Replicating spectro-temporal dynamics in neurobiologically realistic neural networks via a self-supervised approach

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Abstract

Computational modeling tools provide a precise platform to investigate theories and hypotheses in neuroscience. However, current neuronal circuit models fail to achieve realistic neural dynamics without non-physiological assumptions. One class of models can be trained to generate those dynamics with high computational performance but are biophysically unrealistic (e.g artificial neural networks). Another class of models are designed to be biophysically realistic yet most of these models heavily rely on manual tuning. In this study, we have implemented a self-supervised learning algorithm called generalized Stochastic Delta Rule (gSDR). With this rule, we have trained biophysical neural circuits to achieve specific responses, such as resting membrane potential, firing rate and oscillatory dynamics. These models can also be trained to reproduce observed neurophysiological data (e.g task modulated oscillatory dynamics). We test this by training the model to reproduce a visually evoked oscillation shift from alpha-beta ($\sim$ 10-30Hz) to gamma ($\sim$ 40-90Hz) based on high-density electrophysiological recordings. These gamma-beta interactions emerged by self-modulation of synaptic weights via gSDR. We demonstrated that this approach can be used to understand both neuronal circuit mechanisms as well as the computations they perform.

Keywords: Modeling; Dynamics; Learning; Neurophysiology;

Introduction

Computer-based simulation (In-silico) enhance our testing capabilities by reducing majority of experimental limitations existing in-vivo/vitro. Many studies leverage in-silico models to explore and test hypotheses rooted in neural dynamics observed in electrophysiology (Bastos et al., 2015), cell types(Lichtenfeld et al., 2024), excitatory-inhibitory (E-I) interactions and neurochemicals (e.g neurotransmitters In-vivo/vitro)(Ardid et al., 2019). Also, brain inspired computational modeling such as the artificial neural networks (ANNs) revolutionized artificial intelligence (AI) and deep learning(Niu, Zhong, & Yu, 2021).

Unlike most of the computational models in deep learning and AI, biological neural circuits rely on biophysics. By these biophysical interactions neural circuits are able to change the state of them at any scale, large or small neural ensembles, single neurons and even at the receptors and synapses. Eventually, different neuronal cell types with specific neuromodulators inhibit or stimulate other neurons, adding biophysical interactions resulting in spectro-temporal dynamics. In addition, since our goal is to test theoretical hypotheses about the brain in single neuron, microcircuit and/or neuronal population scales, we cannot rely on the models not aiming to be as consistent as possible with neurobiology. Regrading this issue, many of the recent studies have focused on biophysical details of neural microcircuits (J. Sherfey, Ardid, Miller, Hasselmo, & Kopell, 2020), (Wacongne, Changeux, & Dehaene, 2012). However, most of these models require manual tuning and optimization prior to the simulation due to non-linearity, complexity and biophysical constraints. Thus we proposed a learning algorithm for brain-like models with biophysical complexities. The goal of this learning algorithm is to gain insight into how the brain switches between oscillatory motifs (e.g, from beta to gamma).

Methods

Since our goal is to work with biophysically detailed neuronal models, we added our methods as a toolset called "Dynalearn" on Dynasim toolbox on Matlab (J. S. Sherfey et al., 2018). In this toolbox, network models represents a cortical population with distinct cell types modeled by corresponding Hodgkin-Huxley Hodgkin and Huxley (1952) circuit parameters. In addition, some other mechanisms (e.g, receptors & ion channels) have been added to Hodgkin-Huxley equation model based on the other studies. General form of these neurons is shown in the equation (1):

$$C_m \frac{dV}{dT} = -I_{inp}(t,V) + -\sum I_{int} - \sum I_{syn} \tag{1}$$

Where t is time (ms), C_m is the membrane capacitance, I_{int} denotes the intrinsic membrane currents (such as I_{Na}, I_K, I_{Leak}), $I_{inp}(t,V)$ is the current reflecting inputs from external sources and I_{syn} denotes synaptic currents from the other neurons driving this neuron. Using this framework, we are able to define detailed neuronal models with multiple populations of similar or different cell types and various synaptic connection mechanisms (such as $I_{AMPA}, I_{GABA}, I_{NMDA}, ...$) between them.

There are various optimization or learning methods in Dynalearn but here we focus on the generalized Stochastic Delta-Rule (gSDR) which is inspired from the stochastic delta rule (N & SJ, 2020) and spike-timing dependant plasticity (Markram, Gerstner, & Sjöström, 2012). The general form of our algorithm is shown in equation (2):

$$V_t = V_{t-\Delta t} + (\delta(\lambda)L + \alpha).R \tag{2}$$

Where V_t is all variables at time t that model can change, $\delta(\lambda) \sim uniform(-\lambda, \lambda)$ (λ : exploration factor) is a random

sample from a uniform distribution, L is the output of evaluation function ($\sum(metric - target)^2$) at that time, α is the unsupervised factor (if $\alpha = 0$, model will no longer have unsupervised changes) and R is the mutual-correlation dependant plasticity (MCDP) function output around the step time $(t - \Delta t, t)$ based on $X_{t,(N \times t)}$ which is a matrix containing the membrane potential of all (N) neurons. This function acts as an approximation of spike-timing dependant plasticity (STDP) depending on the time length Δt. Details are in this equation (3):

$$R = MCDP(V_t, \Delta t) = \frac{r - \mu}{\sigma_r}, r_{N \times N} = Corr(X_t) \quad (3)$$

Consider that there are two component in gSDR; one is the part that the value of loss or reward affects how the model will change its parameters (self-supervised) and the MCDP part that is completely unsupervised. In addition, value of R will be 1 for any variables in V_t that is not a synaptic weight, in case if other model parameters such as channel properties are included in the simulation.

For runing simulations, after implementing a Dynasim model object, it has to be passed to Dynalearn. Also, Dynalearn will interact with the model according to the tuning, training or task instructions such as restrictions, metrics, objectives and targets. In fact, Dynalearn acts as an interface between the supervisor and the neuronal model (Fig.1).

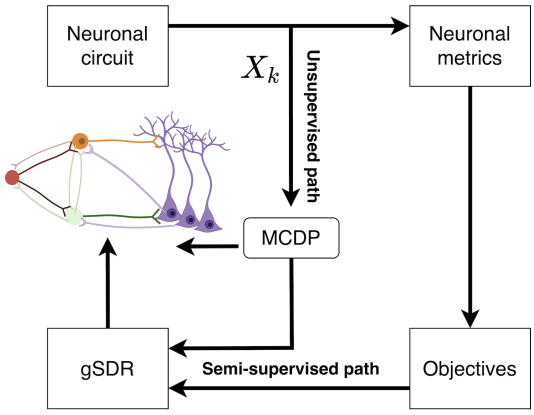

Figure 1: Simplified Dynalearn-Dynasim interaction flowchart

Results

Replication of electrophysiology We began by recording high-density neurophysiology spiking data from awake macaque monkeys observing a visual drifting grating stimulus. We perform these recordings in area MT/MST, areas that have strong selectivity to this type of stimulus. For this work, a single neurophysiology recording session was used with 93 single neurons. In Dynasim, we modeled the underlying MT/MST as a neural network with a total of 70 excitatory and 30 inhibitory interneurons. The synaptic connectivity between these neurons was initialized using a random uniform distribution. Background synaptic inputs to the model were provided using a random gaussian noise process. Visual stimulation was simulated by providing strong tonic input current to all excitatory neurons from 1000ms to 1500ms. Using Dynalearn, we modeled the spectral shift from beta (10-30Hz) to gamma (40-90Hz) that occurs from pre-stimulus (0-1000ms) to post-stimulus (1000ms-1500ms) processing. We asked Dynalearn to minimize the difference between the neurophysiologically observed power spectrum of the spiking response to the model's power spectrum response in both post and pre-stimulus periods. After training, both the individual spiking activity (raster plot in Fig.2) and the population power spectrum showed a high accuracy fit to the neurophysiological data. In particular, the model was able to fit the shift from pre-stimulus alpha-beta to post-stimulus gamma. In ongoing work, we plan to explore different interneuron types and connectivity structures that can best explain this spectral shift.

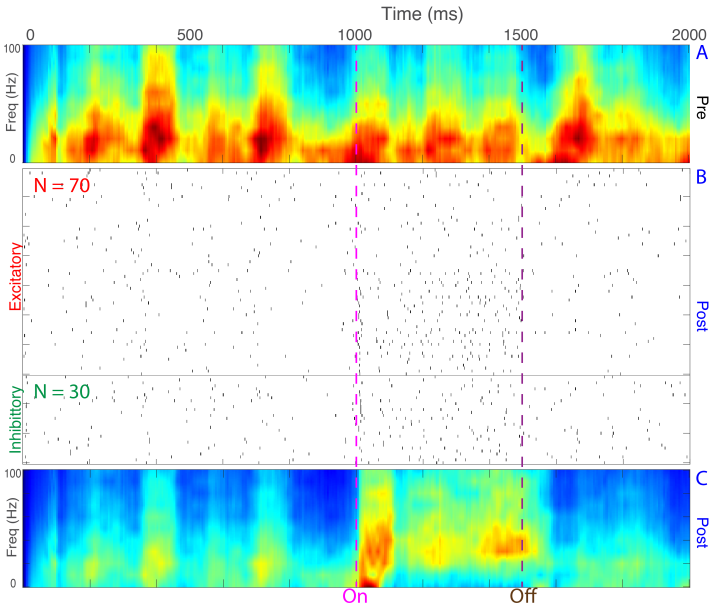

Figure 2: Simulation results; pre-training (A) and post-trainin (C) relative power spectrogram (B) post-training raster plot. (Time axis is aligned for all subplots and onset-offset of the stimulus is indicated by the dashed lines.)

Discussion

This abstract expanded computational approaches in neuroscience by proposing an automated process of studying highly-detailed neural circuits. The main advantage of precise biophysical neural models is that they are more comparable to the brain. In addition, several unknown mechanisms contributing to computations performed by brain may be revealed by unsupervised explorations. Moreover, our algorithm does not assume model types and may be useful for non-physiologic models such as ANNs and transformers. Our aim is to use Dynalearn for testing hypotheses in predictive coding/routing in order to evaluate proposed mechanisms such as the adaptation, prediction and inference.

Acknowledgments

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