MIA CAMERON

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EDUCATION

University of California, San Diego　　　　　　　　　　　　　　　　Expected Jan 2025

B.S. Mathematics - Computer Science

Minor in Biology

- **Relevant Coursework:** Calculus and Linear Algebra, Data Structures and Algorithms, Software Engineering, Real Analysis, Probability and Stochastic Processes, Statistics, Machine Learning, Cellular and Systems Neuroscience, General Biology and Chemistry

RESEARCH PROJECTS

Biologically-plausible deep learning with reciprocal feedback　　　　　　Jan 2024 - Present

Salk Institute for Biological Studies　　　　　　　　　　　　*Computational Neurobiology Lab*

- Independently developed and extended a biologically-plausible learning rule based on the predictive coding framework to deep neural network architectures. Provided a mathematical proof of how it worked, and its relationship to Newton-like optimization.
- Implemented in PyTorch using custom autograd functions, with preliminary results showing it outperforms comparable biologically-plausible algorithms on MNIST and CIFAR-10 classification tasks.
- Submitted as a first-author conference paper to ICLR 2025 as "A biologically-plausible alternative to backpropagation using pseudoinverse feedback"

Predictive Coding in the Hippocampus　　　　　　　　　　　　　　July 2022 - Present

Salk Institute for Biological Studies　　　　　　　　　　　　*Computational Neurobiology Lab*

- Developed a new, biologically-plausible learning algorithm for sequence storage and replay in RNNs as part of a larger project modeling sequence storage, prediction and learning in the trisynaptic circuit. [link to GitHub repo]
- Published in Neuron as "Predictive sequence learning in the hippocampal formation".
- Presented work on the learning rule at the 2022 INC Winter School on Brains and Computation.

Phage Genomics Research Initiative　　　　　　　　　　　　　Sept 2020 - June 2021

UC San Diego　　　　　　　　　　　　　　　　　　　*Dutton Lab and Pogliano Lab*

- Presented original research at the Undergraduate Research Symposium on potential functions of an unknown, novel protein in Erwinia bacteriophage RAY.
- Managed large datasets between collaborators and developed scripts to automate bioinformatics pipelines and repetitive processes.
- Contributed to the publication Prichard et al., (2023) *Identifying the core genome of the nucleus-forming bacteriophage family and characterization of Erwinia phage RAY*, Cell Reports 42.

PUBLICATIONS

- Chen, Y., Zhang, H., **Cameron, M.**, & Sejnowski, T. (2024). *Predictive sequence learning in the hippocampal formation*. Neuron, 112(15). doi:10.1016/j.neuron.2024.05.024 [link]

SUBMITTED CONFERENCE PAPERS

- **Cameron, M.**, Chen, Y., & Sejnowski, T. (in-review). *A biologically-plausible alternative to backpropagation using pseudoinverse feedback*. ICLR 2025. [submission] [slides]

POSTERS AND PRESENTATIONS

- **Cameron, M.** (December 16th, 2022). *Predictive Recirculation: A model of encoding and replay of sequences in a recurrent neural network* [Presentation], 2022 INC Winter School on Brains and Computation - Student Session. [slides]

- **Cameron, M.**, Asavavimol, A., Spencer, T., Prichard, A., Dutton, R., Pogliano, J. (April 2021). *The Predicted Function and Phylogeny of Erwinia phage RAY gp153* [Poster], Undergraduate Research Conference, UC San Diego.

SKILLS

Programming: Python (NumPy, PyTorch, Matplotlib), MATLAB, Java, C++
Tools: Git, Linux, Latex, Blender, Adobe Illustrator
Analysis: Neural Networks, Linear Algebra, Matrix Calculus, Optimization
Communication: Scientific writing, Scientific Presentation skills, Literature review