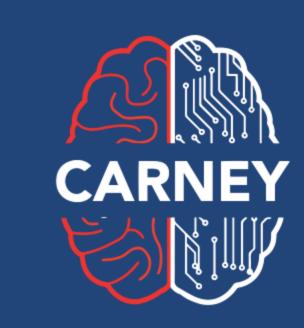


# Ultrafast connectivity optimization of large-scale biophysical network models with deep learning

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# Large-scale biophysically detailed models are useful but challenging to implement

Detailed biophysical models provide interpretable, mechanistic predictions about neural data<sup>1-3</sup>, however...

### They're hard to use due to:

- 1) High computational cost
- 2) Difficult to fit parameters<sup>4</sup>

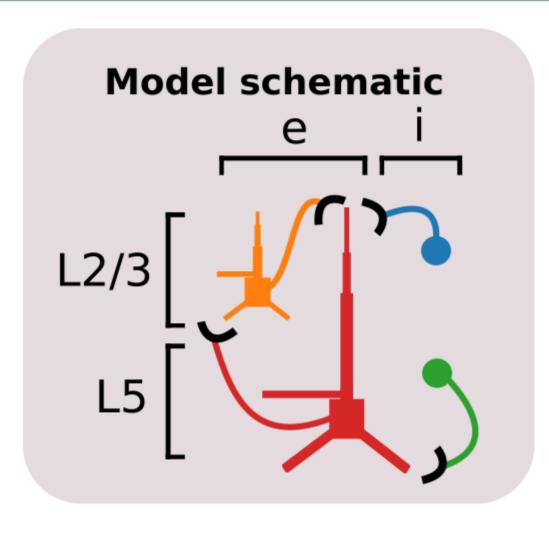
#### **Solution: surrogate models**

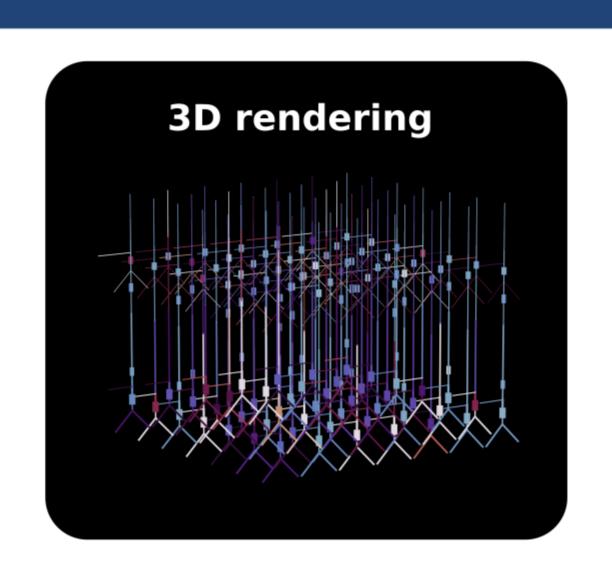
Deep neural networks trained to replicate activity of detailed neurons

#### Surrogate models can help by:

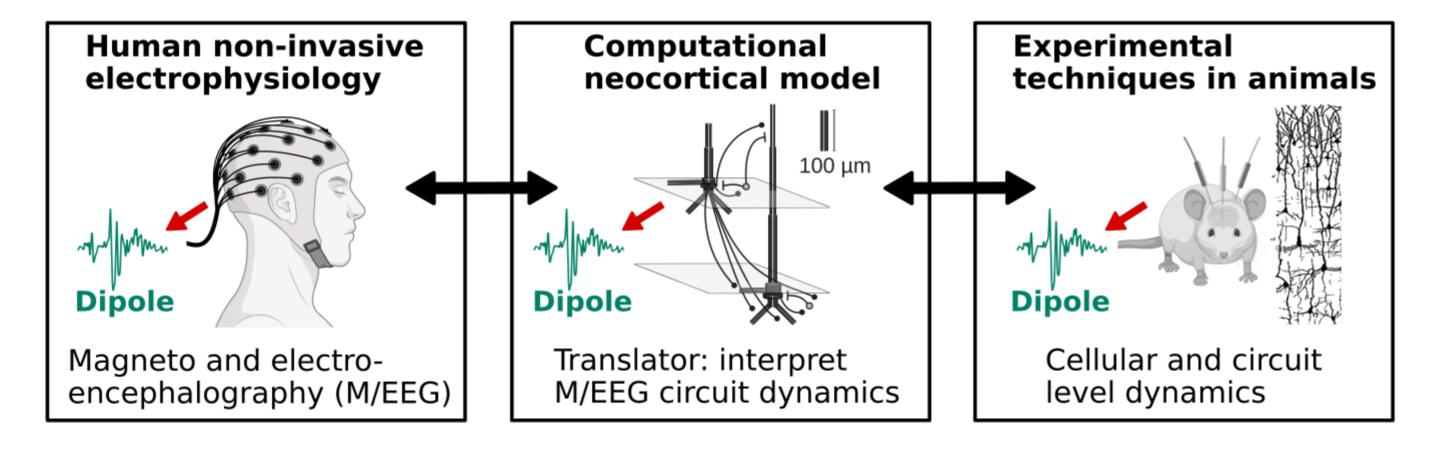
- 1) Approximating simulators with faster deep neural networks<sup>5,6</sup>
- 2) Optimizing parameters through gradient descent, a **novel approach**

# The Human Neocortical Neurosolver (HNN): a large-scale modeling framework to study the origins of M/EEG



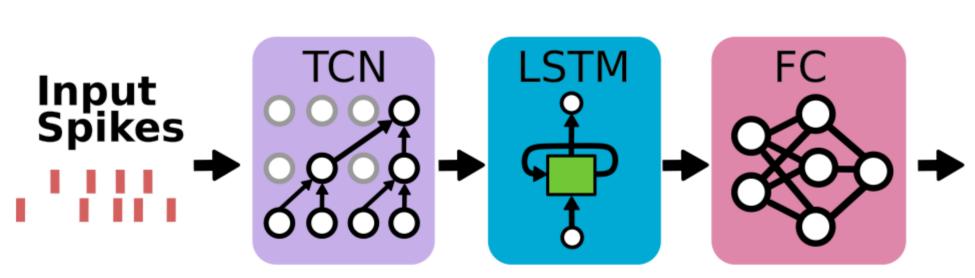


HNN (hnn.brown.edu) simulates a large-scale network of biophysically detailed cortical neurons, and is designed to bridge macroscale M/EEG to microscale cell and circuit level phenomena



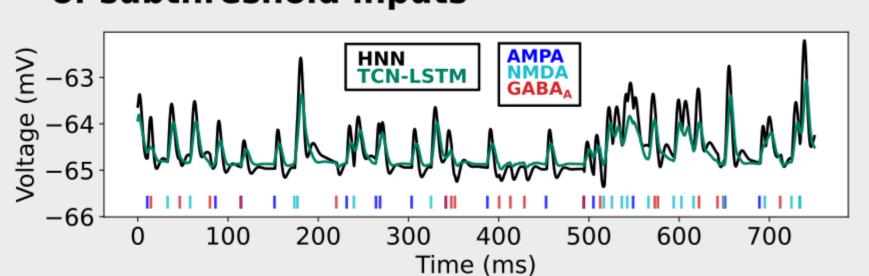
# Deep neural networks can be used as surrogate models of biophysically detailed neurons

A TCN-LSTM architecture was used to learn the voltage response of single neurons to input spikes (i.e. the **surrogate model**)

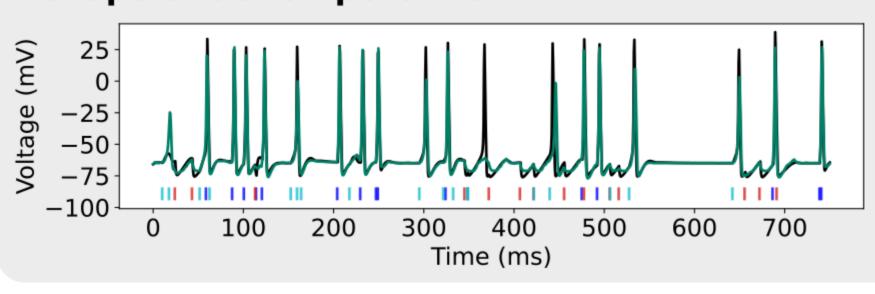


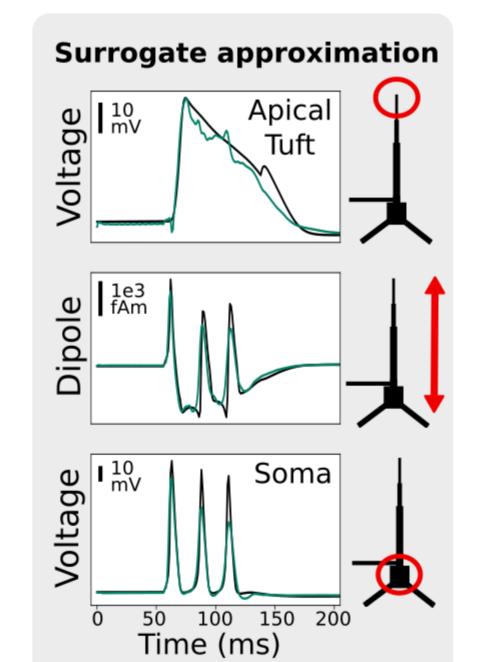
**Training data** was generated by simulating Poisson spike times that activated random sets of synapses spanning sub- and suprathreshold synaptic strengths

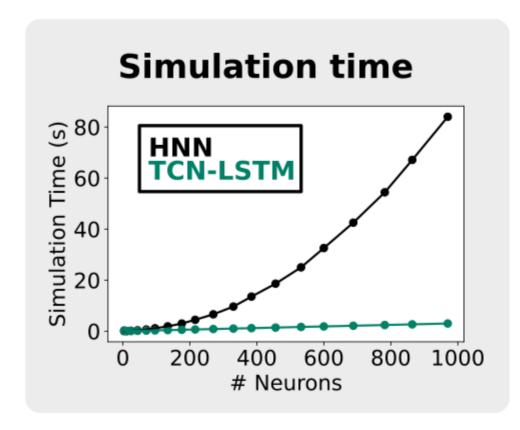
#### Surrogate model learns temporal summation of subthreshold inputs



#### Surrogate model learns firing threshold and shape of action potential



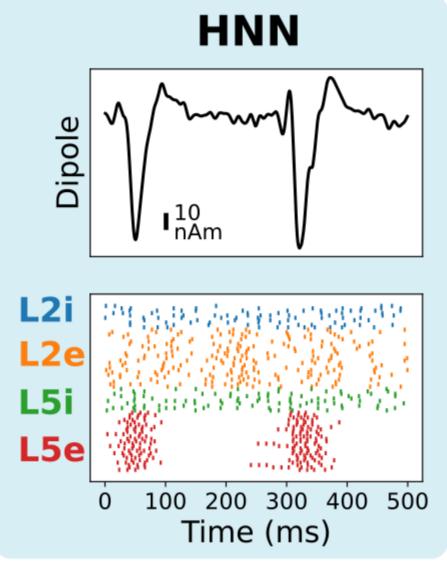


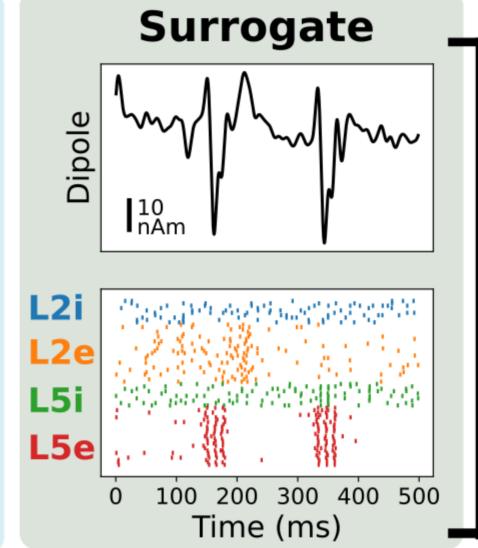


Savings in simulation time enable **massive scaling** of simulated **network size** 

## Surrogate network models approximate features of network activity even with changed connectivity

Surrogate models of each cell type in HNN were connected in a large-scale neocortical circuit



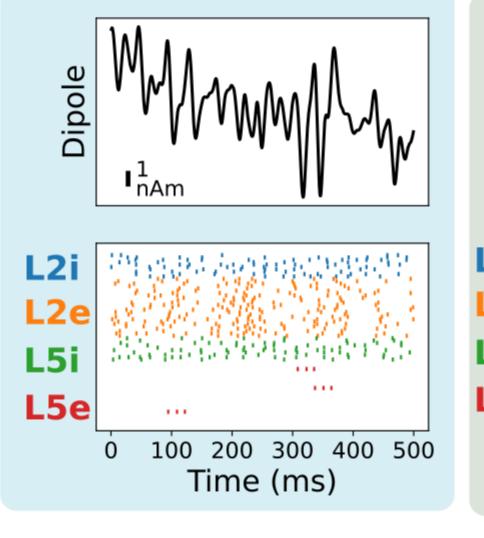


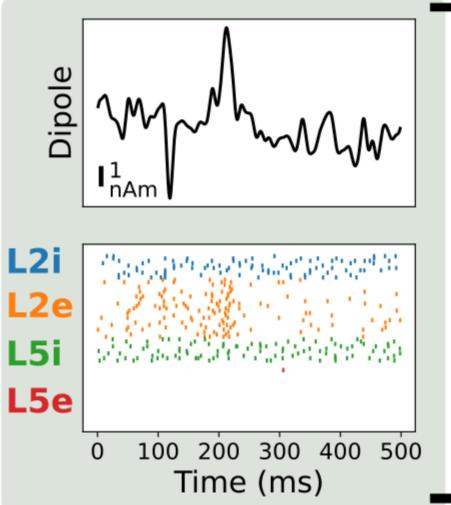
### **Default connectivity**

Network level simulations produce spontaneous oscillations given noisy drive to proximal synapses

Close agreement between surrogate model and HNN

Dipole signal is largely created by synchronous spiking of L5e neurons





### Increased L5i → L5e

L5e spiking is disrupted due to inhibition by L5i

Surrogate model accurately captures changes in network activity due to connectivity

This allows us to efficiently optimize connectivity without retraining

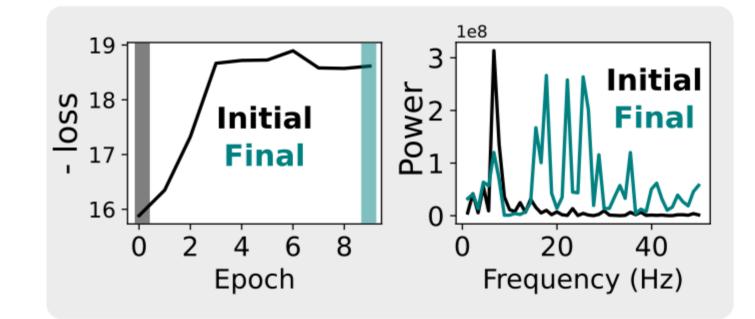
## Connectivity can be efficiently optimized with gradient descent in surrogate network models

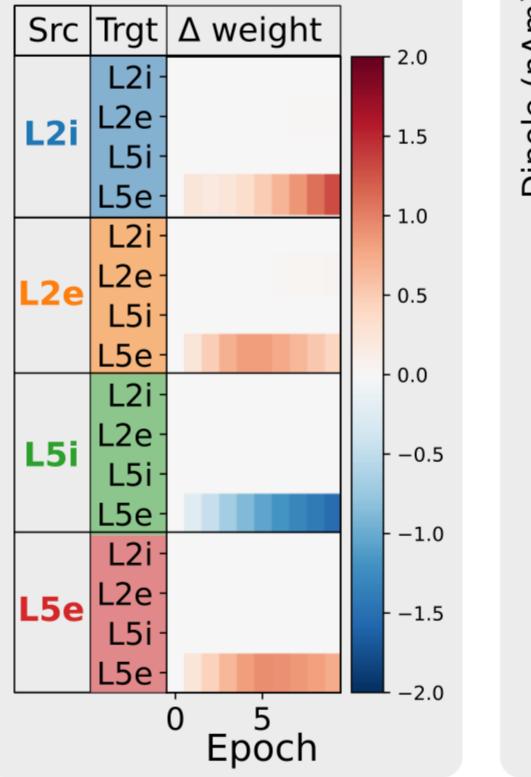
Given a network that generates alpha (10 Hz) oscillations with noisy inputs, can I find a connectivity configuration that produces high frequency (15-60 Hz) oscillations?

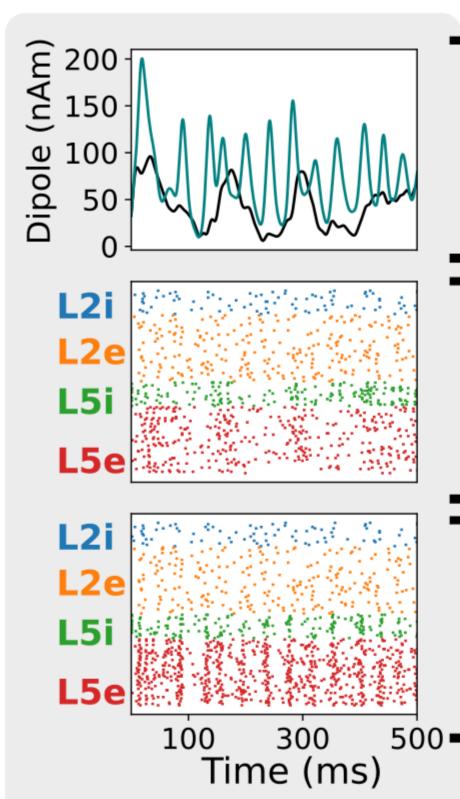
We treated a single TCN-LSTM (neuron) as a node in a spiking neural network (SNN), this approach allows:

1) Fitting connectivity parameters with off-the-shelf deep learning optimizers (e.g. Adam)

2) Complex optimization objectives (é.g. maximize band power)







**Gradient descent** was used to find the optimal connections for spontaneous high frequency oscillations

Initial connectivity produced alpha frequency (10 Hz) oscillations

Final connectivity produced higher frequency beta (13-30 Hz) oscillations

### **Conclusions and future directions**

- 1) Deep neural network-based surrogate models decrease simulation time, and enable rapid connectivity optimization
- 2) Surrogate modeling can permit large scale biophysically detailed simulations previously restricted to abstract, mathematically tractable models (e.g. examination of cortical traveling waves)
- 3) Future work is necessary to improve training efficiency of surrogate models, and better understand when gradient descent may fail to optimize parameters











[1] Jones et al., J. Neurophysiol. (2009) [2] Neymotin et al., eLife (2020) [3] Sherman et al., Proc. Natl. Acad. Sci.

(2016) [4] Tolley et al., PLoS Comput. Biol. (2024) [5] Oláh et al., eLife (2022) [6] Verhellen et al., bioRxiv (2023)