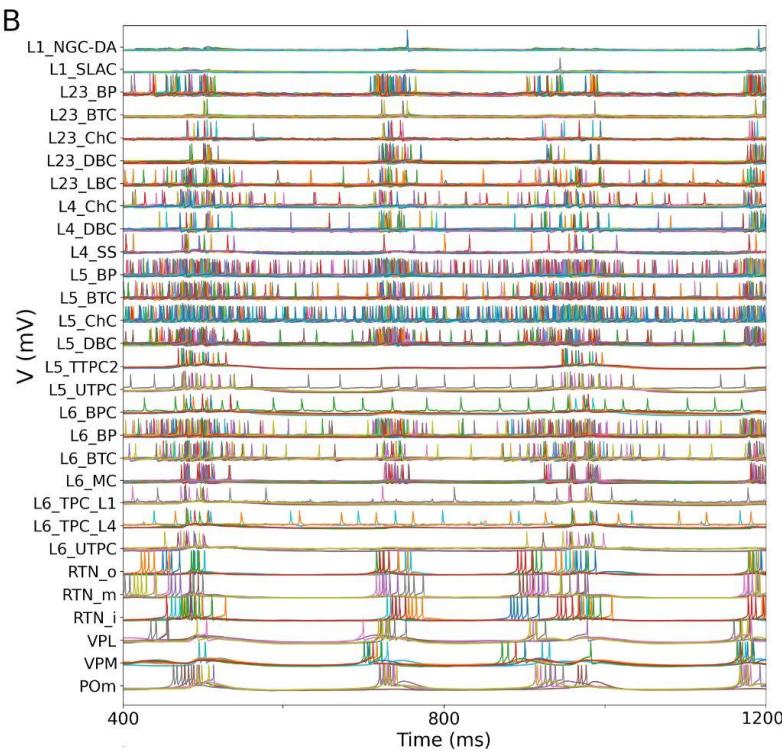
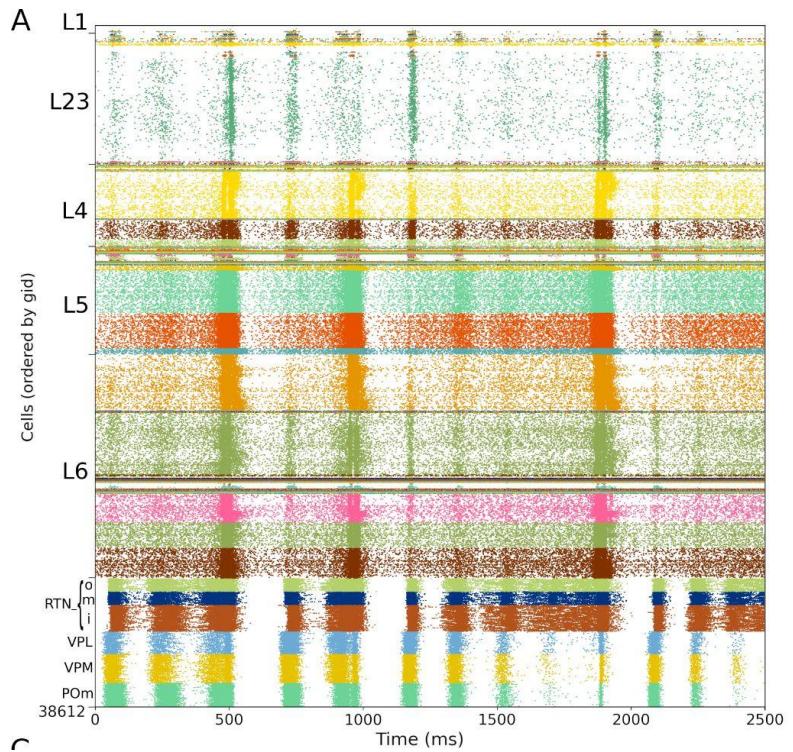
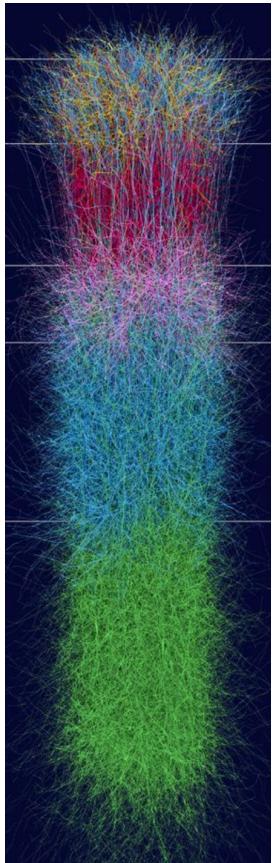


Somatosensory thalamocortical circuits

- Reimplemented in NetPyNE
- Replicated cell properties and connectivity
- Extended to include thalamus



Somatosensory thalamocortical circuits



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