

Anatomically and Functionally Constrained Bio-Inspired Recurrent Neural Networks Outperform Traditional RNN Models



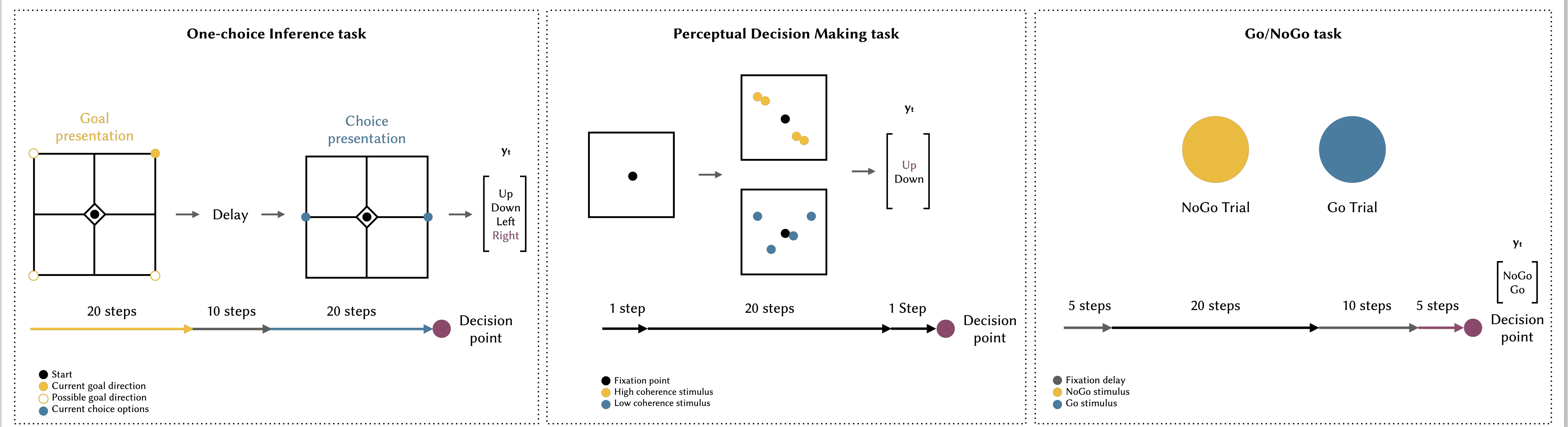
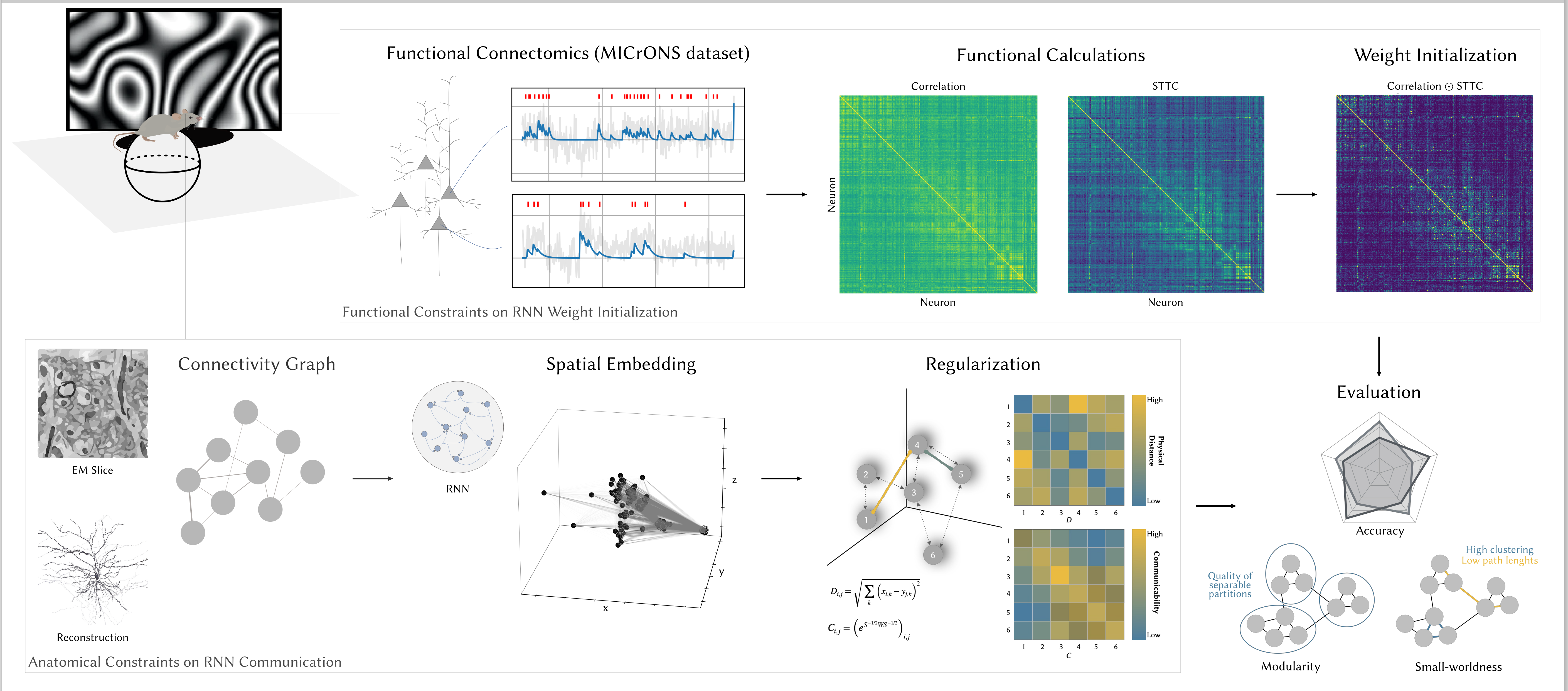
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1. Functional connectomics data from the MICrONS dataset was retrieved and processed to spatially embed an RNN

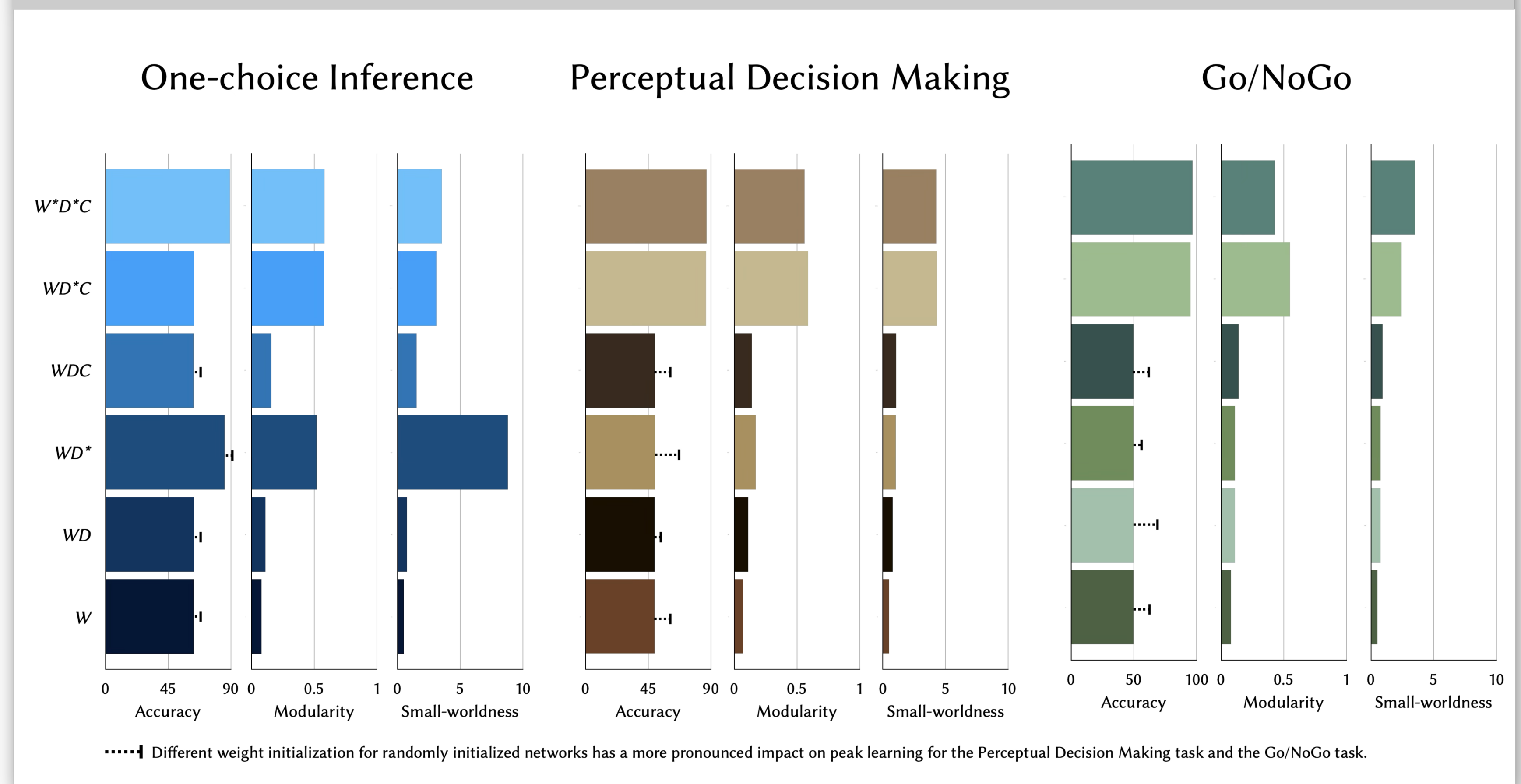


2. Models use different regularizations

Model Name	Bio Weight Init.	Spatial Embedding	Communicability	Regularization
W^*D^*C	Yes	Real (D^*)	Yes (C)	$\lambda \ W^* \odot D^* \odot C\ $
WD^*C	No	Real (D^*)	Yes (C)	$\lambda \ W \odot D^* \odot C\ $
WDC	No	Grid (D)	Yes (C)	$\lambda \ W \odot D \odot C\ $
WD^*	No	Real (D^*)	No	$\lambda \ W \odot D^*\ $
WD	No	Grid (D)	No	$\lambda \ W \odot D\ $
W (Simple RNN)	No	None	No	$\lambda \ W\ $

Model configurations incorporating combinations of biological constraints: biological weight initialization (W^*), spatial embedding using real neurons (D^*) or artificial grid (D) coordinates, and communicability-based regularization (C).

3. W^*D^*C models perform better and exhibit modular, small-world architecture



4. Work Description

Motivation

Understanding how neural circuits drive sensory processing and decision-making is a central neuroscience challenge. Traditional Recurrent Neural Networks (RNNs) capture temporal dynamics but fail to represent the structured synaptic architecture seen in biological systems [1]. Recent spatially embedded RNNs (seRNNs) add spatial constraints for better biological relevance [2], yet they do not fully exploit detailed anatomical and functional data to enhance task performance and neural alignment. This study aims to address this gap by integrating anatomical and functional constraints to create networks that not only perform better on tasks but also mirror biological network characteristics like modularity and small-worldness.

Summary

We introduce and train a bio-inspired RNN that integrates detailed anatomical connectivity and functional data from the MICrONS dataset [3]. It offers nanometer-scale reconstructions of ~75,000 neurons, along with functional imaging data recorded from neurons via two-photon calcium microscopy. Among these, ~12,000 excitatory neurons have both structural and functional data aligned. Using neuronal positions, synaptic connections, functional correlations, and Spike Time Tiling Coefficients (STTC) [4]—a robust metric that eliminates firing rate biases—from a subset of these neurons, we constrain our model using biologically informed weight initialization, communicability metrics, and a regularizer that favors short, communicative connections to reflect realistic network properties.

Results

The biologically constrained model variant (W^*D^*C) achieved the highest performance across three decision-making tasks. In addition to accuracy, the model also showed high modularity and small-worldness—structural properties observed in real cortical networks—making it both functionally and structurally superior to traditional RNNs.

Takeaway

Adding biological realism—via functional and anatomical constraints—not only improves model accuracy but also produces networks with brain-like modular and small-world properties. It opens the door to more realistic and interpretable AI systems modeled after the brain's architecture.

References

- [1] Perich (2020). Rethinking brain-wide interactions through multi-region 'network of networks' models. Current Opinion in Neurobiology.
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- [3] The MICrONS Consortium (2025). Functional connectomics spanning multiple areas of mouse visual cortex. Nature.
- [4] Cuts (2014). Detecting Pairwise Correlations in Spike Trains: An Objective Comparison of Methods and Application to the Study of Retinal Waves. The Journal of Neuroscience.

Acknowledgements

N.D. is supported by NIH Grant R24MH117295. The authors thank NIH for sponsoring DANDI archive, which provided the open-access data used in this study. M.S., R.R., and M.M. thank Neuromatch Academy for its support and resources for young scholars and this study. They also thank the DataJoint team for their help and guidance.

