

EPFL

Blue Brain Project

Soplata Job Talk, 2024-05-09, For HNN Software Engineer Position

Download this talk here:
asoplata.com/talk

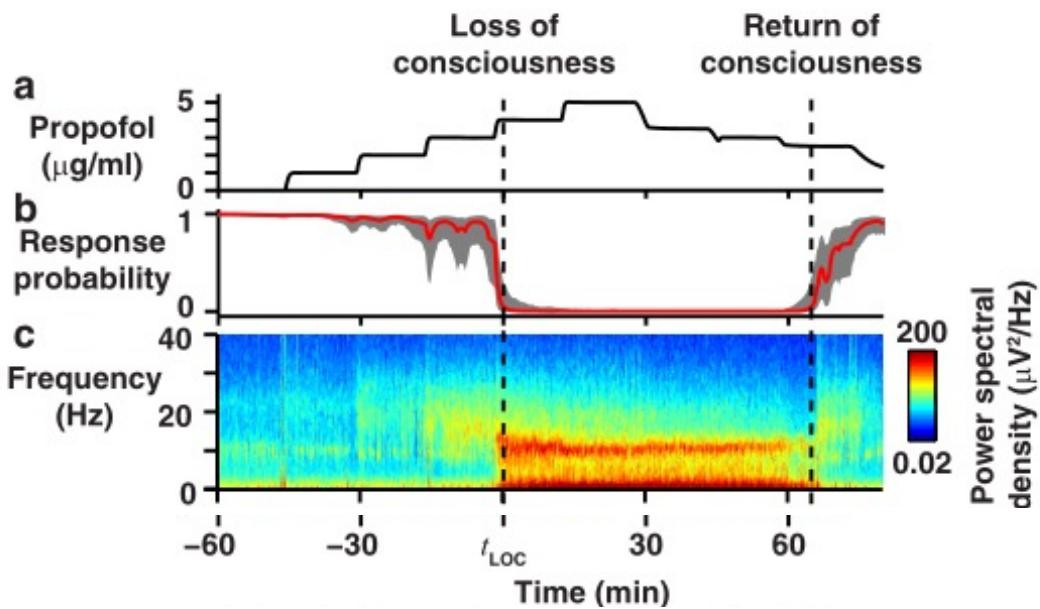
Austin Soplata, PhD
Postdoc for Thalamus Special Region, Circuits Team

The thalamus: If you're reading this, you have one (probably)



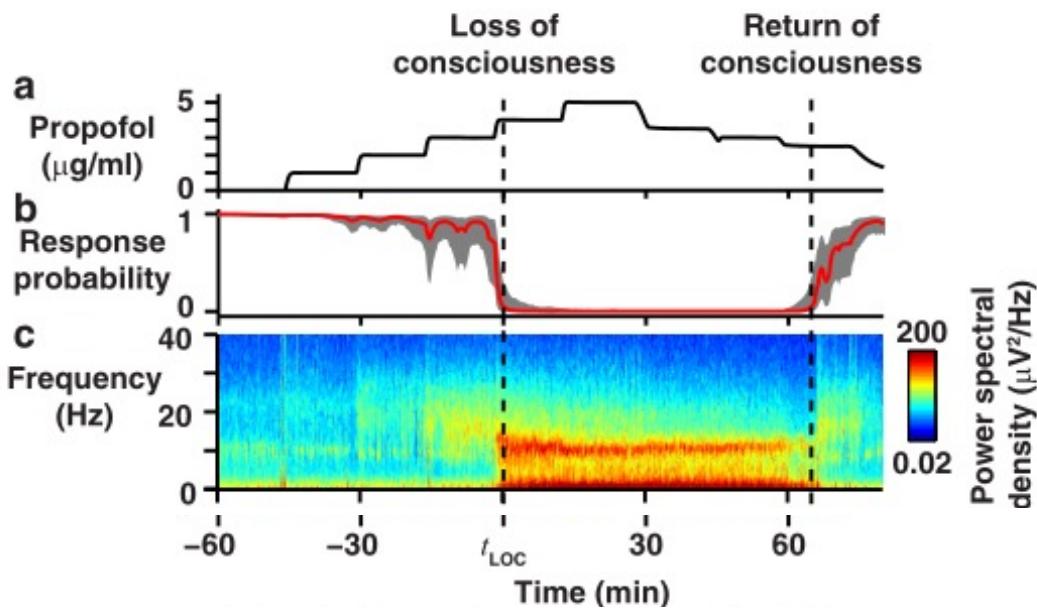
(not to scale)

PhD and first postdoc: Understanding propofol anesthesia via modeling EEG oscillations



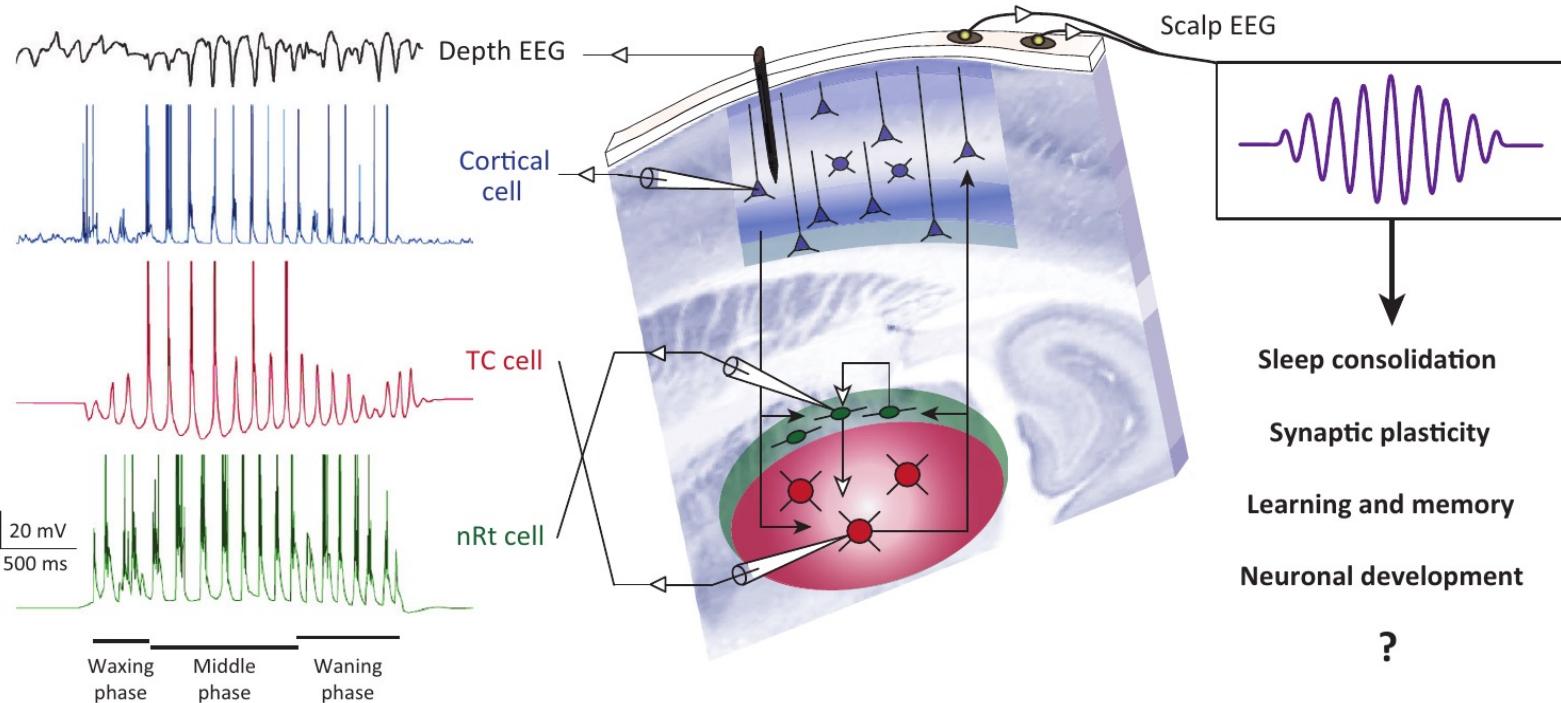
- What causes **Alpha Oscillations (8-14 Hz)** in propofol anesthesia?
- What causes **Slow Wave Oscillations (SWO, 0.1-2 Hz)** in propofol anesthesia?
- What causes the change in **Phase-Amplitude Coupling** between alpha and SWO?

PhD and first postdoc: Understanding propofol anesthesia via modeling EEG oscillations

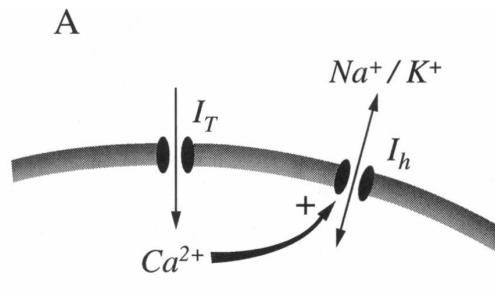
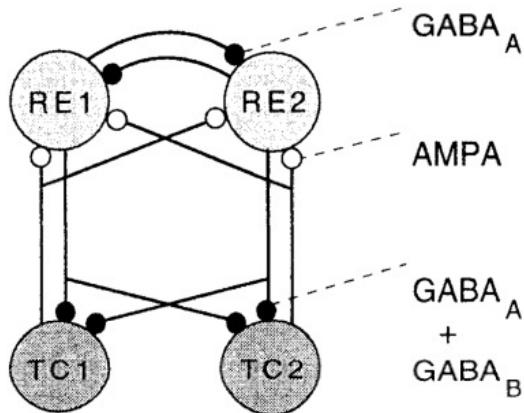


- What causes **Alpha Oscillations (8-14 Hz)** in propofol anesthesia?
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Propofol alpha is same frequency as Thalamic Sleep Spindles (8-16 Hz)

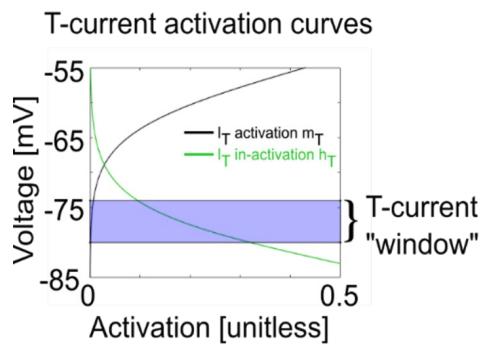
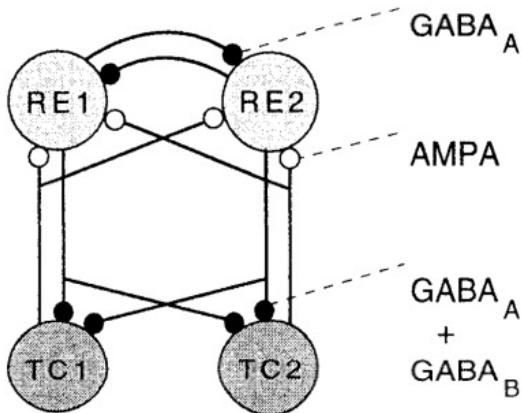


Destexhe Model of Thalamic Spindles

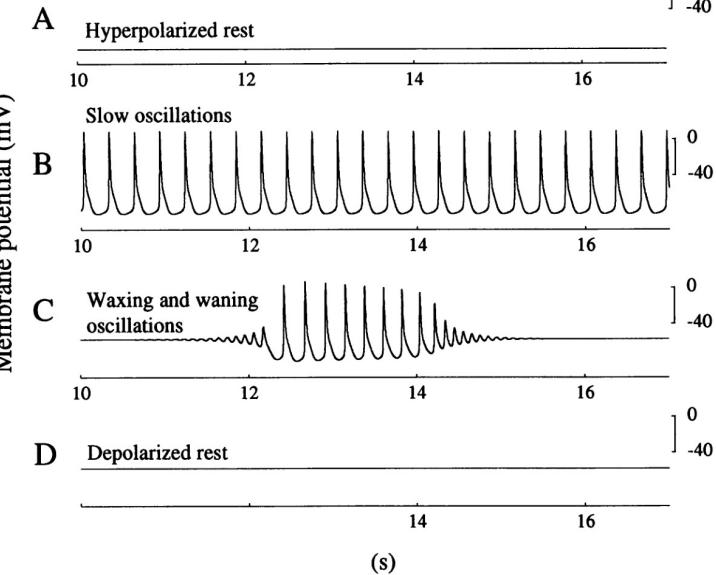


$$C_m \dot{V}_T = -g_L(V_T - E_L) - I_T - I_h - I_{KL} - I_{Na} - I_K - I_{GABA_A T} - I_{GABA_B} \quad (1)$$

Destexhe Model of Thalamic Spindles



Different H-current simulations



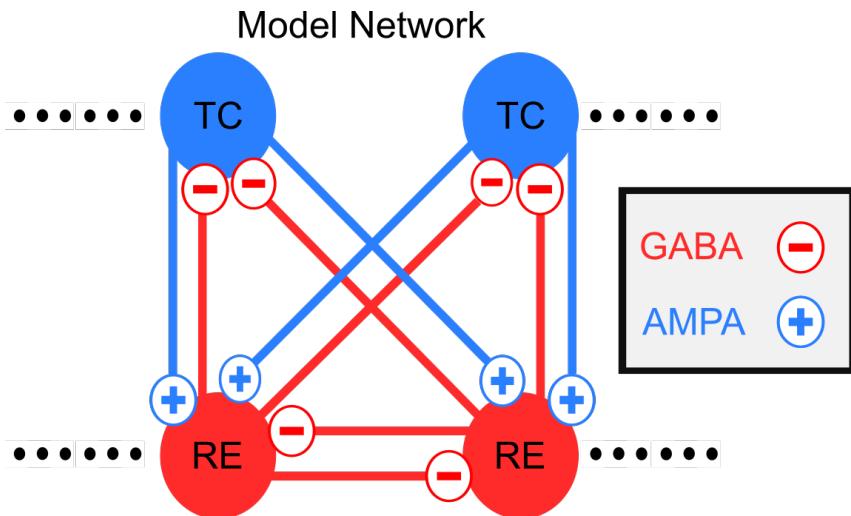
$$C_m \dot{V}_T = -g_L(V_T - E_L) - I_T - I_h - I_{KL} - I_{Na} - I_K - I_{GABA_A T} - I_{GABA_B} \quad (1)$$

DynaSim: A MATLAB Toolbox for Neural Modeling and Simulation

Jason S. Sherfey^{1,2}, Austin E. Sopkota³, Salva Ardid¹, Erik A. Roberts⁴, David A. Stanley¹, Benjamin R. Pittman-Polletta¹ and Nancy J. Kopell¹*

- Easy vectorization of ODEs
- Plug-and-play mechanism functionality like NEURON MOD files
- Built-in parameter grid search and batch job submission on clusters/HPC
- ...however, not actively developed for the last 2-3 years

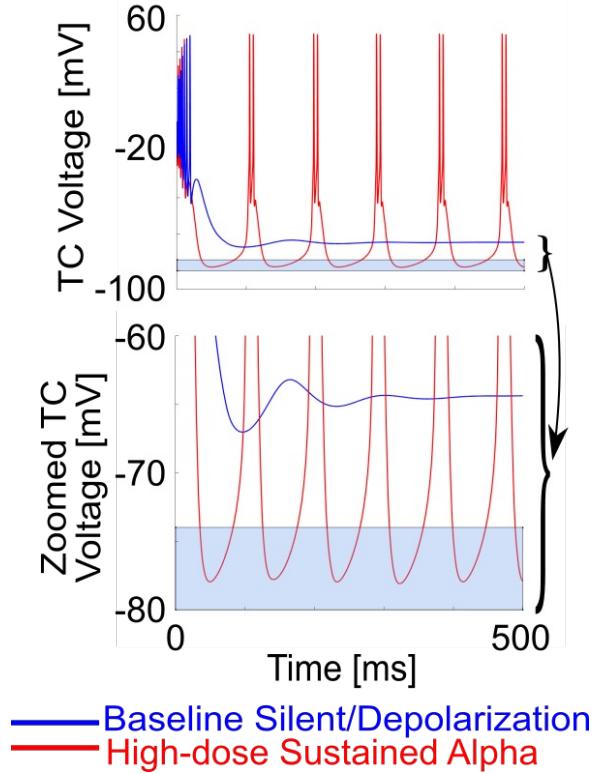
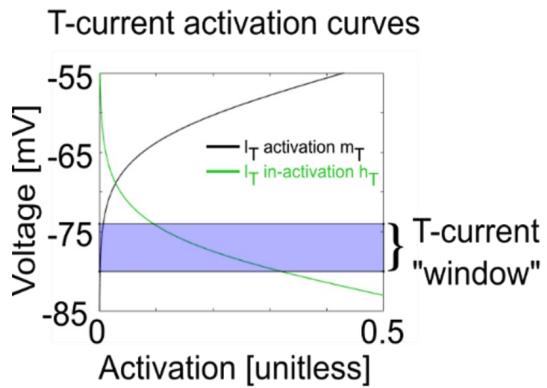
First Thalamic Circuit



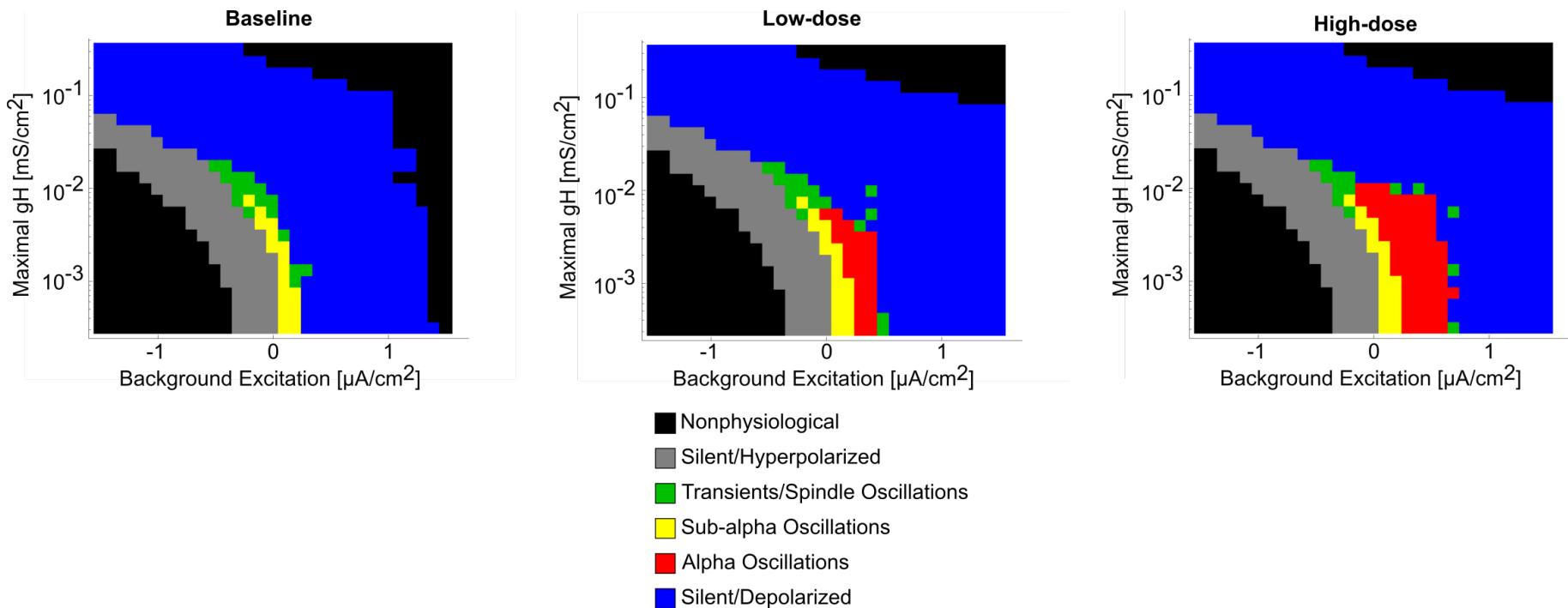
Propofol direct effects

- Increases \bar{g}_{GABA_A}
("strength of inhibition")
- Increases τ_{GABA_A}
("how long inhibition lasts")
- Decreases \bar{g}_H
(TC cell H-current strength)
- Decreases Background Excitation

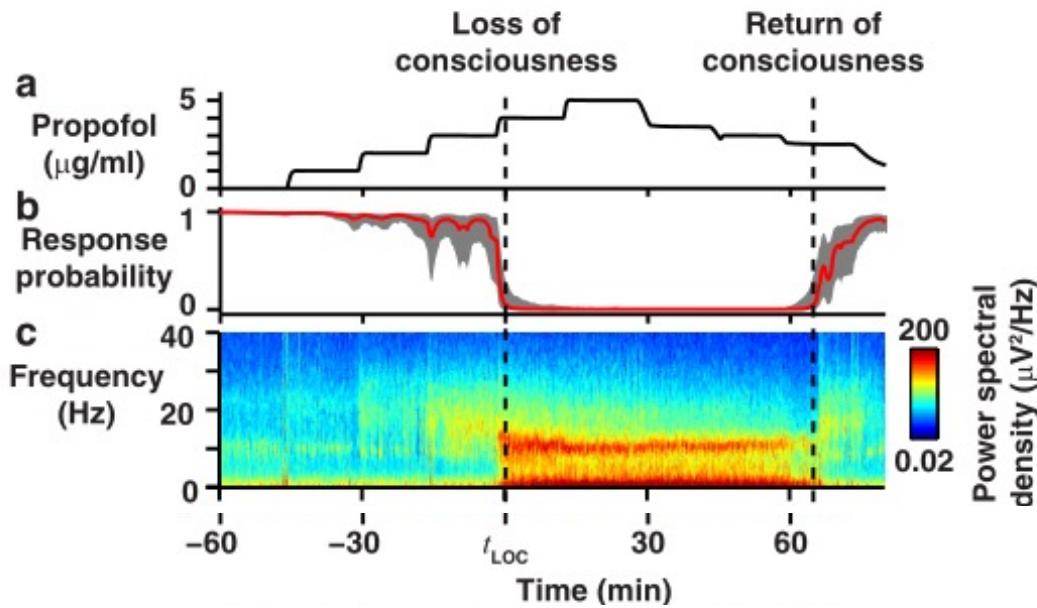
Enhanced GABA_A inhibition enables Alpha



Propofol changes to **GABA_A** and H-current affect the likelihood of **Alpha**

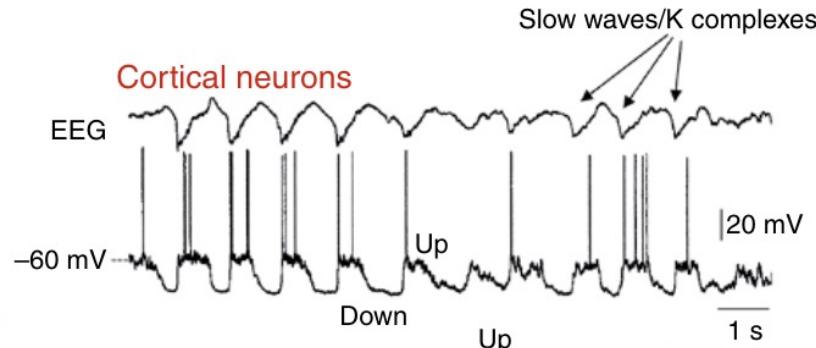


Understanding propofol anesthesia via modeling EEG oscillations



- What causes Alpha Oscillations (8-14 Hz) in propofol anesthesia?
- What causes Slow Wave Oscillations (SWO, 0.1-2 Hz) in propofol anesthesia?
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Sleep Slow-Wave Oscillations (SWO) (~1 Hz)



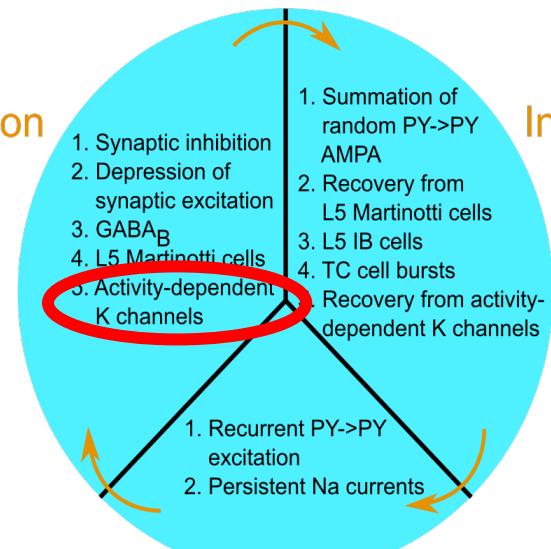
SWO "onset"

- 1. Neuromodulators affecting K-Leak
- 2. Decrease in PY-PY excitation

Slow Wave Oscillation Mechanisms

Termination

Initiation



Second, Thalamo-cortical circuit

Cortical Slow Wave Mechanism:
K(Na)-current

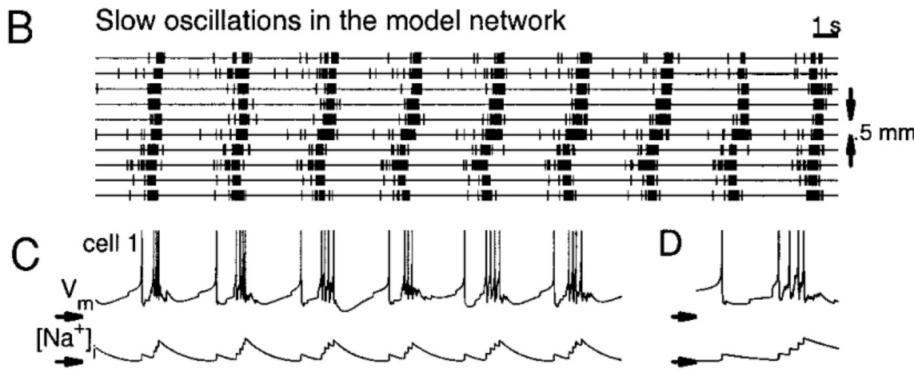


Image from (Compte et al., 2003)

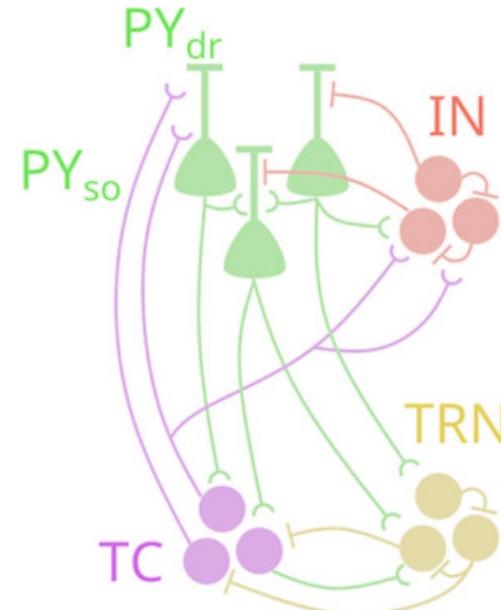
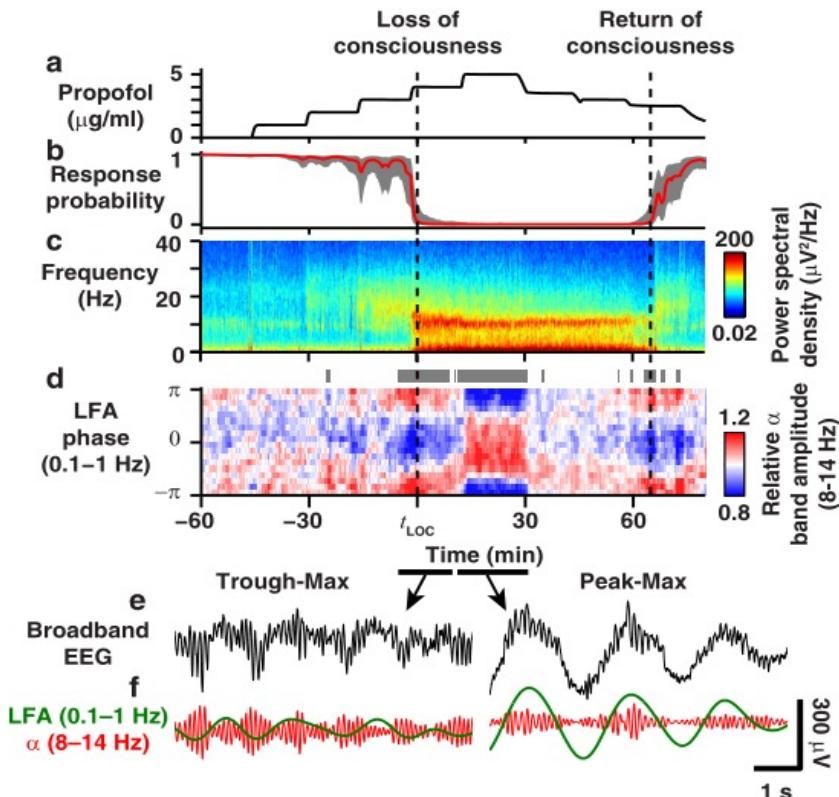


Image from (Soplatá et al., 2023)

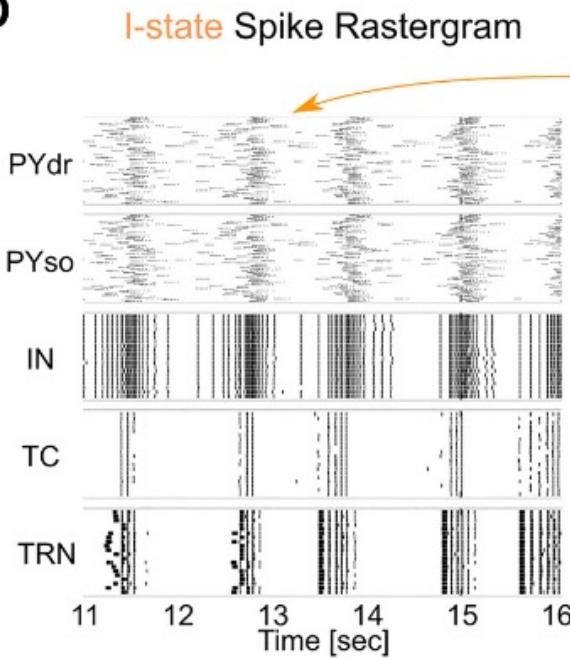
Understanding propofol anesthesia via modeling EEG oscillations



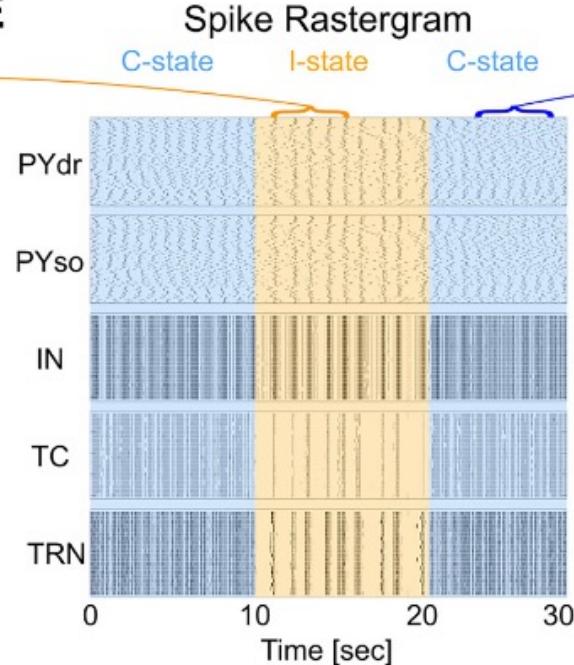
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Our thalamocortical circuit would randomly switch between two oscillatory states

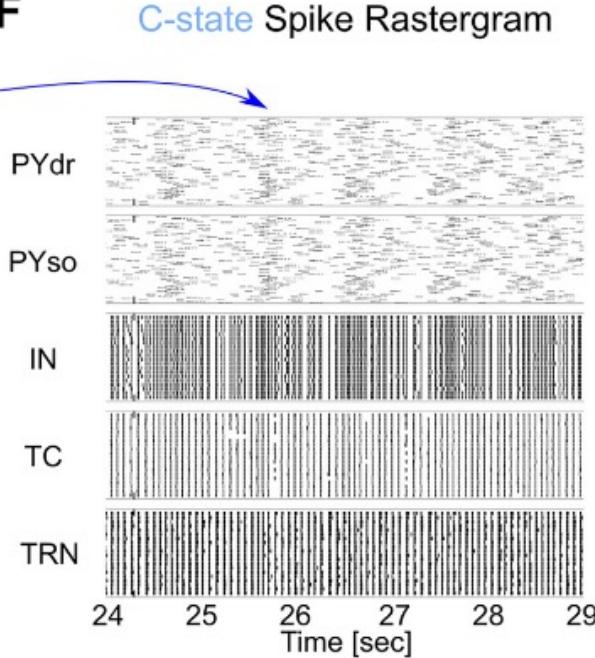
D



E

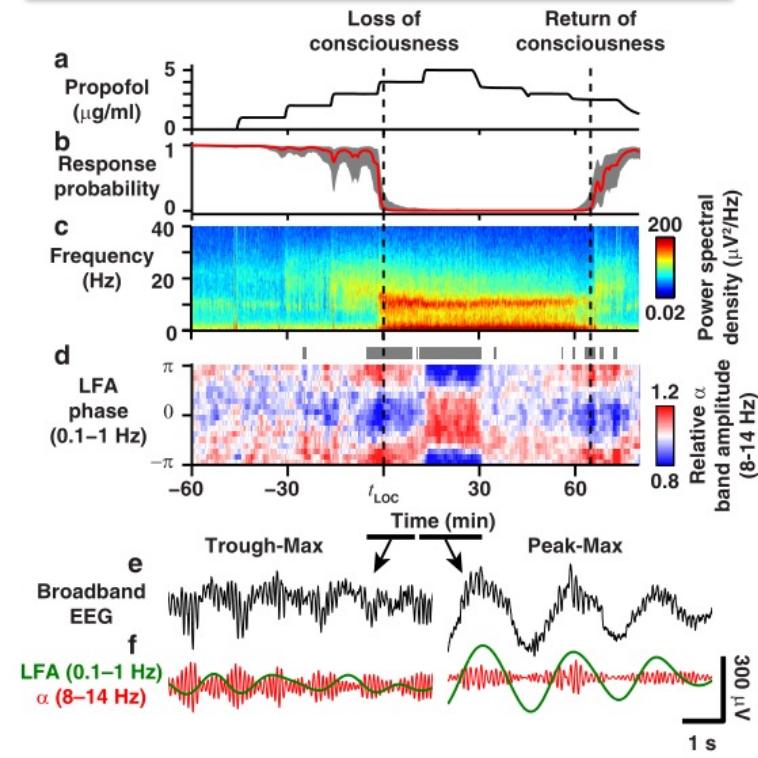


F



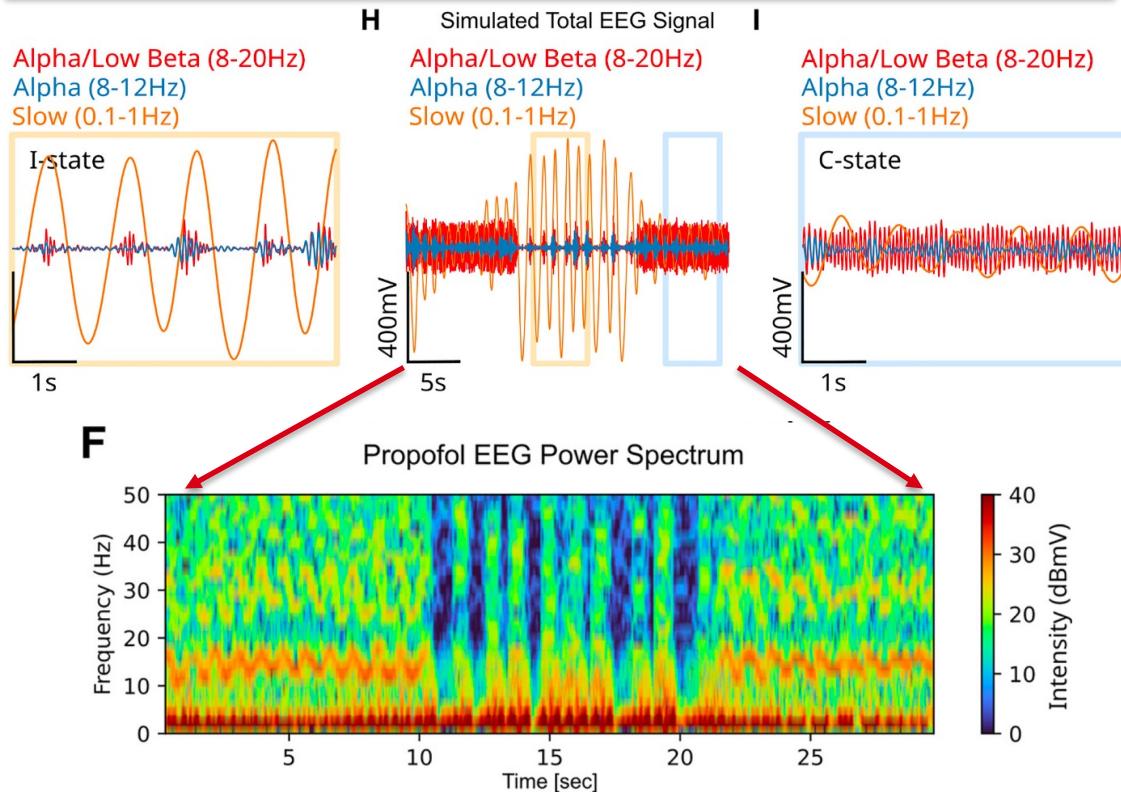
The two simulated states were phase-amplitude coupled like propofol EEG data

Experiment



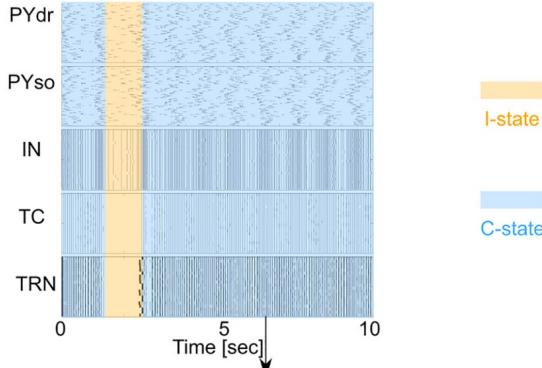
EPL

Simulation

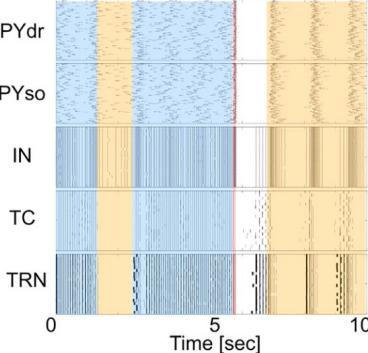


The thalamocortex switched coupling type based on dynamic cortical synchronization level

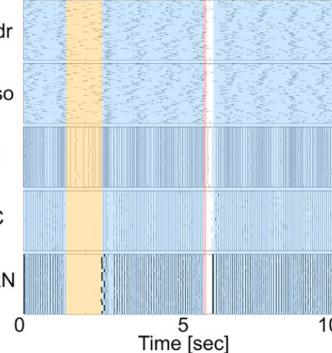
A Baseline mostly-C-state simulation



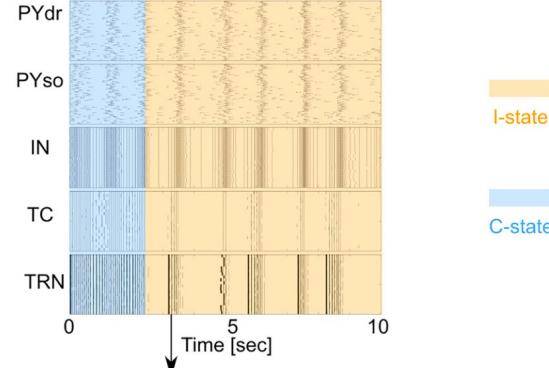
B Example Simulation where Synchronizing Input Applied at time 5700 ms



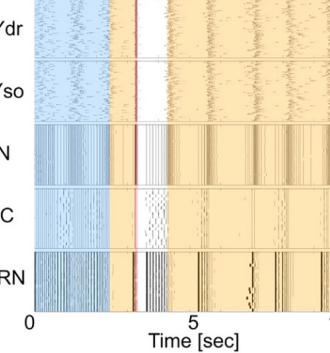
C Example Simulation where De-synchronizing Input Applied at time 5700 ms



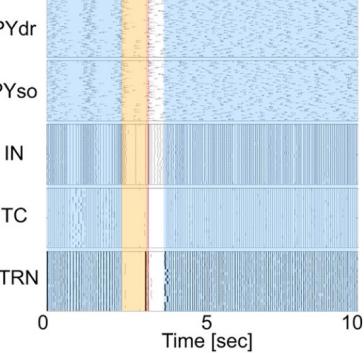
A Baseline mostly-I-state simulation



B Example Simulation where Synchronizing Input Applied at time 3200 ms

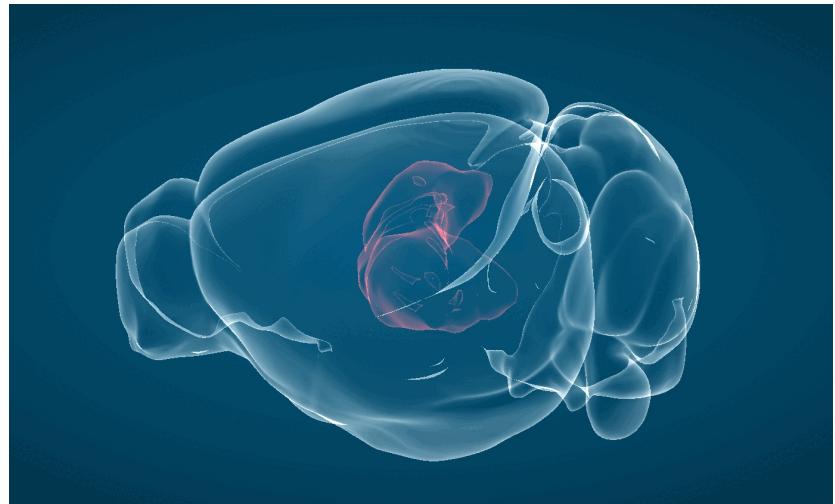


C Example Simulation where De-synchronizing Input Applied at time 3200 ms



Second postdoc: Blue Brain Project

- Here since beginning of 2023
- 90% of my time has been learning how to use, and quickly get up to speed with, many internal and some external Python libraries
- (Yes, this has left very little time for “doing science”...)
- Most of what I will show is unpublished and internal, but will be open-sourced at end of 2024.
(If you want, I can send you a copy now, just ask)

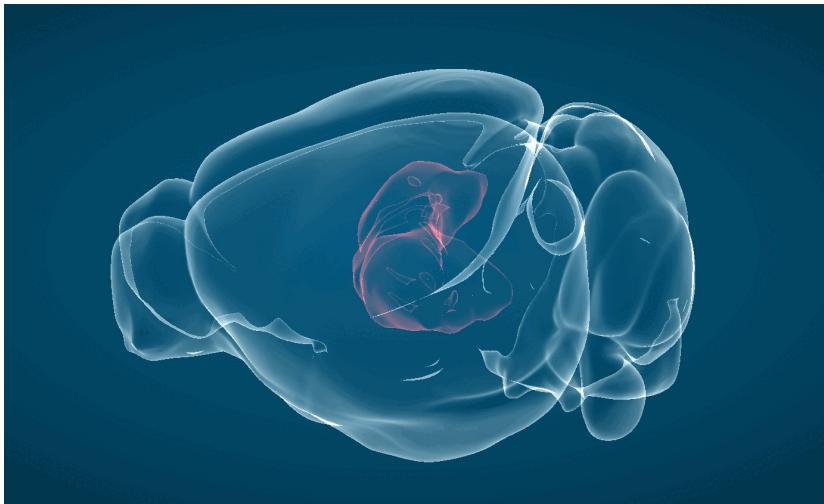


NEURON Caveats

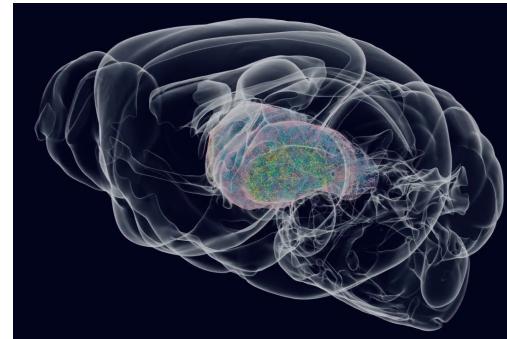
- To be clear, 99% of “NEURON programming” is handled by other teams:
 - **Cells Team:** Scientists who fit single-cell models based on reconstructed cell morphologies and electrophysiological data. They provide parametrized celltypes for our models.
 - **Neuroscientific Software Engineering:** SoftWare Engineers (SWEs) who do general software management and maintenance, including "production-izing" scientific code. They support software that "builds" all the different models.
 - **High-Performance Computing:** SWEs specializing in running NEURON at-scale on our supercomputer, including environment management. They support us "running" the models.
 - **Circuits Team** (the one I'm on): Scientists who work with everyone else to "assemble" **specific** models (such as for Thalamus) and attempt to "do science" using the models.
 - Many other teams (Data/Knowledge Engineering, Visualization, etc.)
 - Caveat to the caveat: I have used NEURON and models built in it from before BBP

How do we go from mouse brain spatial regions to simulations?

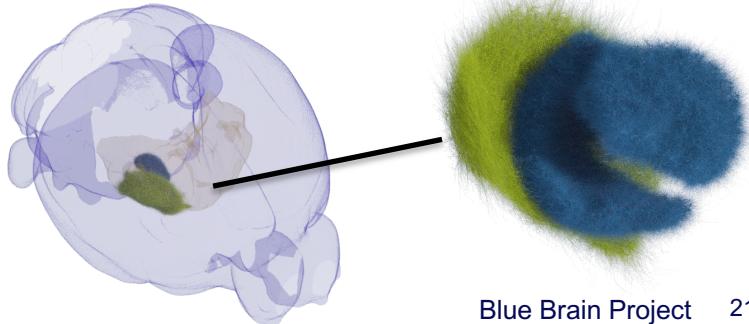
Allen Institute Mouse Brain Atlas
Version CCFv3



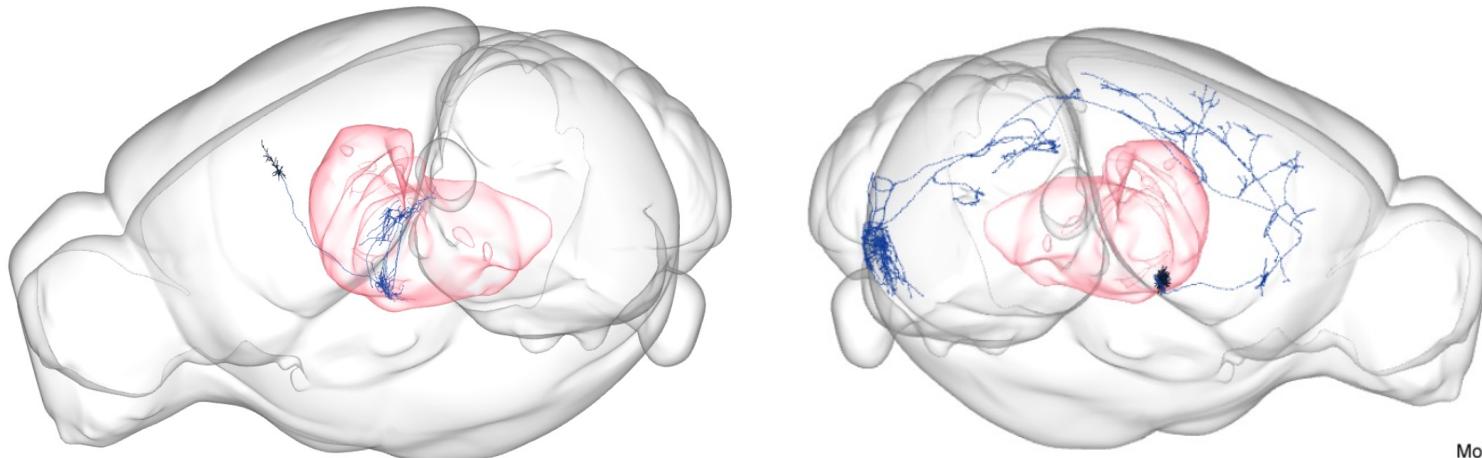
Whole thalamus model



Somatosensory thalamus model

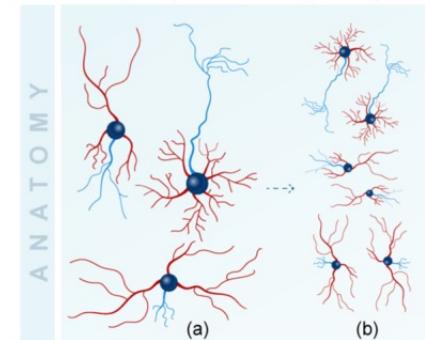


We begin with cell shapes, or “morphologies”

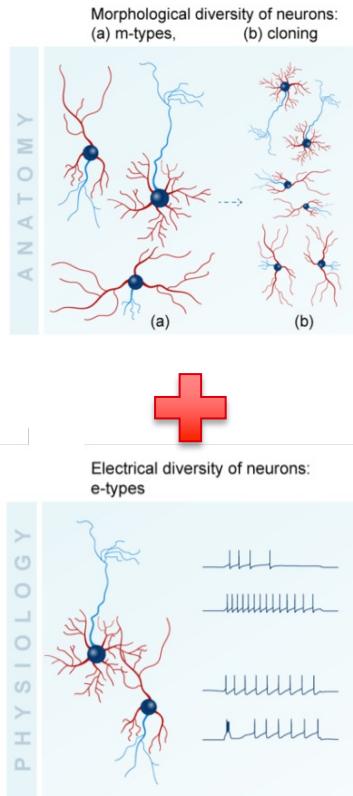


Morphological diversity of neurons:
(a) m-types,
(b) cloning

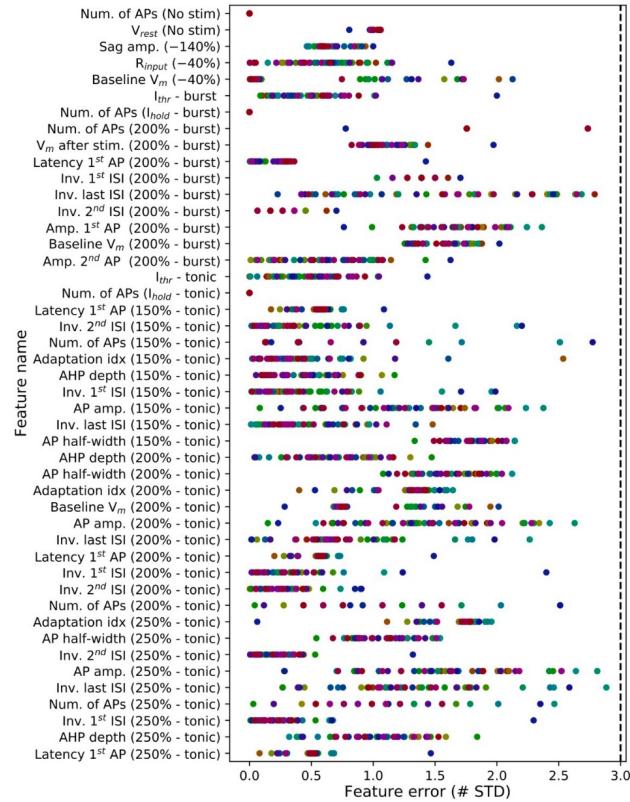
- We start with "reconstructed" morphologies of real cells provided to us by multiple labs. Only some are provided in "mouse brain space".
- I have helped to validate whether these morphologies are located in the "correct" spatial regions, including between different coordinate systems (Allen's CCFv3 vs Janelia's "legacy CCFv2.5").



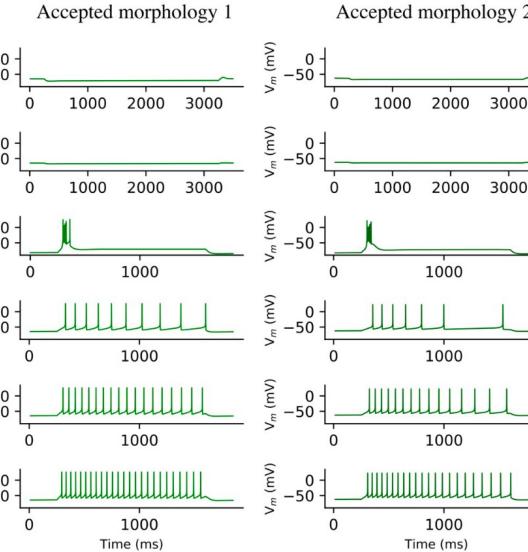
We then create MANY “morpho-electric” celltypes by fitting electrophysiological data to our morphologies (not me though)



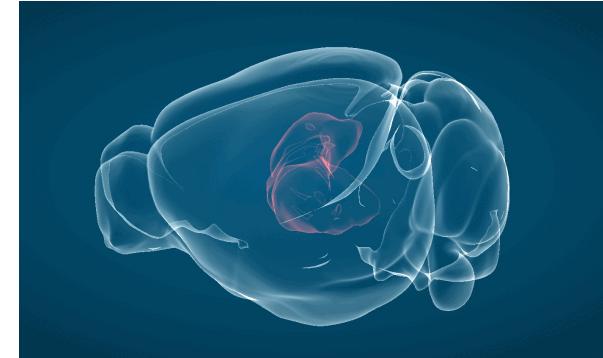
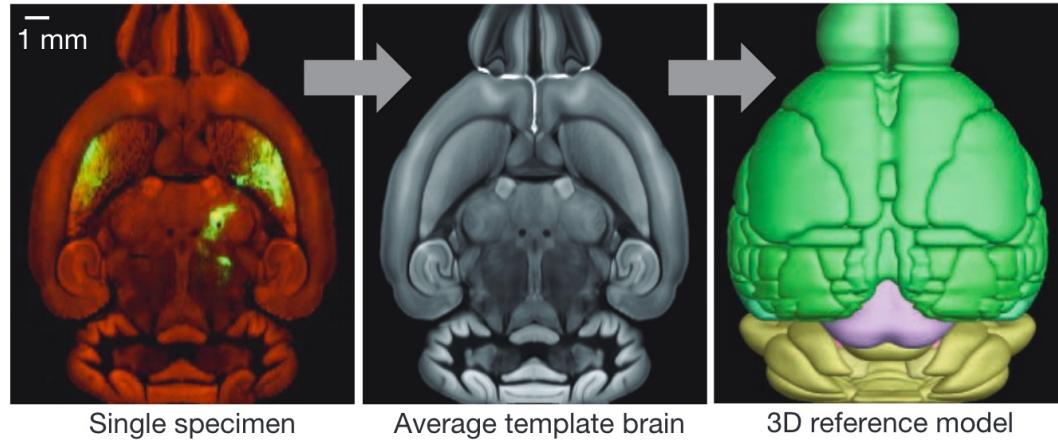
A Feature errors of different model/morphology combinations



B Voltage traces of different model/morphology combinations



Where do we put our cells? Regions: The Allen Mouse Brain Atlas

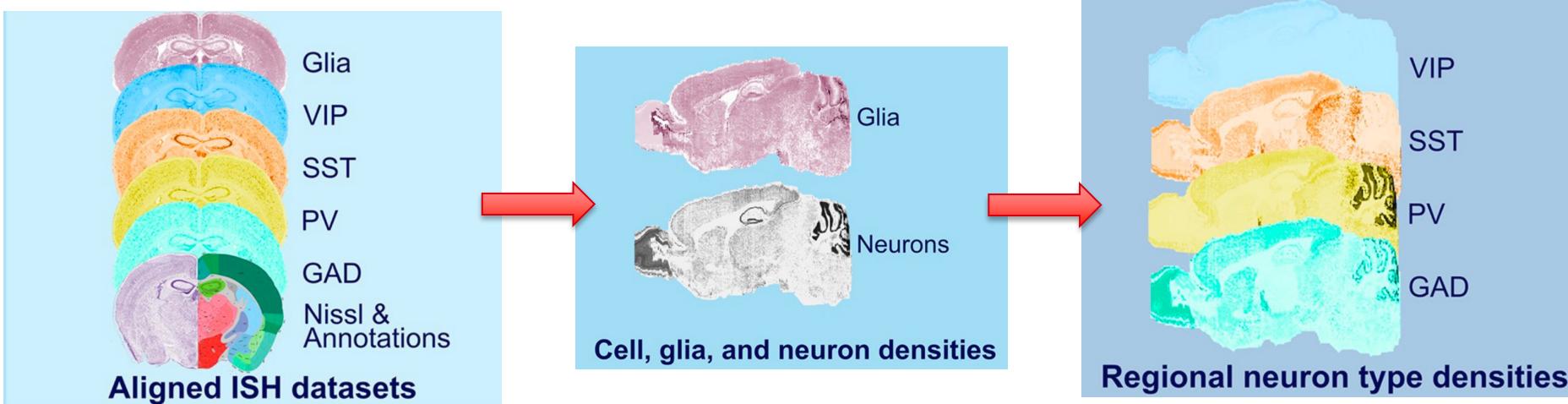


Consists of:

1. A 3-dimensional NRRD “annotation” file that assigns every 25 μm^3 voxel to a single region ID
2. A “hierarchy” JSON file that identifies (almost) every region in the brain

```
{  
    "id": 733,  
    "atlas_id": 374,  
    "ontology_id": 1,  
    "acronym": "VPM",  
    "name": "Ventral posteromedial nucleus of the thalamus",  
    "color_hex_triplet": "FF8084",  
    "graph_order": 649,  
    "st_level": 9,  
    "hemisphere_id": 3,  
    "parent_structure_id": 709,  
    "children": []  
},
```

Where do we put our cells? Cell densities: The BBP Atlas

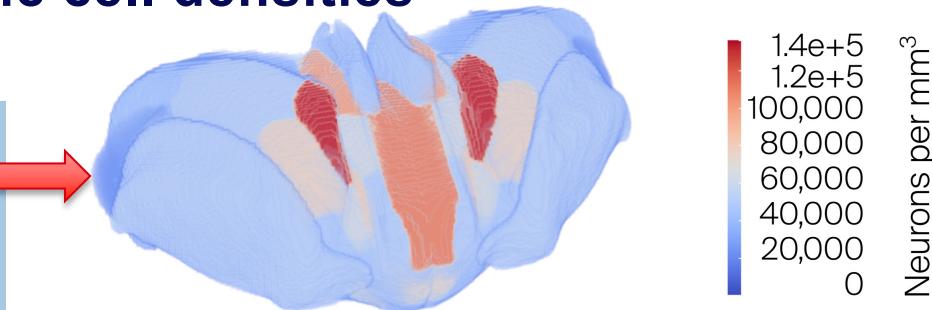
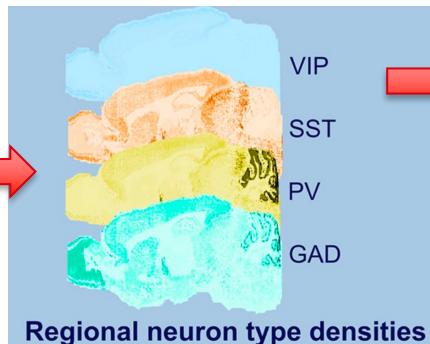
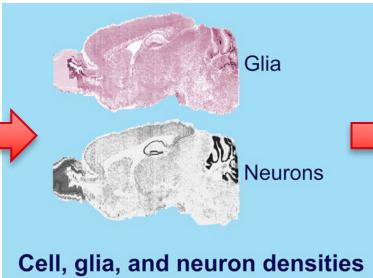


The **BBP Atlas**, which is based on the Allen Atlas, is the result of an extremely complex piece of software, which estimates the “cell density” (cells / mm³) for most cell types in all brain regions.

This consists of:

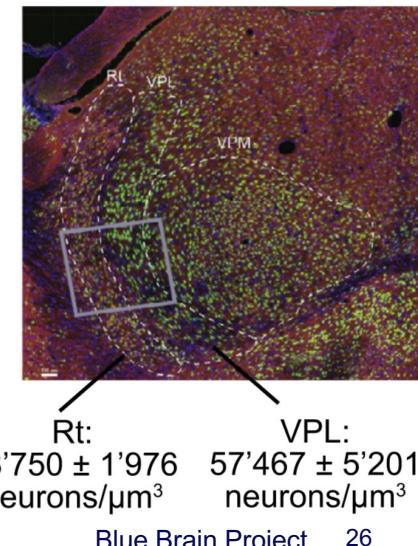
1. A “hierarchical” JSON file identifying brain regions (including changes from Allen)
2. Hundreds of 3-dimensional NRRD files for densities of different celltypes
3. Other files, including compilations of literature data values

Where do we put our cells? Thalamic cell densities

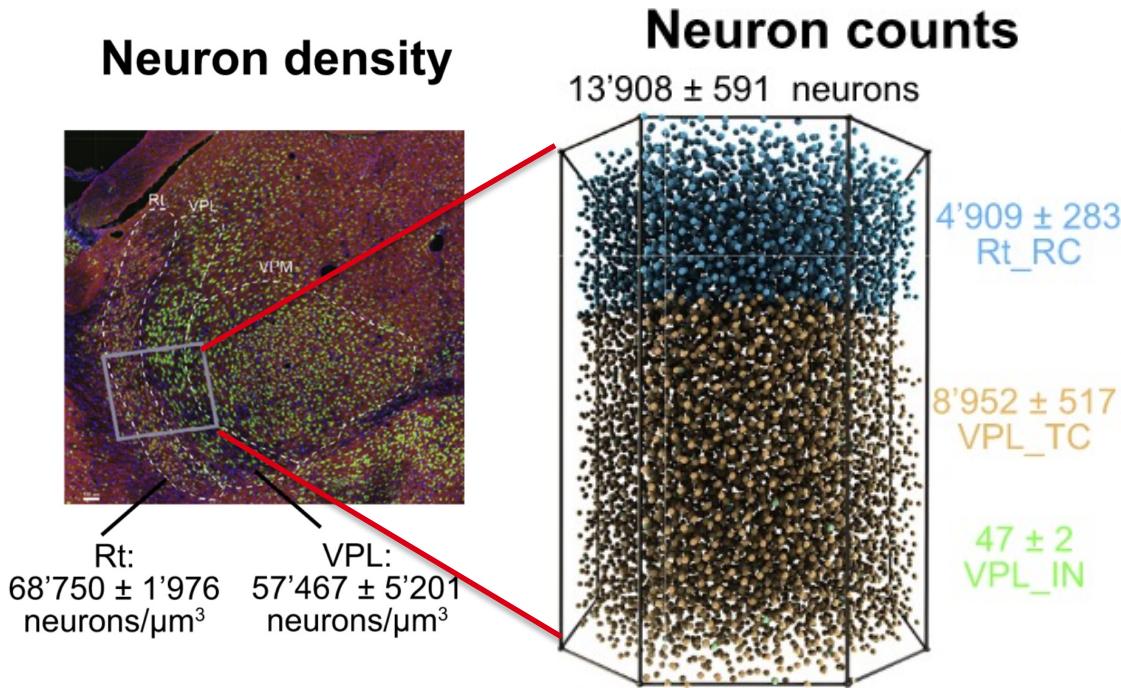


As with most things at BBP, the BBP Atlas was only validated for cortex. This required me to do:

- Assistance in creation of Singularity containers to make the BBP Atlas Pipeline reproducible (including a brief foray into Docker)
- Significant debugging of its consumption of our “Nexus” data storage / knowledge base and API
- Validation and correction of our thalamus cell density values at different stages across the Pipeline

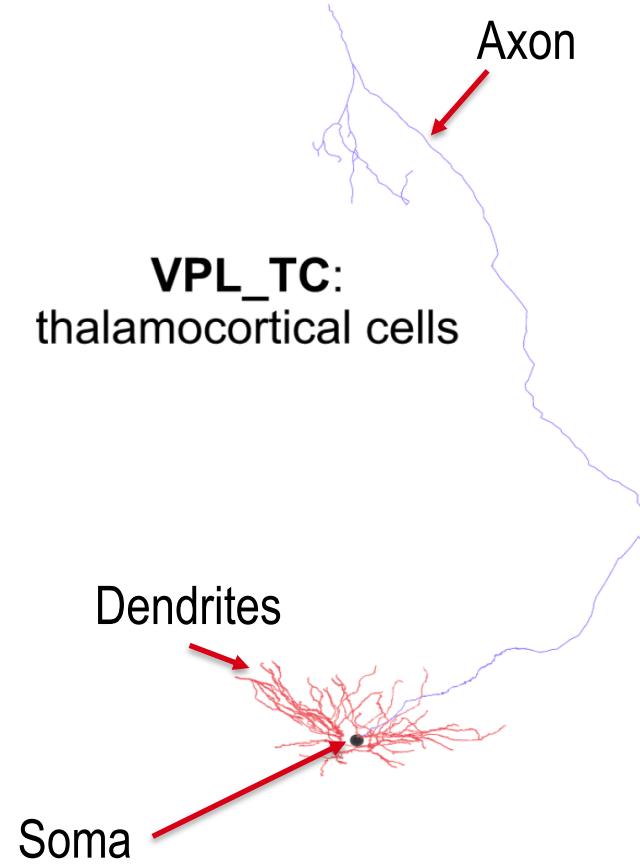


We've got soma positions, let's go! Example columnar circuit



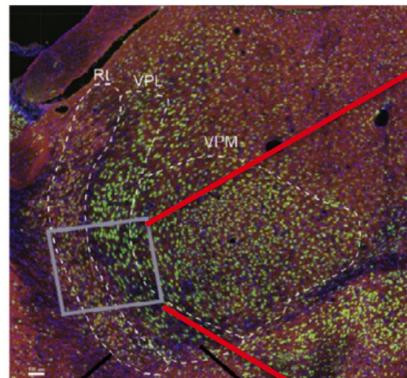
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Ref: (Iavarone, et al., 2023 <https://doi.org/10.1016/j.celrep.2023.112200>)



We've got soma positions, let's go! Not so fast...WHERE are we going?

Neuron density

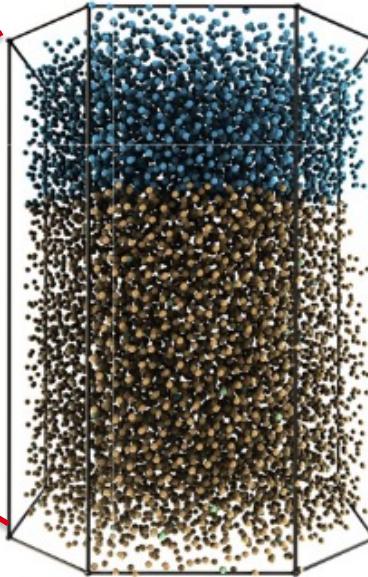


Rt:
 $68'750 \pm 1'976$ neurons/ μm^3

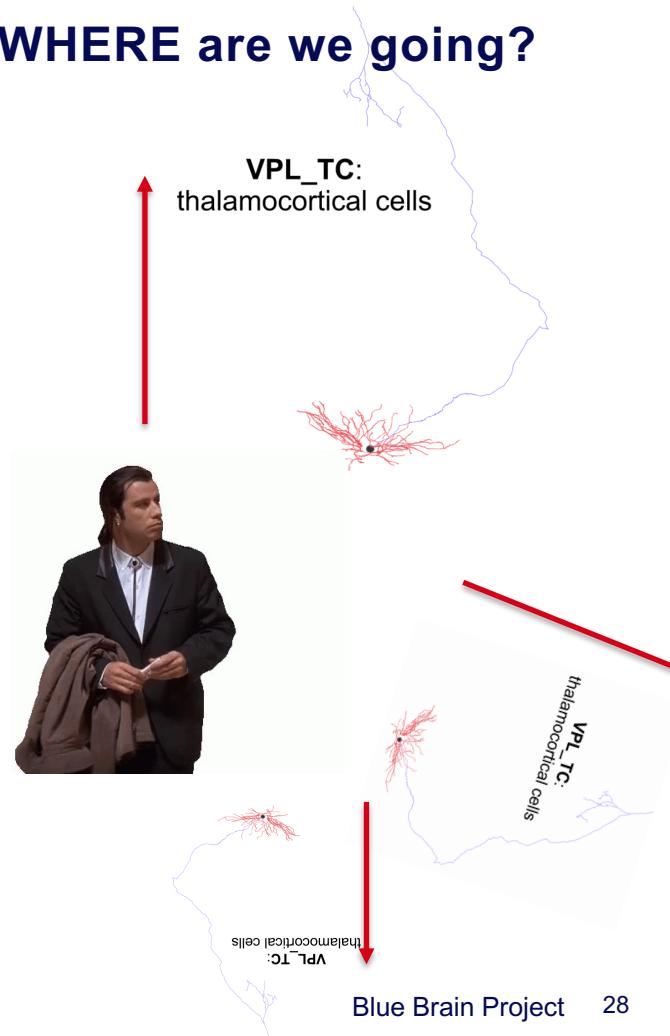
VPL:
 $57'467 \pm 5'201$ neurons/ μm^3

Neuron counts

$13'908 \pm 591$ neurons

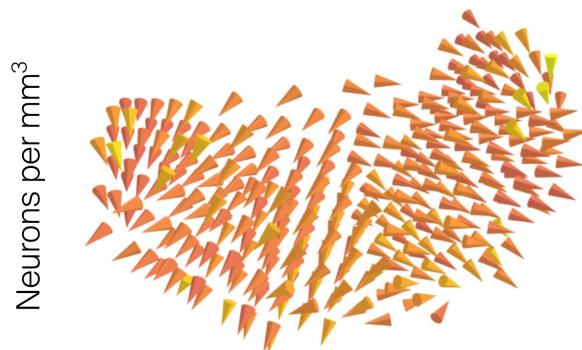
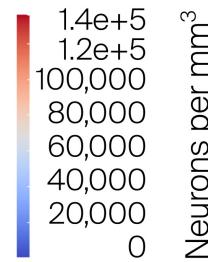
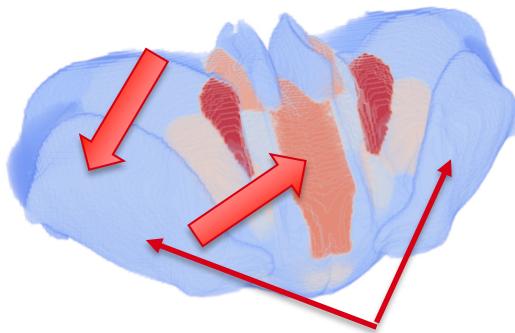
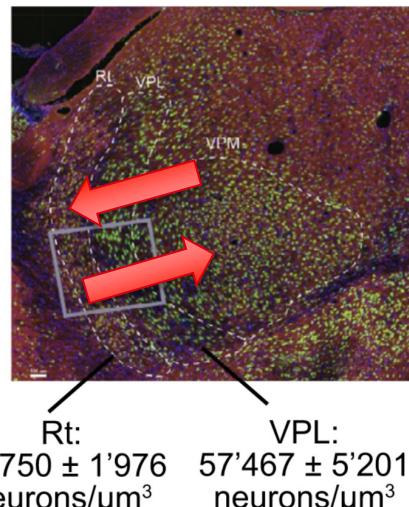


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We need to orient the “direction vectors” of our thalamic cells

Neuron density



RT regions

We know from literature that TC cells from inside the thalamus project outwards the RT, and RT cells project in the opposite direction.

A predecessor had made code years ago to create thalamic direction vectors via blurring a gradient, starting from the brain midline and ending at the RT. I updated this code to use our modern toolset, and fixed some major calibration errors.

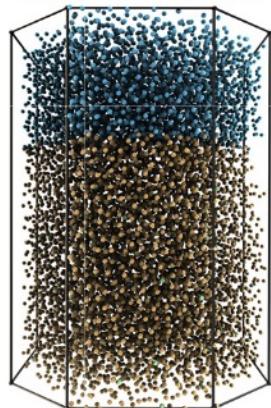
(Note that cells can be defined to go with or **opposite to** the vectors.)

This code is public: <https://github.com/BlueBrain/atlas-direction-vectors>

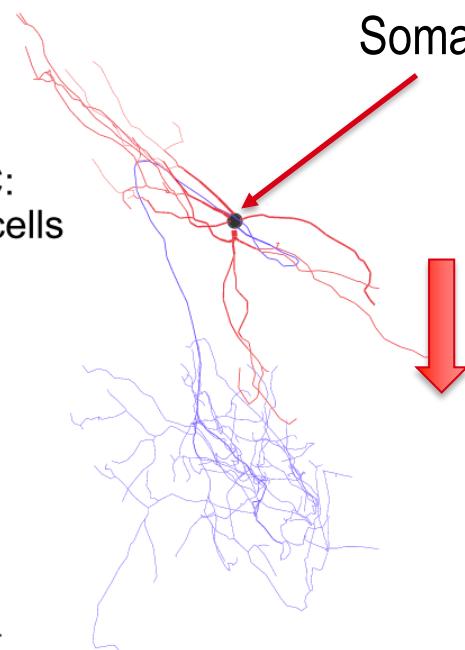
We've got our direction / orientation vectors for every voxel

Neuron counts

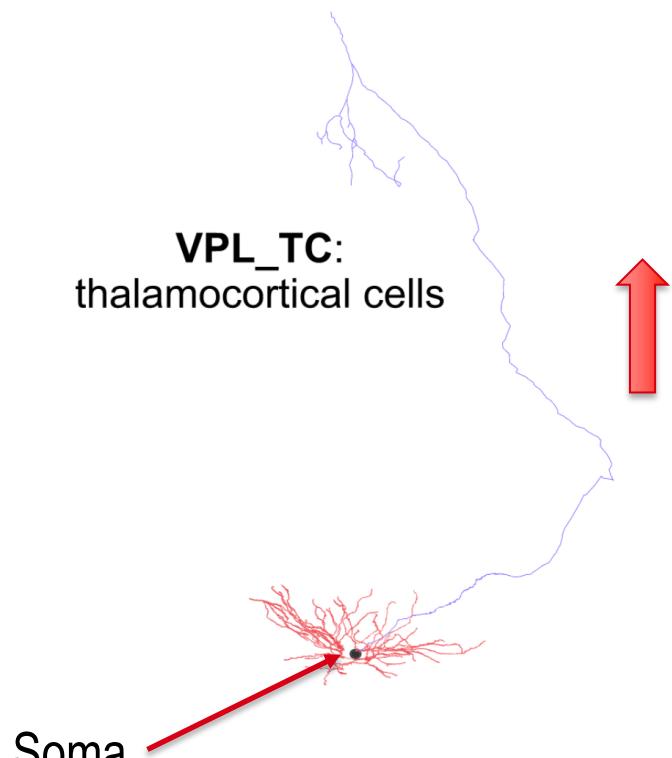
13'908 ± 591 neurons



Rt_RC:
reticular cells

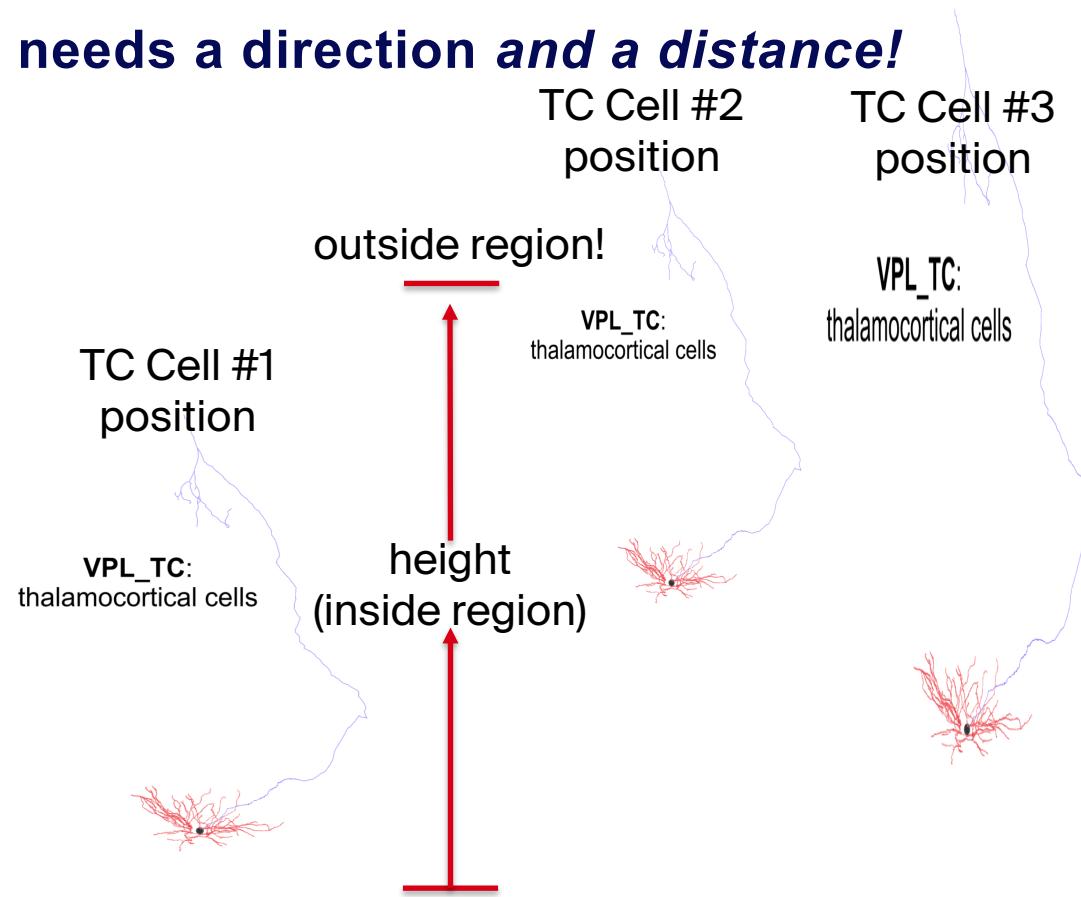
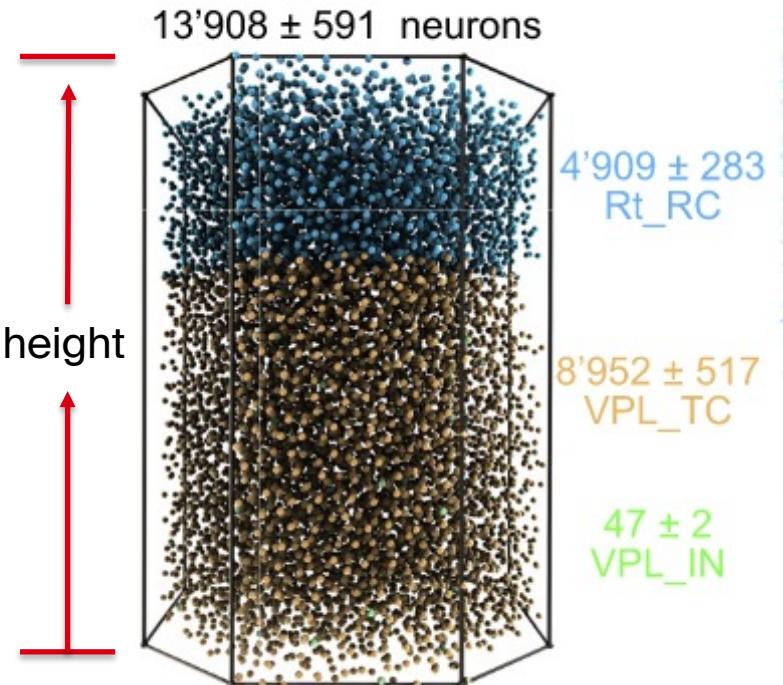


VPL_TC:
thalamocortical cells

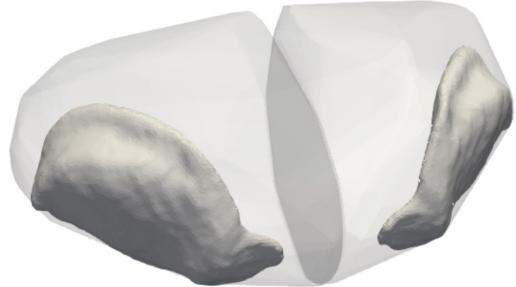


However, any good road trip needs a direction *and* a distance!

Neuron counts



We need to calculate our “distance hints” *along each direction-vector*, for every voxel

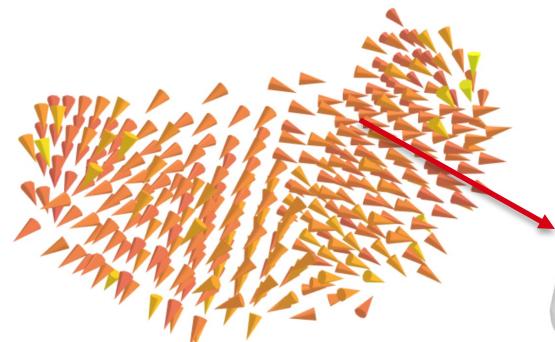


Step 1. Create 3D polygons (“meshes”) of different parts of thalamus.

Step 2. "Draw" lines (“ray-tracing”) along each direction vector, and find the distance of that voxel to every mesh intersection.

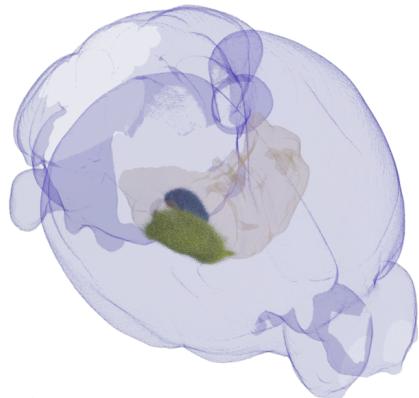
This complex technique was also created by a predecessor, but required significant rebuilding for both quality issues and much technical debt.

<https://github.com/BlueBrain/atlas-placement-hints>

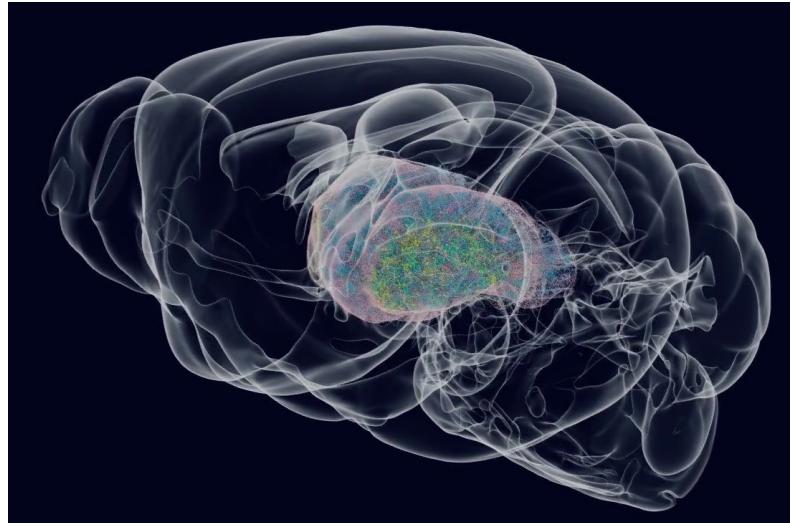


Okay...can we place the cells now??? Yes! (Reproducibly!)

Somatosensory thalamus circuit

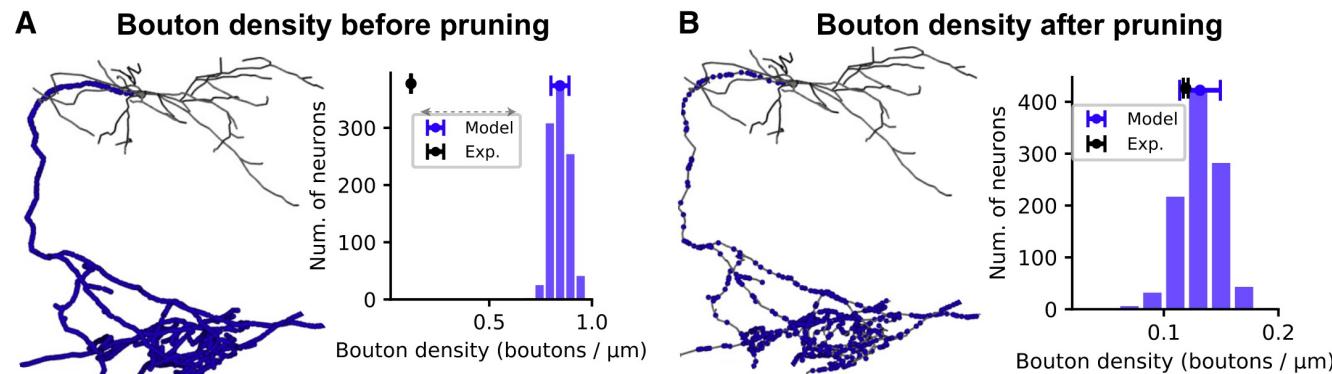
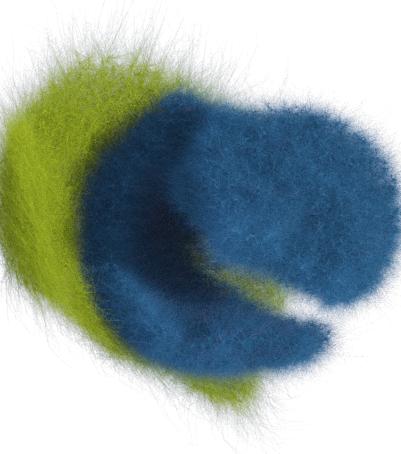


Whole thalamus circuit



However, there's a word I haven't said in a while...“synapse”

This thalamus circuit looks pretty “fuzzy”...



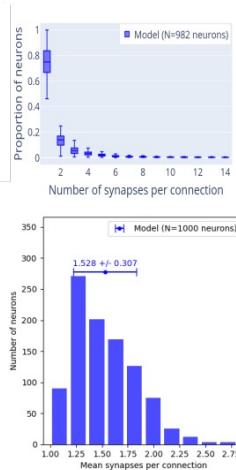
Fortunately, synapses are easier to deal with:

Step 1. Find the locations of **possible** synapse locations based on how close source cell axon compartments are to target cell dendrites.

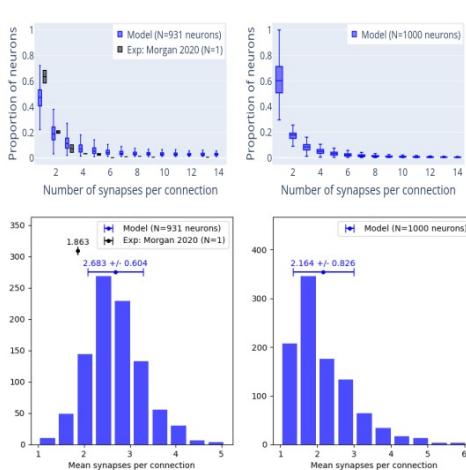
Step 2. “Prune” the number of synapses down to experimentally-measured levels for that type of connection.

Connectivity validation

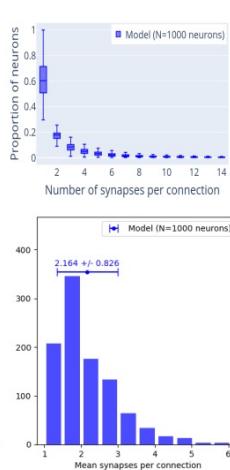
TC



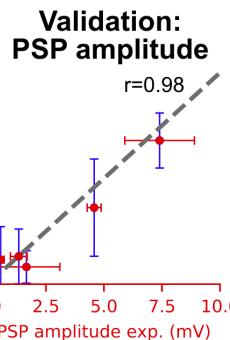
IN



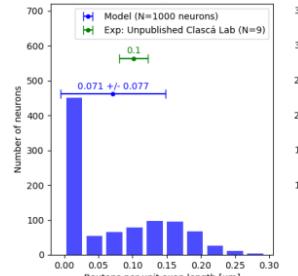
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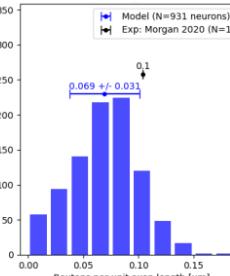
J



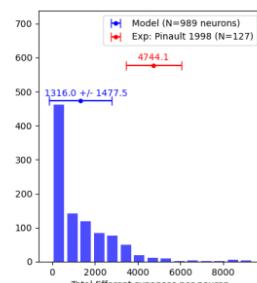
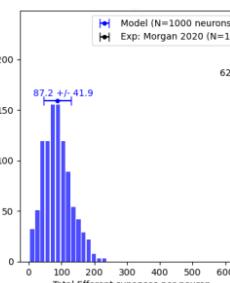
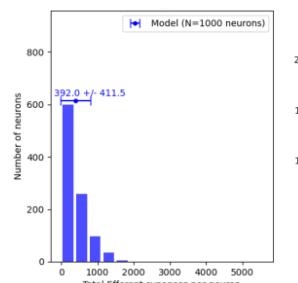
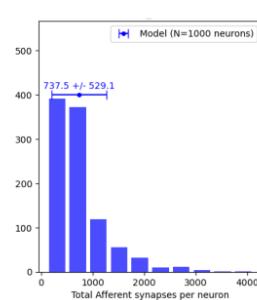
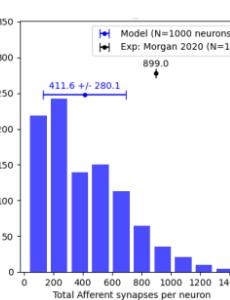
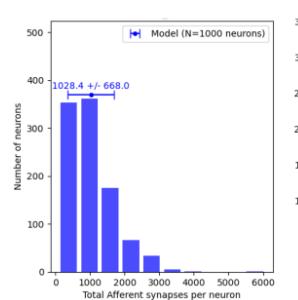
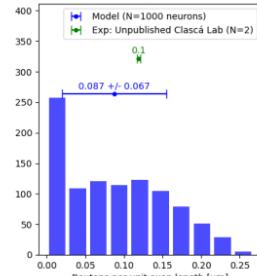
TC



IN



RT



For validating “static” synaptic connectivity, I consolidated and parallelized a large amount of thalamus validation code spanning several years. This code can be quickly adapted to run on any SONATA circuit. (Code not public yet)

However, the dearth of precise thalamus synapse data is a big limiting factor for us (there is MUCH more for cortex!)

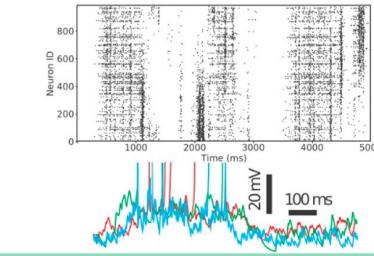
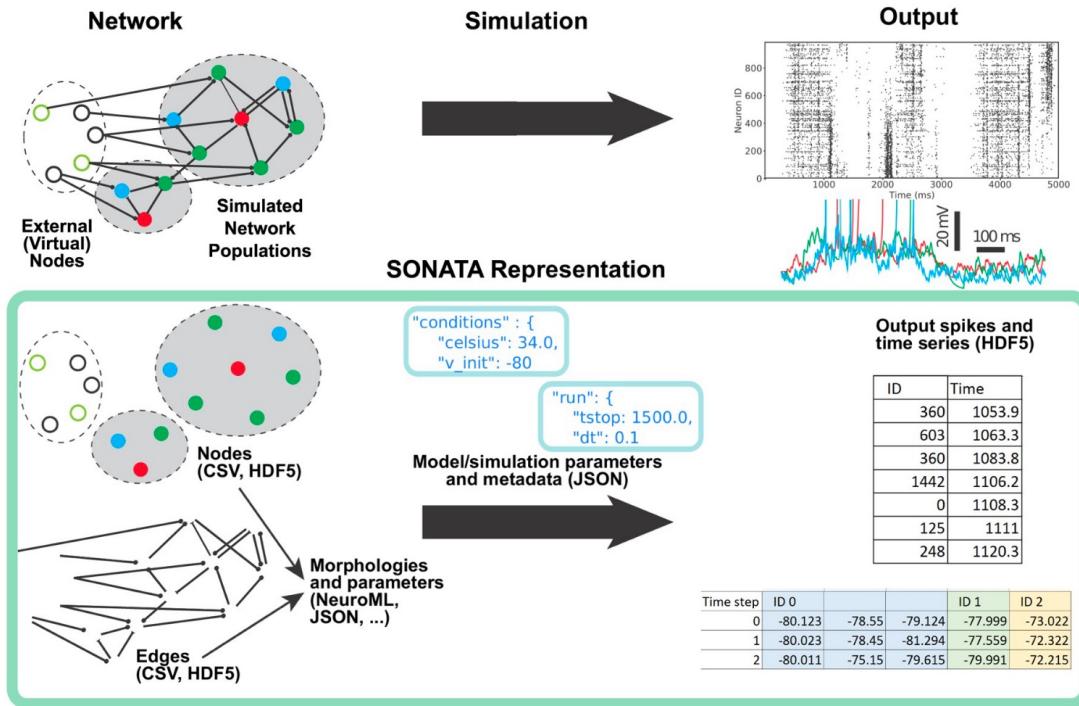
Parallelization: SONATA circuits and CoreNEURON

If y'all ever plan to run BIG simulations fast (100,000 x N cells), these will be important.

SONATA is an efficient, scalable specification for representing both your neural circuit and its output. It was co-developed between BBP and the Allen Institute and is mostly comprised of HDF5 and JSON files.

CoreNEURON is a BBP-created NEURON “engine” optimized for memory usage and speed, and has been added to NEURON as an option.

All BBP and Allen Institute circuits use SONATA format. NetPyNE has support too.



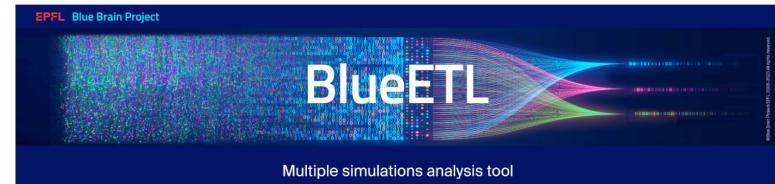
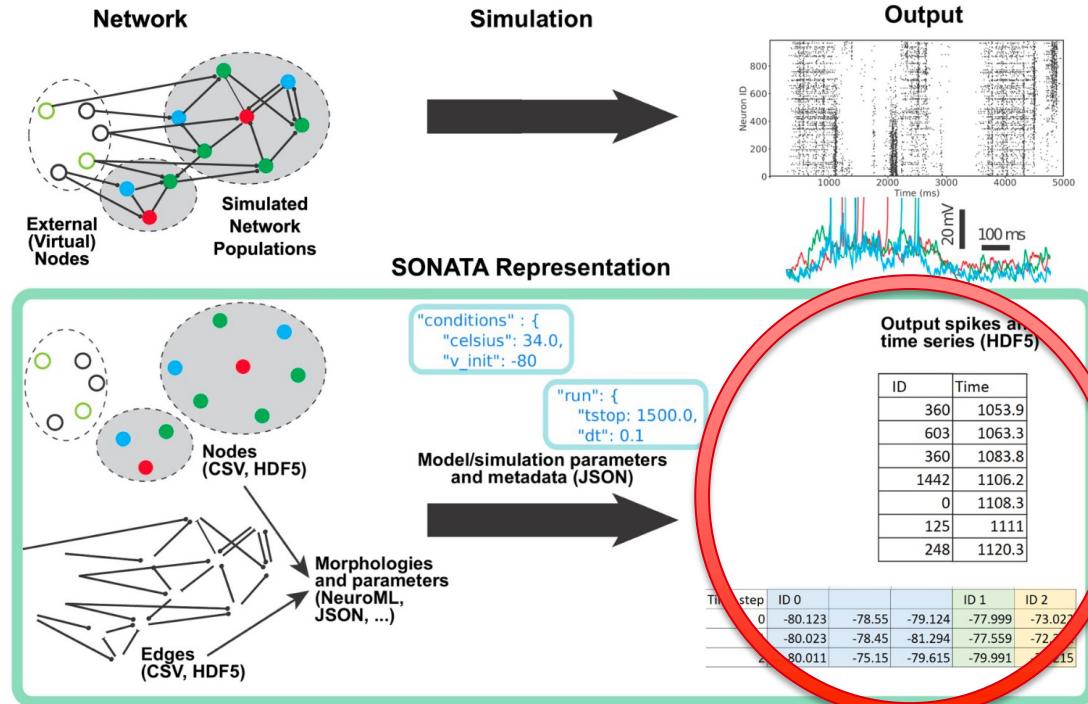
| Time step | ID 0 | ID 1 | ID 2 |
|-----------|---------|--------|---------|
| 0 | -80.123 | -78.55 | -79.124 |
| 1 | -80.023 | -78.45 | -81.294 |
| 2 | -80.011 | -75.15 | -79.615 |

Parallelization: SONATA circuits and analysis

Raw SONATA (especially HDF5) is efficient, but not human-friendly. SNAP helps you interact with your circuit, and BlueETL runs parallel analyses on your output.

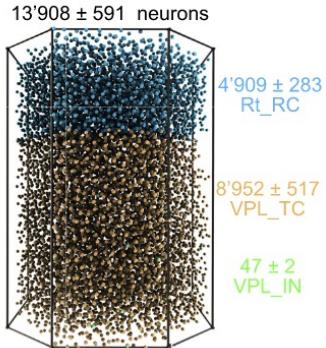
I did not help create these, but I have spent significant time learning SONATA, SNAP, and BlueETL.

BlueETL is named after the “Extract-Transform-Load” paradigm for data, and is built around Pandas’ DataFrames, which are very powerful in the right hands!

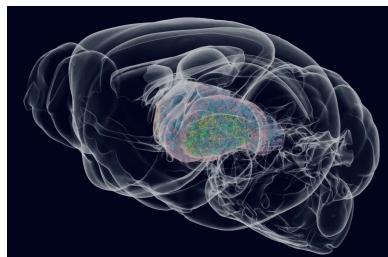
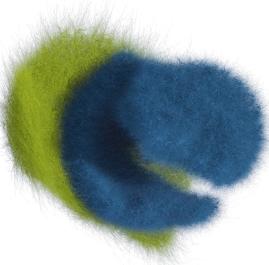
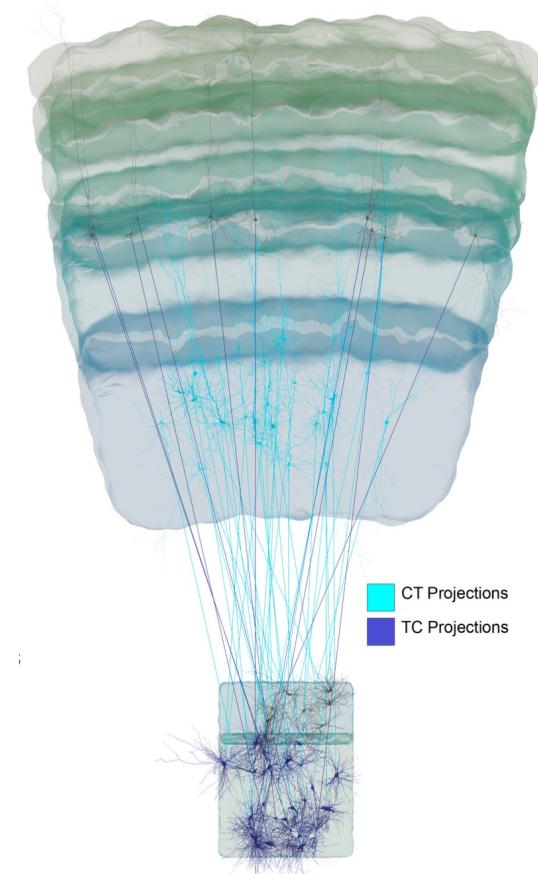
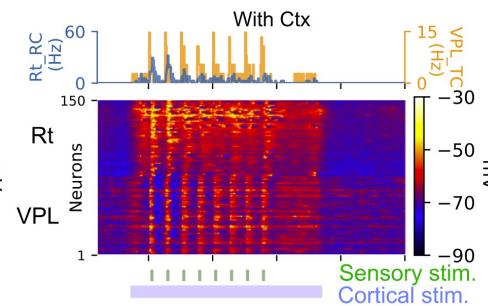
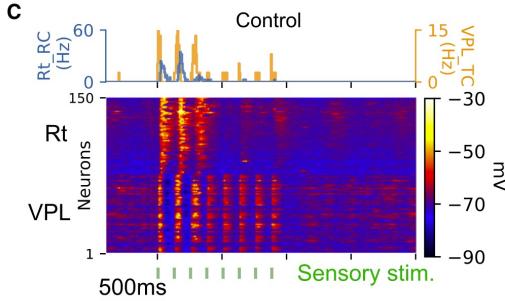


If this sounds more like “Methods” than “Results”, it is...

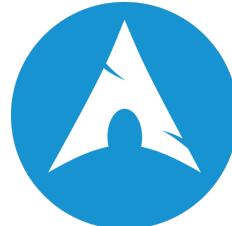
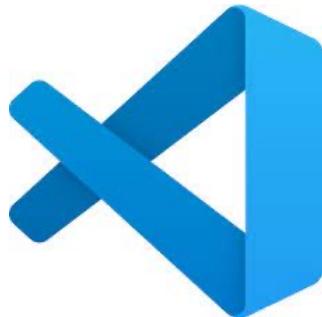
Neuron counts



c



Curios



GitHub

<https://github.com/asoplatan>

Thanks for the opportunity to come speak!

Acknowledgements:

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Weina Ji

And many more...