Neuro-constrained Bio-inspired Recurrent Neural Network

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Introduction

Understanding neural population activity is fundamental to unraveling how the brain processes information. However, traditional Recurrent Neural Networks (RNNs) are designed with random connectivity patterns and do not incorporate constraints based on biological structure, such as the spatial arrangement of neurons or the specific patterns of synaptic connections—features critical to biological neural networks. Our research aimed to overcome this limitation by creating a neuro-constrained bio-inspired RNN that incorporates functional and anatomical constraints derived from the Machine Intelligence from Cortical Networks (MICrONS) dataset, a comprehensive resource detailing the mouse visual cortex. We evaluated the bio-inspired RNN on a 1-step inference task, demonstrating a significant performance improvement over other networks. This work underscores the importance of true synaptic connectivity in neural modeling. It suggests that biologically informed models could enhance neuroscience and artificial intelligence by fostering more realistic neural networks.

Description

Neural population activity underpins brain function, from sensory processing to decision-making, yet computational models often oversimplify the brain's complexity. Traditional RNNs, widely used to emulate neural dynamics, assume uniform or random connectivity, neglecting the true synaptic connectivity of neurons (Perich Rajan, 2020). This discrepancy limits the ability of traditional RNNs to accurately replicate behavior, prompting the need for models that integrate anatomical data. Achterberg et al. pioneered the integration of spatial constraints into recurrent neural networks (RNNs) to bridge the gap between artificial models and biological neural systems. Their work demonstrated that spatially embedded RNNs (seRNNs) exhibit enhanced task performance and biologically plausible connectivity patterns. In this work, by integrating anatomical and functional information from biological neurons into an RNN, we aimed to create a model that better reflects the brain's architecture, offering insights into how structure shapes function. Our approach involved extracting and preprocessing data from the Machine Intelligence from Cortical Networks (MICrONS) dataset, constraining the RNN with anatomical and functional features, and evaluating its performance against baseline models. Below, we detail the datasets, tools, theoretical frameworks, and analytical methods employed.

Dataset: We utilized the MICrONS dataset, a unique resource in neuroscience, offering large-scale connectomics from the primary visual cortex and three higher visual areas in mice (MICrONS Consortium, 2021). It provides detailed anatomical information on over 200,000 cells and 523 million synapses, with two-photon microscopy functional imaging data capturing the visual responses of approximately 75,000 neurons. We focused on a subset of neurons, extracting neuronal position) and connectivity data via synapse queries. The functional data used in this study were derived from deconvolved calcium imaging recordings (session 6, scan 6, field 2) of 312 neurons available in the dataset, which captures neuronal activity in the mouse visual cortex during stimulus presentation. This dataset was chosen for its high-quality anatomical detail, enabling us to map neurons' physical locations and connections accurately.

Data Preprocessing and Tools: The anatomical data extraction was facilitated by the CAVEclient, a Python library interfacing with the MICrONS dataset, and DataJoint, which streamlined database queries. Neuronal coordinates were converted into a 3D Euclidean space, and synaptic connections were compiled into a connectivity matrix, which constructs a sparse matrix of synaptic weights. This matrix, combined with Euclidean distances between neurons, and the initialization of the bio-inspired weight matrix formed the basis for constraining the RNN. The recurrent weight matrix was initialized using biological constraints derived from the MICrONS dataset. First, lognormally distributed weights were generated. These weights were combined with normalized functional correlation and Spike Time Tiling Coefficient (STTC) matrices (Figure 1b). Both matrices were min-max scaled to [0, 1], and element-wise multiplication was applied:

$$W_{\text{Bio}} = W_{\text{lognormal}} \odot \text{norm}(\text{corr}) \odot \text{norm}(\text{STTC})$$

The weights were scaled to a target mean (0.1), thresholded (> 0.01), and adjusted to ensure spectral radius for stability. Pairwise Pearson correlations between neuronal activity traces were computed from the MICrONS functional imaging data (session 6, scan 6, field 2). The matrix was normalized to [0, 1] using min-max scaling. The STTC is a measure used to quantify the level of temporal synchrony between the spike trains of two neurons (Cutts Eglen, 2014). It is designed to address the problem of biases in firing rates that can affect other measures of synchrony, making it a robust metric in the context of neural firing patterns. For neurons $\boldsymbol{i}$ and $\boldsymbol{j}$, it is defined as:

$$\text{STTC}(i, j) = \frac{1}{2} \left(\frac{N^i_{\text{overlap}}}{N^i_{\text{total}}} + \frac{N^j_{\text{overlap}}}{N^j_{\text{total}}} \right)$$

N_{overlap} counts spikes that co-occur within a defined temporal window, while N_{total} represents the total number of spikes for each neuron. The STTC matrix derived from the MICrONS dataset was min-max normalized to the range $[0, 1]$ and combined with a functional correlation constraint to inform the recurrent weight matrix. Both the STTC and correlation matrices were loaded from preprocessed files, normalized, and integrated into the recurrent layer of the spatially embedded RNN (seRNN). To refine connectivity patterns, spatial regularization was applied—penalizing long-distance connections while promoting network communicability. The bio-inspired seRNN was implemented using TensorFlow's SimpleRNN, with the custom SeRNN regularizer. Neuron coordinates were defined based on their actual soma positions extracted from the MICrONS dataset.

Theoretical Framework and Model Development: Inspired by Achterberg et al. (2023), our seRNN incorporates a custom regularizer, which penalizes connections based on spatial distance and communicability—a measure of network efficiency. Unlike traditional RNNs with unconstrained recurrent layers, our model embeds neurons in a 3D space reflecting their anatomical positions. We implemented this in TensorFlow 2.3.0, defining a sequential model with a Gaussian noise layer, a 128-unit SimpleRNN layer with the custom regularizer (strength = 0.3), and a softmax output layer for classification. The regularizer combines spatial costs (derived from MICrONS coordinates) with communicability, encouraging biologically plausible connectivity patterns.

Analytical Methods and Evaluation: We trained the seRNN on a 1-step inference task (Figure 1a) using a maze-like dataset generated by mazeGeneratorI, simulating a decision-making process where the network predicts the next step (left, up, right, down) after observing a goal, delay, and choice options. The dataset comprised 5,120 training, 2,560 validation, and 2,560 test samples, batched at 128. Training ran for 10 epochs with the Adam optimizer and categorical cross-entropy loss. Performance was compared to baseline RNNs with random initial positions or embeddings, using accuracy as the primary metric. For a visual summary of the methodology, please refer to the flowchart provided later in the document.

Results: The bio inspired seRNN (bio seRNN) outperformed baseline models, achieving a 37% increase in accuracy on the 1-step inference task compared to networks with random embeddings (Figure 1c). This improvement highlights the critical role of spatial organization in enhancing predictive accuracy.

Discussion and Implications: These results demonstrate that integrating anatomical and functional data from biological neurons into both seRNNs and RNNs significantly improves their performance on the defined task. The performance boost suggests that spatial constraints enable the network to capture biological systems' dynamics better. This approach refines hypotheses about how brain structure shapes function by integrating anatomical and functional constraints from actual neurons into neural networks, providing a concrete tool to test and validate theories of neural dynamics in silico. For artificial intelligence, it suggests a path toward efficient, brain-inspired architectures.

Conclusion: Our development and evaluation of the bio-inspired RNN reveal that integrating anatomical and functional data from biological neurons, enhances the modeling of neural population activity, achieving a 37% performance increase over traditional RNNs. By incorporating MICrONS-derived anatomical and functional data, we propose a model that performs better and mirrors biological network properties. This work underscores the value of biologically informed computational models and sets the stage for future research into scaling seRNNs.

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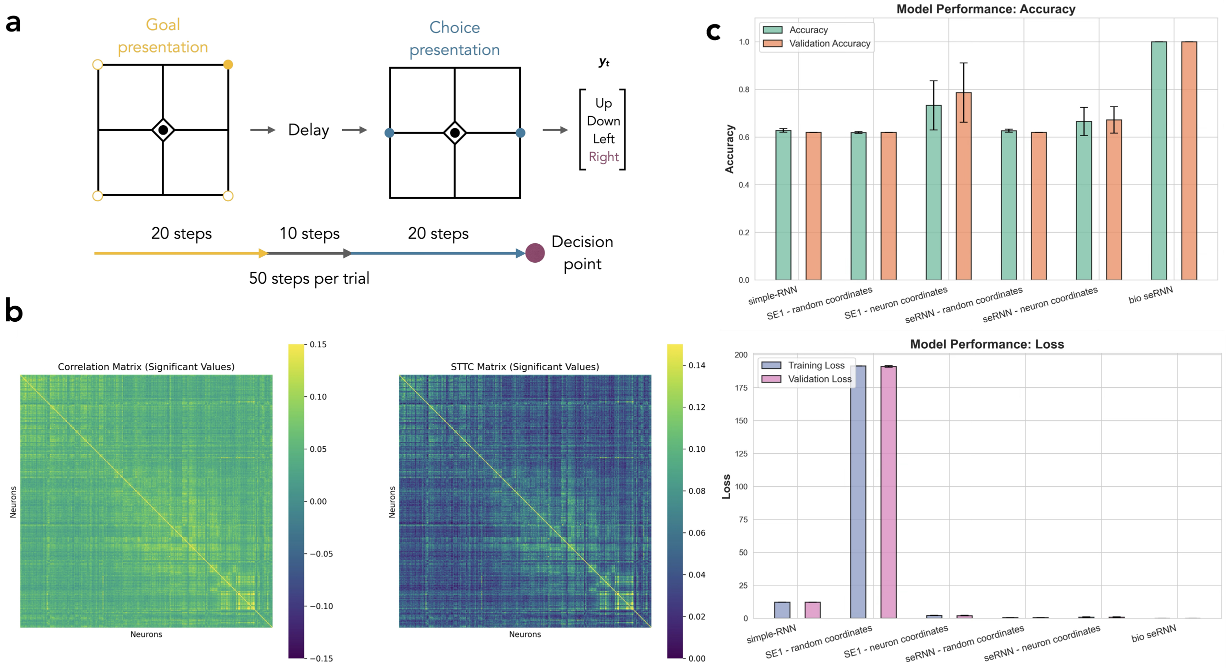
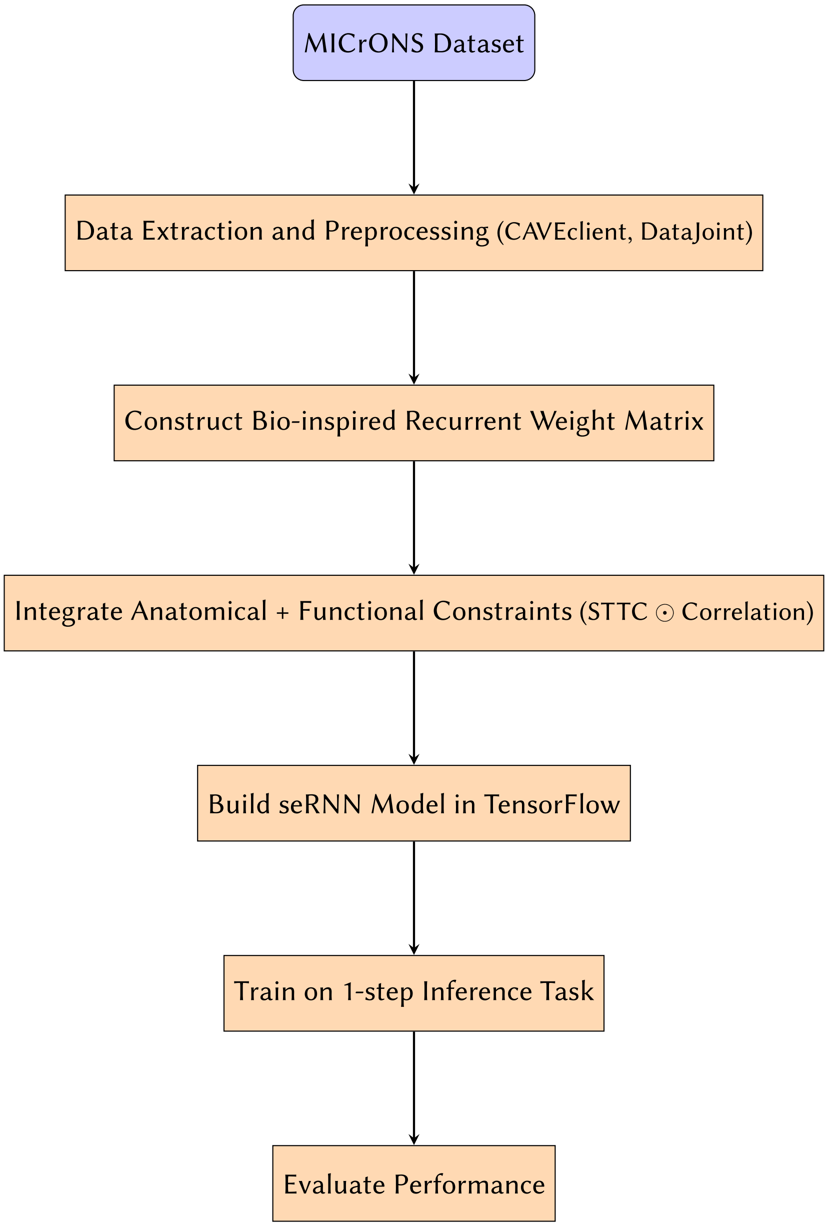


Figure 1: **(a)** Task design for the 1-step inference task. The maze-like decision-making paradigm involves goal presentation, delay phases, and choice options (left, up, right, down). **(b)** Left: Functional correlation matrix of neural activity from MICrONS functional data. Right: STTC matrix quantifying pairwise neuronal synchrony. **(c)** Performance comparison. After 10 epochs, the bio seRNN achieves a 37% accuracy improvement over baseline RNNs with random embeddings.



Flowchart summarizing the methodology for developing the neuro-constrained bio-inspired RNN.