Dynamics, Networks and Computation

Homework Exercise #3

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1 Submission Guidelines

Submission deadline is Thursday, May 22nd 2025, at 23:59

1.1 Submission

Submit a single .zip file containing

1. A .ipynb file (Jupyter notebook) with your answers to the questions. (Python code cells for code questions, MarkDown cells for text/math).

2. Any other files needed to run the code in the notebook.

1.2 Working in Groups

You're allowed to discuss questions and code implementations with other students, but the final answers should be yours alone. In particular, you should write all code yourself.

2 Hopfield Networks

Choose two images, and transform them into $n \times n$ binary matrices (you may use the helper functions in the attached .py file). Choose n so that the images are clear, but not too big or else the simulations in the following part may be too demanding.

2.1 Planting Memories in a Network

Design a weight matrix so that your two images are attractors with respect to the Hopfield (deterministic) update equation. Does the system reliably converge from random initial conditions?

2.2 Stochastic Update

Implement a stochastic transition rule between states which will ensure the system converges to desired Boltzman distribution

$$p(\mathbf{S}) \propto e^{-\beta E(\mathbf{S})}$$

How does β affect the convergence from Q2.1?

2.3 Multiple Memories

Try adding more images. At what point does the system no longer reliably converge to one of the stored memories?

Bonus: Try doubling the number of neurons n. What changed? Can you explain intuitively?

2.4   Local Fields

Adjust the update rule so that a neuron S_i is connected only to a $d \times d$ window centered around S_i. Try running one of the variants of the network from the previous question which converged reliably to one of its stored memories. Does it still converge? What is the effect of d?

3   Evolving Optimal Regulation in a Noisy Environment

In recitation we explored a model for the conditions in which regulation is beneficial. In the model, an organism may find itself in one of two environments E_1 and E_2 w.p. p and $1 - p$ respectively, and it can produce some resource Z with cost $c < b$ which is beneficial in E_1 with benefit b, but useless in E_2. The organism can produce sensory and regulatory mechanisms which allow it to generate Z only in E_1, but this decision has cost r.

In reality, sensory apparatus are never infinitely accurate, and an organism may be wrong about what environment it actually is in. Expand the model from recitation to include the possibility of noise in environmental signals. The modelling details are up to you, but the model should include some parameter/s which control the degree of reliability of environmental signals (the simple model above has perfect reliability). Explore the behavior of your model as a function of this parameter/s and provide plots to support your analysis and conclusions.

4   Evolution With No Selection of Protein Networks

So far, we treated evolution as an optimization process whose products may always be thought of as have been selected for some function. However, there are many reasons for evolutionary products to have a clear signature, but which is not optimized for any purpose. In this question we will explore one example, supplying us with yet one more null model for comparing biological network characteristics to.

4.1   Protein Interaction Network Degree Distribution

Download the protein interaction network from here (network #5).

What is the shape of the network's degree distribution? Try visualizing the distribution using a log-log plot to better observe the behavior of the tail. Compare this shape to a simple null model.

4.2   Duplication Mutation Networks

Implement a function which, starting from an initial seed (undirected) graph, gradually grows it to a desired size n by iteratively

1. Selecting a random node

2. Duplicating the node, together with all of its edges

3. Removing each of the duplicated nodes edges independently with probability δ

This process is meant to model biological network evolution where gene duplication is often the source of novel genes, which then go on to mutate and acquire new function.

Use your function to generate an appropriate null model for the protein interaction network starting from a seed graph with two connected nodes (making sure the final sampled graph has the same number of nodes and roughly the same number of edges as the protein network).

4.3   Duplication Mutation Network Properties

Compare the degree distribution of your new null model to the protein interaction network. How sensitive are the results to changing the seed graph from which you grow the duplication-mutation graph?

4.4 Other Properties of the Protein Interaction Network

Can you find any properties of the protein interaction network which *aren't* explained by the duplication-mutation null?

Good Luck!