APMTH 226 — Project Proposal

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Auto-Associative Neural Networks for Protein Interaction Dynamics: Reproduction, Stability Analysis, and Learning-Rule Extensions

Project Idea

This project will reproduce and extend the work of Samarasinghe et al. [1], which modeled a 12-protein mammalian cell-cycle network using auto-associative neural networks (AANNs). The original study showed that AANNs with sigmoid neurons accurately captured protein dynamics, while linear or randomly connected networks failed to do so.

Reproduction + Extension

I will reconstruct their experiments using the published connectivity matrix and weight tables, implementing masked AANNs in PyTorch. Without access to their simulated dataset, I will simulate data that mimics described dynamics. My goals will be to replicate training-loss and trajectory results for linear vs sigmoid AANNs, confirm that accurate dynamics can emerge without correct structural edges, and verify that adding recurrence improves fidelity.

To extend the analysis, I will perform the following investigations:

- Perform a fixed-point and Jacobian eigenvalue analysis of the learned network to study stability and attractor structure, drawing parallels to Hopfield-network energy formulations.
- Re-train the same network using a biologically plausible contrastive Hebbian learning rule [2] and compare convergence and generalization against gradient-based training.
- Quantify structure-function non-identifiability by testing how many weight configurations yield near-identical dynamics, relating this to Gardner's capacity framework.

Expected Outcomes

Reproduced AANNs should match reported dynamics (low MSE for sigmoid networks, degraded fits for linear ones). Eigenvalue and Lyapunov analyses are expected to reveal stable attractors corresponding to cell-cycle states. Contrastive Hebbian training should reach comparable accuracy but slower convergence, illustrating trade-offs between biological plausibility and efficiency. The final report will include quantitative results, phase-portrait visualizations, and theoretical discussion linking these findings to Hopfield-style dynamics and capacity limits.

References

[1] Sandhya Samarasinghe, Tran Nguyen Minh-Thai, Komal Sorthiya, and Don Kulasiri. Neurons and neural networks to model proteins and protein networks. *BioSystems*, 258:105613, 2025.

[2] Javier R. Movellan. Contrastive hebbian learning in the continuous hopfield model. In David S. Touretzky, Jeffrey L. Elman, Terrence J. Sejnowski, and Geoffrey E. Hinton, editors, *Connectionist Models*, pages 10–17. Morgan Kaufmann, 1991.