

Life Finds A Way: Emergence of Cooperative Structures in Adaptive Threshold Networks

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Abstract

There has been a long debate on how new levels of organization have evolved [21]. It might seem unlikely, as cooperation must prevail over competition [22]. One well-studied example is the emergence of autocatalytic sets [9], which seem to be a prerequisite for the evolution of life. Using a simple model, we investigate how varying bias toward cooperation versus antagonism shapes network dynamics, revealing that higher-order organization emerges even amid pervasive antagonistic interactions. In general, we observe that a quantitative increase in the number of elements in a system leads to a qualitative transition.

We present a random threshold-directed network model [24] that integrates node-specific traits with dynamic edge formation and node removal, simulating arbitrary levels of cooperation and competition. In our framework, intrinsic node values determine directed links through various threshold rules. Our model generates a multi-digraph with signed edges (reflecting support/antagonism, labeled “help”/“harm”), which ultimately yields two parallel yet interdependent threshold graphs. Incorporating temporal growth and node turnover in our approach allows exploration of the evolution, adaptation, and potential collapse of communities and reveals phase transitions in both connectivity and resilience.

Our findings extend classical random threshold and Erdős-Rényi models [8], offering new insights into adaptive systems in biological and economic contexts, with emphasis on the application to Collective Affordance Sets [19]. This framework should also be useful for making predictions that will be tested by ongoing experiments of microbial communities in soil.

1 Introduction

Life drives — and is driven by — interactions. Each organism brings a unique and vast combination of causal properties into its environment, continuously adapting and “tinkering” to establish beneficial interactions or mitigate harmful ones. Despite evolutionary pressures and competition, we regularly observe that complex, self-

sustaining networks of mutual support routinely emerge in living systems [22]. Understanding how and why such networks reliably form is central to both theoretical biology and complex systems science.

Microbial communities illustrate this phenomenon particularly well. Despite (or, possibly due to) immense biochemical and ecological diversity, stable interdependent communities arise repeatedly. Even when initial interactions are predominantly antagonistic, microbes find ways to coexist or even benefit each other, forming what can be viewed as "collective affordance sets" [19]: jury-rigged, self-organized structures that exploit combinations of causal properties among community members.

To empirically examine this phenomenon, ongoing experimental work aims to mix 56 bacterial and 56 fungal species, to observe if and how novel stable ecosystems emerge from a huge potential space of interaction patterns. While our primary interest is in complex soil communities of microorganisms, this concept extends beyond biology. Human economies share remarkably similar dynamics. Technological innovation and market diversity are driven by recombinations of existing products, services, and ideas. As more firms or inventors enter the market, new products and services find "niches," creating a self-reinforcing and evolving web of interdependence.

In this paper, we present an adaptive threshold network model with simple assumptions, designed to explore the conditions that foster stable, cooperative structures. Rather than focus on specific evolutionary games or particular ecological scenarios, our model investigates the broader space of possible interaction patterns, identifying conditions under which large, strongly connected communities (SCCs) reliably form and persist. Moreover, because "alternative community states can arise as a consequence of system dynamics without being driven by environmental differences" [11], the broad, environment-agnostic design of our model is well justified.

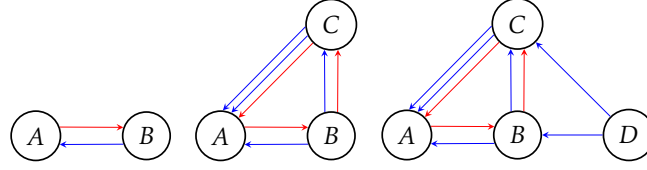
Using a simple model, our results demonstrate that networks of mutual support robustly emerge even when antagonistic interactions predominate, provided certain thresholds of cooperation and species longevity are met. Moreover, these emergent communities exhibit distinctive patterns, such as stable configurations of key cooperative nodes and systematic turnover influenced by antagonism. Thus, our findings offer insights not only into the formation of biological ecosystems but also into analogous processes in economics and social systems, highlighting universal principles underlying collective organization and adaptive complexity.

2 Model

2.1 Description of Vanilla Model

Using the python library Networkx, we dynamically generated a Directed Multi-Graph $G = (V, E)$ where V is the set of vertices (or nodes) and E is the set of edges (or links). At each discrete time-step the model adds one new vertex to the digraph and endows it with four independent traits that represent a subset of its causal properties to give or receive help and harm. The newcomer then "tests" every pre-existing vertex in both directions. For each ordered pair, the absolute difference between the relevant traits is compared with a random Poisson-scaled threshold: if the gap is small enough, then an edge is created. This threshold is also modulated by a global help-to-harm ratio, and a

small random multiplicity is allowed, so a single pair can accumulate several parallel edges (we set a maximum of 6 to calculations, but this can be altered) to represent multiple affordances or adverse interactions.



Visualization of Possible Simulation:

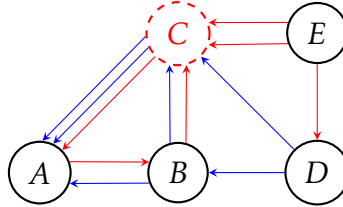
Step 1: Node A is added.

Step 2: Node B added, harm (red) edge added $B \rightarrow A$ as $|A_{\gamma_{in}} - B_{\gamma_{out}}| < P_{AB}$, and help (blue) edge added $A \rightarrow B$ as $|A_{h_{out}} - B_{h_{in}}| < P_{AB}$.

Step 3: Node C added, 3 blue and 2 red links added after threshold test between C and existing nodes A,B.

Step 4: Node D added, 2 blue links added after threshold test between D and existing nodes A,B,C.

Once edges are formed, every vertex ages by one tick. A node whose age now exceeds its prescribed lifespan is removed—and all of its incident edges with it—under either of two conditions: it has no incoming edges at all, or more than a fixed fraction (usually 50 %) of its incoming edges are harmful. If there are enough helpful edges, then nodes survive indefinitely. Edges never disappear on their own; they vanish only when one of their endpoints is deleted. Repeating this birth–binding–culling cycle yields the evolving signed network on which the subsequent experiments are run.



Death threshold (η) passed. Node C (and all its incoming and outgoing edges) will be removed if its lifespan is reached.

Some key concepts and parameters are called for at this point:

- **Strongly Connected Component (SCC)** A maximal set of nodes in which each can reach every other via directed edges. Here, a large SCC indicates a self-reinforcing community of mutual “help” interactions that props up structured cooperation even within threatening environments.
- **Lifespan (L_S)**. Maximum number of steps a node may survive before it is culled for (i) having no in-edges or (ii) a non-positive net balance of help minus harm.
- **Bind-range (p_{\max})**. Upper bound on the allowable trait-difference for an edge to form; scaled Poisson noise introduces pair-specific variability.

- **Binding propensity.** Edge probability for a specific pair (i, j) : $P_{ij} = \min[1, k_{ij}p_{\max}]$ with $k_{ij} \sim \text{Pois}(\lambda)$. This is explained in more detail below.
- **Help/Harm ratio (ρ).** Scales bind-range so that overall fraction of potential interactions are harmful are ρ ; $(1 - \rho)$ are helpful.
- **Node traits.** Each new node draws four independent traits: $h_{\text{in}}, h_{\text{out}}$ or "help in" and "help out", and $\gamma_{\text{in}}, \gamma_{\text{out}}$ or "harm in" and "harm out."
 $(h_{\text{in}}, h_{\text{out}}, \gamma_{\text{in}}, \gamma_{\text{out}}) \in [0, 1]^4$ and govern help/harm matching.
- **Removal threshold (η).** A node is deleted once $\frac{\text{harm}_{\text{in}}}{(\text{help}_{\text{in}} + \text{harm}_{\text{in}})} > \eta$. We use $\eta = 0.5$ unless stated otherwise.

Binding propensity p_{\max} We set an *upper-bound parameter* p_{\max} (starting at $p_{\max} = 0.001$ but varies in some simulations) that represents the largest possible difference in pairwise "catalytic potential" between any two nodes. For each ordered pair (i, j) we draw an integer $k_{ij} \sim \text{Poisson}(\lambda)$ and let the effective probability that a directed edge $i \rightarrow j$ appears be

$$P_{ij} = \min(1, k_{ij} p_{\max}).$$

In ecological terms k_{ij} could be read as the (random) count of events that would enable i to facilitate or provide affordances to j within the current time-step, while p_{\max} translates that count into a probability of edge-formation.

What follows are the results from several simulations. When parameters are altered, they are specifically listed below the figure.

3 Experiments & Results

In a systematic way, we explore how shifting the parameters (lifespan, harm-to-help ratio, binding chance) influence the emergence and persistence of strongly connected components (SCCs) in our directed network. Our primary interest was the evolution and robustness of cooperative structures (large SCCs) in networks characterized by varying degrees of antagonism (harm-to-help ratio). Eigen Analysis was performed to give a higher level characterization of the network's behavior short and long run behavior.

We enumerate and briefly explain the results found in the figures below:

1. **Number of Nodes and Edges:** At each time step t , the number of nodes and edges present in the graph. A node is added at every step with its own traits. Edges form based on the threshold rule. As it is the case with many network growth algorithms, existing nodes can create edges only with new nodes. Still, cycles can be formed with the proposed approach.
2. **Fraction of Nodes in an SCC:** The fraction of nodes at time t in the graph that are part of a strongly connected component.
3. **Fraction of Nodes in largest SCC:** The fraction of nodes at time t in the graph that are part of the largest strongly connected component.

4. **In-Degree of Harm and Help Edges:** The distribution of the number of inbound help and harm edges at the end of the simulation. For figures 1-3, after 8,000 steps.
5. **Out-Degree of Harm and Help Edges:** The distribution of the number of outbound help and harm edges at the end of the simulation. For figures 1-3, after 8,000 steps.
6. **Mean Dominant Eigenvalue:** Measure of the density of connections in the direction of the principal eigenvector.
7. **Absolute Mean Dominant Eigenvalue:** Removing the sign of the above reveals just the intensity of any shifts in the principal eigenvector, positive or negative.
8. **Principal Angle:** The angle between the principal eigenvectors between network states.
9. **Spectral Gap:** The difference between the first and second principal eigenvalues: $|\lambda_1| - |\lambda_2|$.

3.1 Harm-To-Help Ratio and Lifespan Dynamics

3.1.1 Below 0.5 Harm-To-Help Ratio

When cooperative interactions dominate (harm ratio $\rho < 0.5$), we observed exponential growth in directed edge formation, resulting in a linearly increasing SCC size relative to the number of nodes in the network. This scenario characterizes a cooperative and expansive community where nodes not only persist, but integrate rapidly into a collective structure. Once such a community emerges, with a majority of help edges, it is would be difficult for its elements to be removed.

Figures 1,2,3 show the results of the simulation from solely increasing the Harm-To-Help ratio from $\rho = 0.3, 0.5, 0.7$ with all other parameters fixed. At first, we can restrict our view to the differences in the number of nodes and edges at step t , the largest SCC size and largest SCC fraction.

3.1.2 When Harm-To-Help > 0.5

For harm-to-help ratios exceeding 0.5, a strongly connected community still emerges and persists, provided nodes' lifespan surpasses ≈ 10 timesteps. Below this number, an SCC will fail to form reliably if $\rho > 0.7$.

Notably here, SCC size does not grow indefinitely; rather, it reaches an upper bound and fluctuates around a steady-state maximum. This equilibrium state depends directly on both lifespan and the binding chance parameters. Increasing antagonism (harm ratio) gradually reduces the steady-state size of the SCC, yet even with extremely antagonistic environments (harm ratio approaching 0.9), some significant level of persistent inter-connectedness remains, as tenuous as it is.

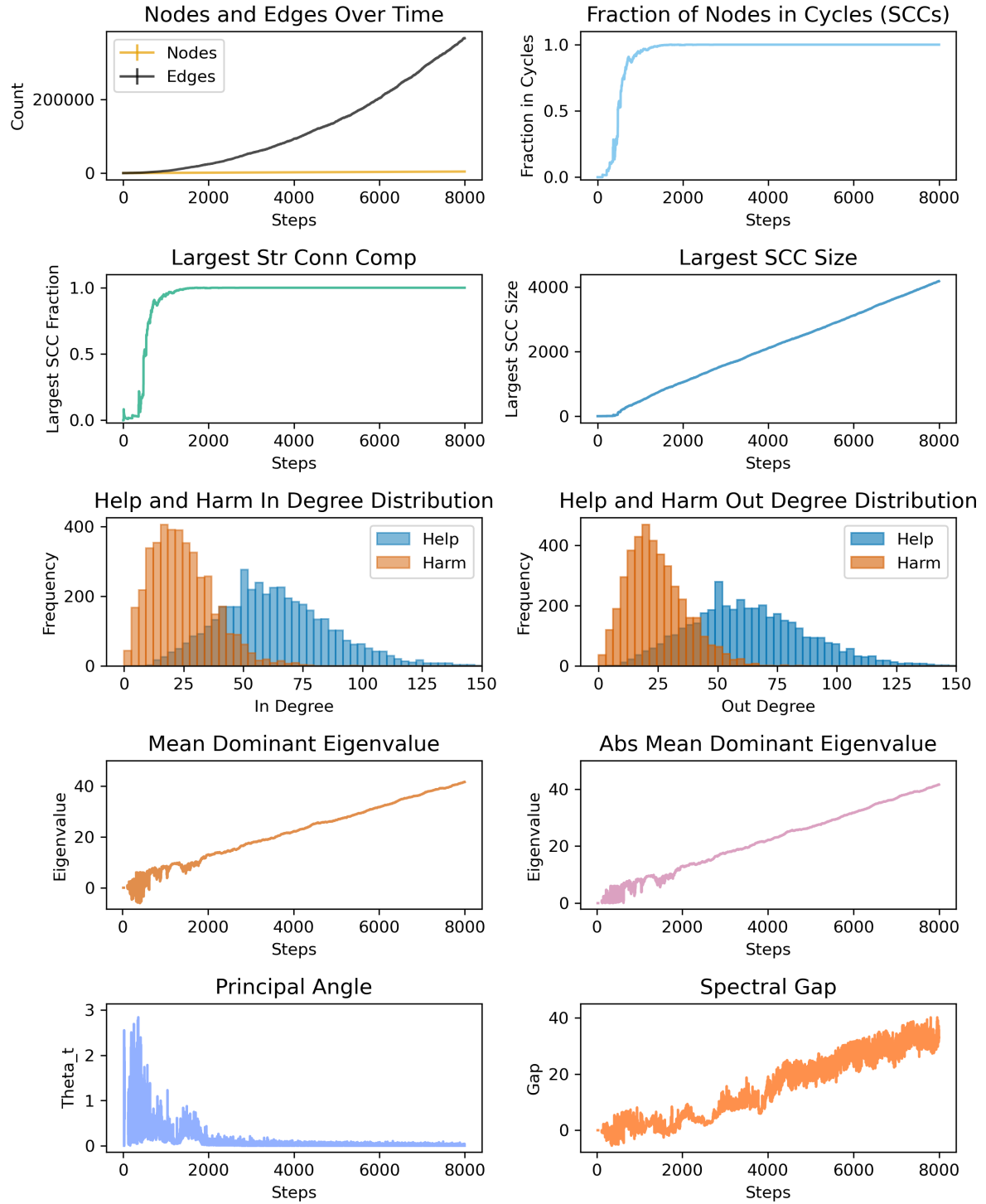


Figure 1: Harm-To-Help: 0.3, Lifespan = 100, Bind-Chance = 0.003

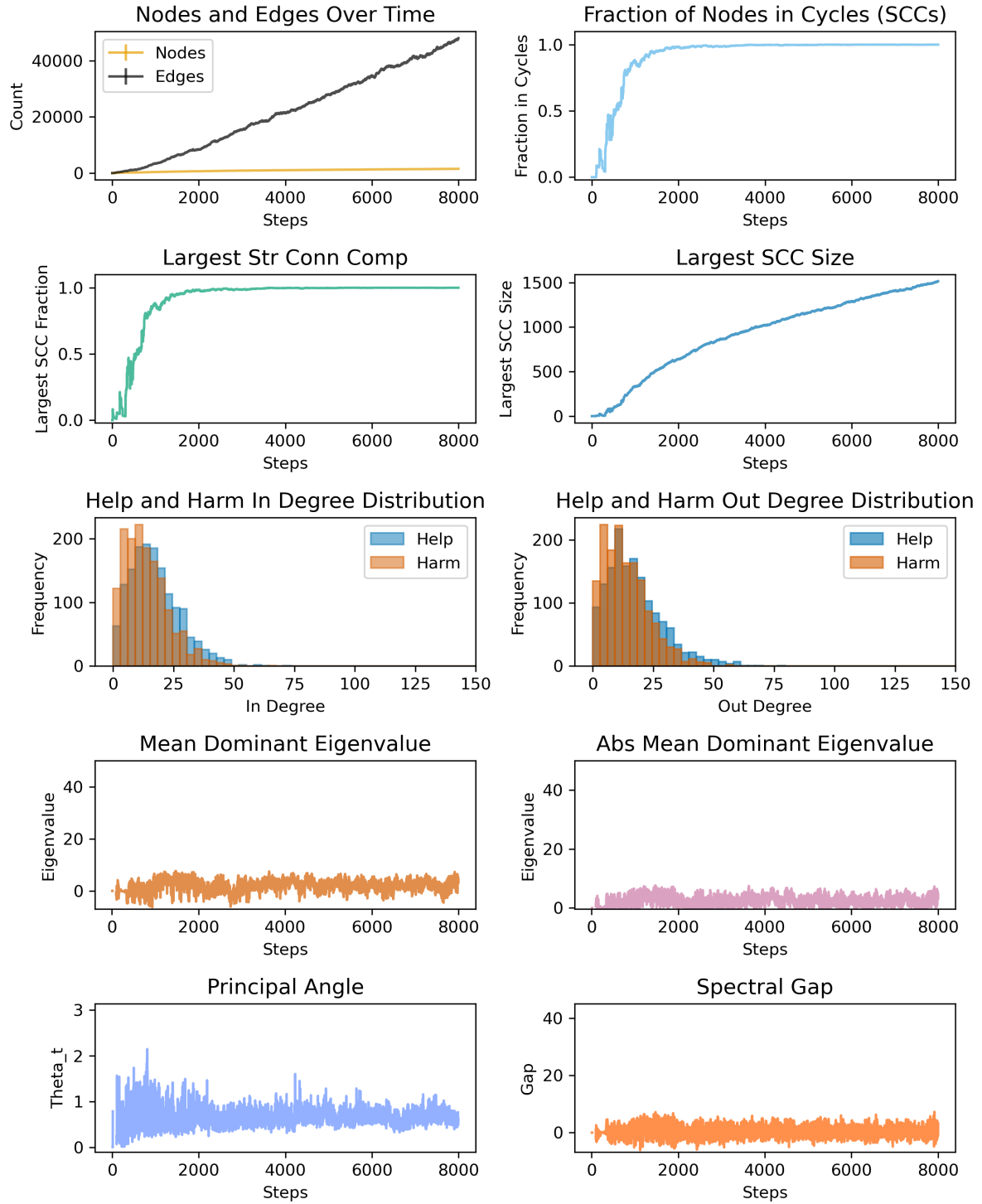


Figure 2: Harm-To-Help: 0.5, Lifespan = 100, Bind-Chance = 0.003

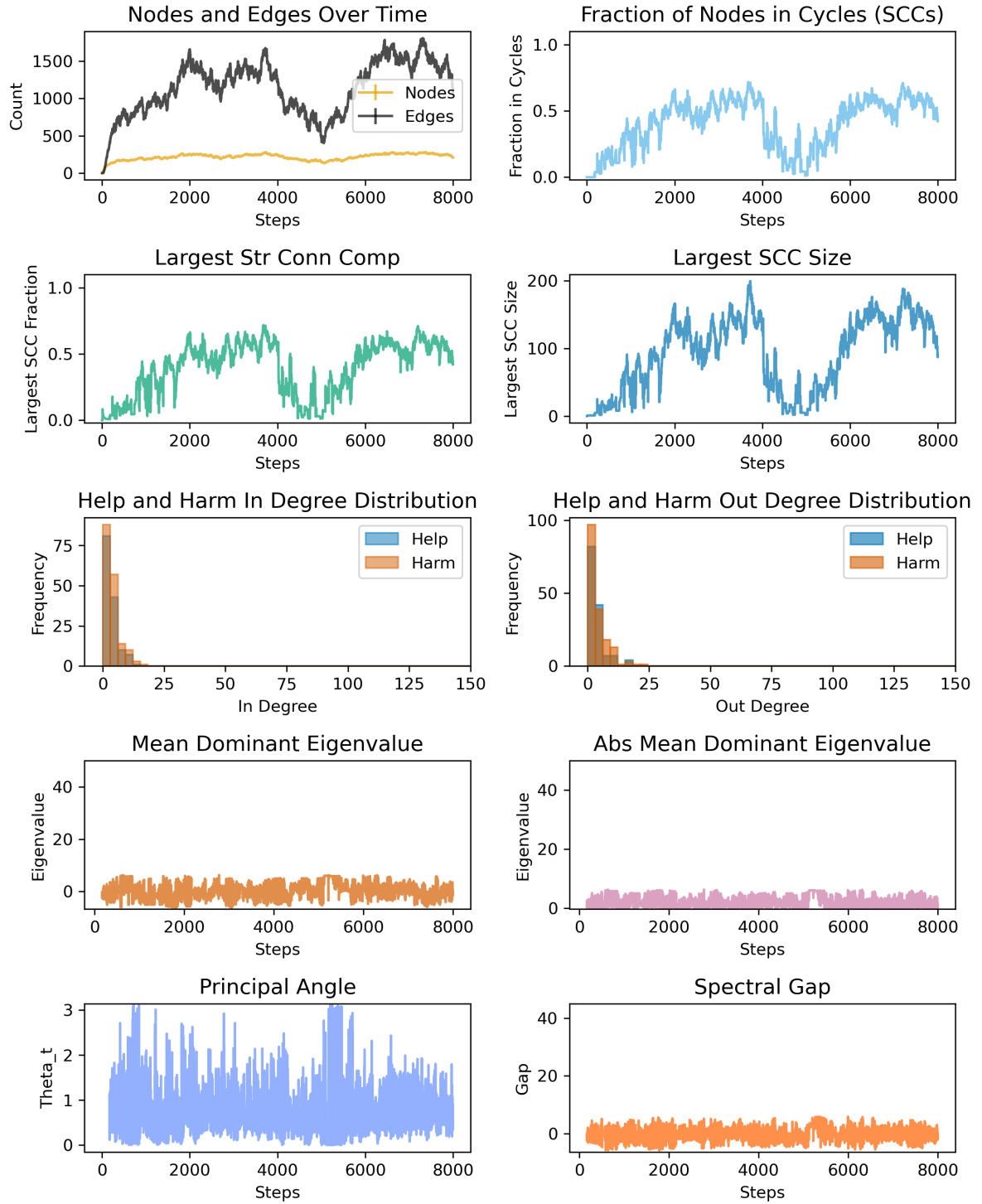


Figure 3: Harm-To-Help: 0.7, Lifespan = 100, Bind-Chance = 0.003

3.2 Influence of Binding Chance

Adjusting the binding chance, p_{max} which scales the likelihood threshold for interactions, primarily impacts the rate of convergence toward the final dynamic state. Increasing this parameter leads more quickly to equilibrium behaviors without substantially altering the qualitative behavior of SCC growth. However, in scenarios where the harm ratio exceeded 0.5, a higher binding chance increased the *fraction* of nodes in the SCC, but overall slightly decreased the number of nodes in the equilibrium size of the SCC. This suggests that increasing the likelihood of interaction partially counteracts the destabilizing effect of widespread antagonism.

p_{max}	Fraction in SCC	Final SCC Size
0.005	≈ 0.8	≈ 210
0.0075	≈ 0.9	≈ 200
0.015	≈ 0.98	≈ 175
0.02	≈ 1.0	≈ 150

30,000 Steps, $L_S = 100$, $\rho = 0.7$.

3.3 Node Age and Persistence

We noted a ‘demographic’ shift among highly-connected nodes (in the top 10% of in-degree) as antagonism increased. Specifically, and perhaps not surprisingly, networks with higher antagonism were increasingly dominated by younger nodes. High-harm environments shorten the node survival significantly, reducing the presence of “older” and more established nodes. Despite this shorter persistence, large SCCs remain viable and indicate a dynamically renewing structure of cooperation, which is resilient amidst high node turnover.

When viewing $\log(\text{age})$ vs $\log(\text{degree})$ we see bands or clustering when Harm-To-Help is < 0.5 which dissipates and trends towards younger nodes as the network is stressed by harmful interactions. See Figure 4.

3.4 Eigen Analysis of Adjacency Matrix

For additional insights into the structure of this adaptive network, we turned to Eigen Analysis which provides a higher level description of the simulation from the lower-level data. [25]

We first generate an adjacency matrix by flattening the MultiGraph to a weighted graph by summing the number of edges: +1 for help edges and -1 for harm edges. For example entry A_{ij} will hold +3 if there are 5 helpful and 2 harmful edges from $i \rightarrow j$. Recall that at most 6 edges of one type (help or harm) can form between two nodes.

At each simulation tick we run a 20-step power iteration to approximate the leading eigenpair. A simple deflation then yields the sub-dominant eigenvalue. The resulting spectral radius, gap, and the angle between successive principal eigenvectors give a coarse but fast-to-compute fingerprint of network cohesion and regime shifts. While this heuristic skips the full, potentially complex spectrum and may miss fine

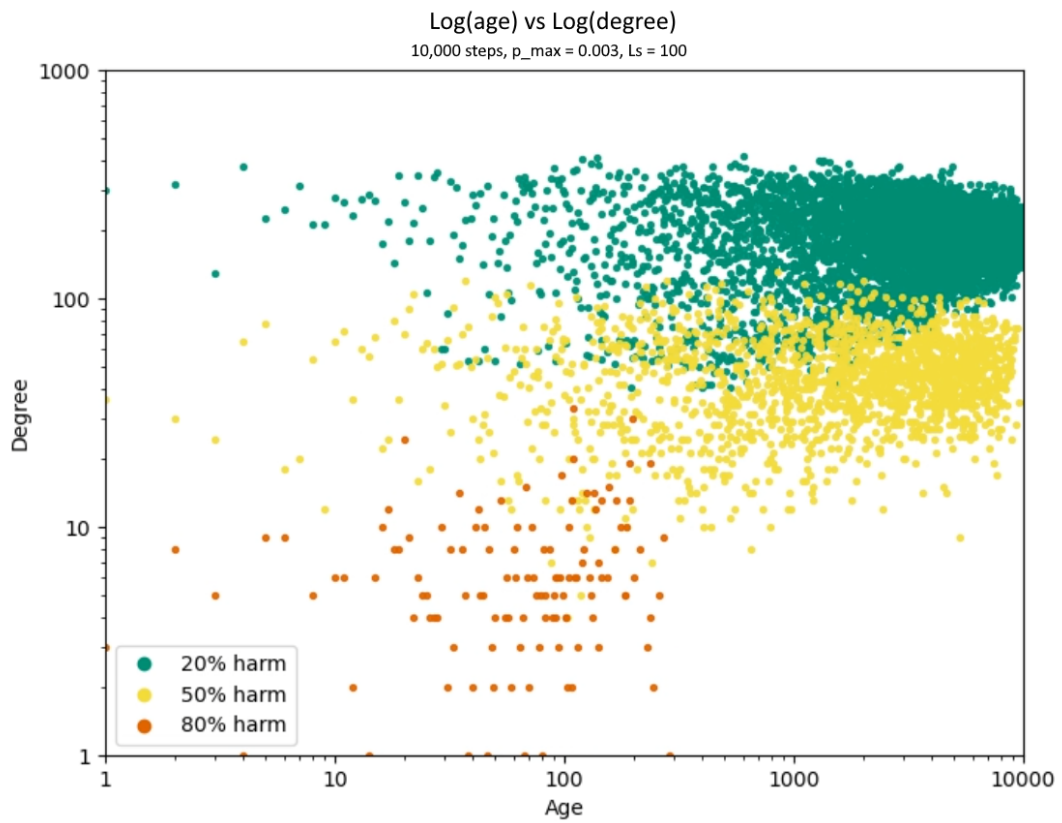


Figure 4: Log(age) vs Log(degree) after completing 10,000 steps of the simulation. $p_{\max} = 0.003$. $\rho = 0.2, 0.5, 0.8$.

detail, it is accurate enough for the qualitative trends we report and avoids the heavy cost of exact eigendecomposition on every time-step.

The **principal eigenvector** for the adjacency matrix encodes the principal or dominant direction of flows or activity in the network. It’s corresponding **principal eigenvalue** gives a measure to the ‘strength’ of that dominance. An increasing steady principal eigenvalue also means that average connectivity (and so the potential for feedback/cooperation or harm) is still growing – the graph hasn’t saturated yet.

Our second measure, the **spectral gap**, is the difference between the two leading eigenvalues: $|\lambda_1| - |\lambda_2|$. A large and growing spectral gap implies there is one cohesive, resilient strongly connected component. In other words, the principal direction of connectivity has ‘pulled away’ from any secondary directions. A small or falling gap would suggest there are many communities and more potential for fragmentation. Put another way, λ_1 tells us how *dense* the connections are, the spectral gap tells us how internally cohesive that density is.

Our third measure, the **principal angle**, reveals how stable the ‘identity’ of the dominant nodes is. It measures the cosine similarity between two successive network states:

$$\theta = \arccos\left(\frac{v_{t-1} \cdot v_t}{\|v_{t-1}\| \|v_t\|}\right)$$

A small, steady angle signals a persistent hub has formed; sharp increases imply regime shifts where new species take over the ‘core’ of the network.

Summary:

- **High eigenvalue** = high density and definition of help/harm interactions
- **Spectral angle** = measures structural change between network states.
- **Spectral gap** = indicates dominance and stability of primary interaction pattern.

4 Discussion

4.1 Robustness of Cooperation under High Antagonism

Our model demonstrates robustness of cooperative structures even when antagonistic interactions (harmful edges) significantly outnumber supportive interactions. This finding could be an extension of the concept of ‘islands of cooperation’ in [14]. Specifically, even with high harm-to-help ratios ($\rho > 0.5$), SCCs consistently emerge and persist at steady-state equilibria. This implies the presence of inherent resilience within the network structure, which allows it to dynamically reconfigure to maintain cooperative viability despite continuous antagonistic pressure. The results on node “age” vs degree distribution lend another perspective on the long run dynamics, which we discuss below.

The stability of these SCCs under high antagonism can be explained in network-theoretic terms: while harmful edges break node support structures, nodes with multiple positive inbound edges form resilient core communities, even when positive edges have a low probability of being formed. This leads to a dynamic steady state characterized by continuous recruitment and turnover of peripheral nodes, rather than collapse of the entire structure. These results align conceptually with robustness observed in dynamic real-world networks under external stresses, pointing to perhaps a broader principle of cooperative resilience inherent to certain threshold-based network structures.

4.2 Critical Thresholds and Phase Transitions

A primary result from our simulations is the clear emergence of a phase transition at the harm-to-help ratio $\rho \approx 0.5$. Below this threshold, the strongly connected component (SCC) grows linearly and steadily with the total node population, indicating robust, widespread cooperation. Above this threshold, however, SCC growth transitions from indefinite linear expansion to a bounded steady state, characterized by persistent fluctuations. The shift marks a clear qualitative boundary in the dynamics of the system.

Furthermore, we observe another critical threshold related to the binding propensity parameter (p_{\max}). When p_{\max} is sufficiently low (around 0.002), there emerges a clear criticality in network density: a minimum population size (approximately 200 nodes, just after 500+ steps, in our simulations, see Figure 5) must first be reached before an SCC becomes viable and begins growing rapidly. This behavior resembles classical phase transitions in percolation theory and random graph models, where a threshold density of connections is required for a "giant" connected component to emerge. [8] Explorations of these transitions using Haantjes curvature [27] have produced promising preliminary results, indicating that mean curvature may reliably increase prior to the formation of the emerging SCC.

Both phase transitions identified here highlight intriguing qualitative boundaries and merit deeper analytic investigation. Future work should include refined analytical treatments and fine-grained numerical explorations, particularly around the critical harm-to-help ratio region $0.5 < \rho < 0.6$, to conclusively determine the precise nature and location of these transitions.

These thresholds offer concrete and testable predictions about the conditions required for cooperative network formation and may be connected to critical phenomena observed in physical and complex systems.

4.3 Eigen Analysis

Eigen Analysis of the network's adjacency matrix provides more insight into structural and dynamical features. The principal eigenvalue (found by power iteration in NumPy) measures overall connectivity strength along the dominant eigenvector direction, which reflects the magnitude and stability of cooperation (or antagonism) in the network. Higher eigenvalues indicate denser and strongly coupled cooperative or competitive interactions. In our simulations, rising mean eigenvalues (observed with

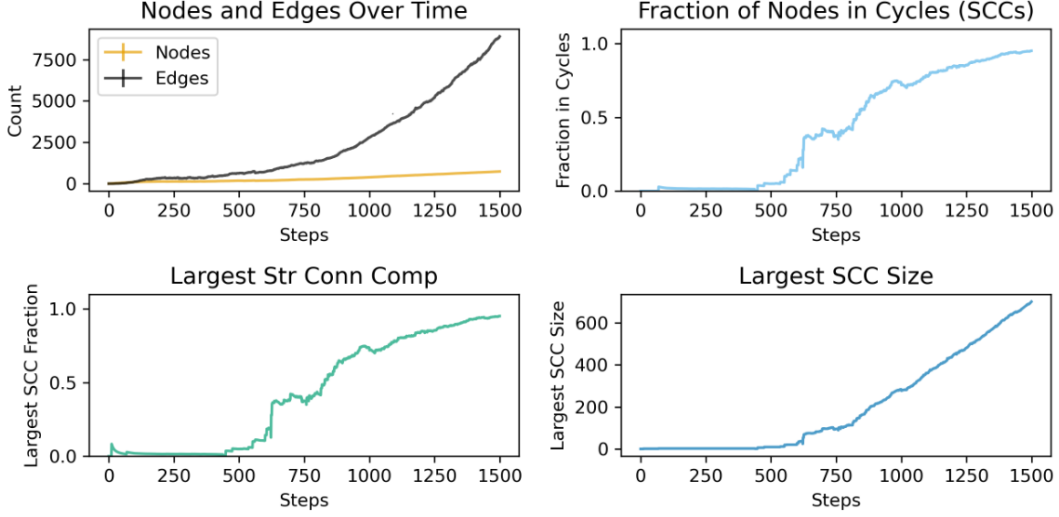


Figure 5: $p_{max} = 0.002, \rho = 0.2$

$\rho < 0.5$) corresponded to increasingly stable and interconnected SCCs.

The spectral gap (difference between the two largest eigenvalues) serves as a helpful secondary indicator, measuring how distinctly the principal ‘mode’ of interaction separates from other competing modes. A widening gap implies a clearly dominant, cohesive community structure, whereas narrowing gaps suggest fragmentation, multiple competing SCCs, or potential instability. Our results consistently showed that networks with high cooperation exhibit both large eigenvalues and pronounced spectral gaps, reaffirming the stability and dominance of a singular cooperative community structure.

Finally, the principal angle between consecutive eigenvectors quantifies the stability of core network structure across simulation steps. Small and stable principal angles indicate persistent dominance by specific nodes or clusters, while sudden spikes highlight structural rearrangements or shifts in network “leadership.” This measure gives additional, nuanced insights into temporal stability and dynamic structural shifts within the network. Consistent with our other measures, when the harm ratio was high, the principal angle fluctuated with increasing magnitude and signaled substantial shifts of influence of the key nodes in the support structure.

4.4 Age Distribution and Community Stability

The interplay between node lifespan and network antagonism produces distinctive patterns in node age (measured in time - birth-step) distributions. Under conditions of low antagonism (low ρ), older nodes with high connectivity become established, reflecting stable core communities. Conversely, increased antagonism rapidly shifts this balance toward younger nodes, as frequent node removal due to harmful interactions reduces node longevity. Interestingly, despite the reduction in older, established nodes, SCCs remain viable by continuously replenishing their core through newly added nodes. This activity reflects a structurally dynamic equilibrium rather than a fixed, static composition. Investigating the details behind the bands and clusters we see in the logarithmic plot may yield more insights. It is notable that at $\rho = 0.5$ we

see a cluster of nodes that are persisting most of the simulation, but have a reduced overall degree.

This age-based dynamic provides additional perspective on network stability and resilience. The continual integration of younger nodes suggests that organization under antagonism relies not on individual node longevity, but the network's capacity for rapid turnover and ongoing renewal. This could mirror adaptive responses observed in other complex systems where dynamic reconfiguration rather than static preservation promotes robustness.

[Click for Video Animation](#)

4.5 Binding Range as Ecological Analog

The binding range parameter, which can be thought of as the probability or "ease" of forming interactions (akin to biochemical or ecological compatibility), accelerates the dynamics of community structuring. It is interesting this parameter does not radically alter long-term outcomes but modulates the speed and slightly reduces the SCC's ceiling under antagonistic conditions. In ecological contexts, this could suggest ecosystems with higher interaction potentials (dense signaling, physical proximity, etc) might achieve stable cooperation more rapidly and sustain slightly larger cohesive structures despite competitive pressures. Nevertheless, even in cases with a low binding range, it is "just a matter of time" before cooperative communities (autocatalytic sets, ecosystems (biological, economic, cultural), etc.) will be formed.

4.6 Emergent Levels of Organization in Diverse Systems

Our adaptive threshold network model, while originally inspired by microbial community dynamics, embodies general principles of emergent cooperation and the formation of higher-level organizational structures. The minimal assumptions we built into the model make it applicable to a wide variety of complex systems.

The dynamics observed here resonate strongly with other computational works [1] and the concept of collective affordance sets [19]: where diverse system elements spontaneously combine their causal properties to create new functional wholes. Our findings illustrate clearly that, given sufficient time and diversity of interactions, these self-sustaining organizational structures are not merely possible but can be robustly expected to emerge.

In economic networks, analogous dynamics are not hard to find. Various goods, services, technologies, and businesses interact through interdependent relationships which support or undermine one another and give rise to intricate webs of economic cooperation. These adaptive networks continuously reorganize as new elements appear and obsolete ones exit, mirroring our model's node addition and culling dynamics. Through this lens, our model can offer quantitative insights into the conditions under which economic ecosystems reliably generate new collective structures, whether clusters of industry specialization, innovation hubs, or resilient supply chains.

Similarly, ecosystems more broadly demonstrate these principles. Rich biodiversity provides a palette of interactions, allowing ecosystems to self-organize into resilient structures such as trophic networks, mutualistic partnerships, and adaptive

community assemblies. Our work aligns with classical general systems theory [29] and recent empirical studies demonstrating self-organizing structures in ecological contexts, such as microbial communities [11] and biofilms [13].

Biofilms represent another powerful biological parallel. Individual bacterial species, each with unique traits and potentially antagonistic interactions, reliably assemble into complex multicellular aggregates. The emergent properties of biofilms such as shared resource utilization, collective defense mechanisms, and coordinated behavior, demonstrate exactly the kind of spontaneous higher-level organization our model predicts. Indeed, such structures can be viewed as an evolutionary step toward multicellularity [13, 7, 5].

Placing our model within the broader framework of major evolutionary transitions [21, 20] also yields valuable insights. It highlights conditions under which Darwinian preadaptations can coalesce into higher-order systems, suppressing or transcending individual-level competition. So, our results offer a theoretical foundation for understanding transitions from simple chemical reaction networks to living cells, from unicellular organisms to multicellular structures, from individuals to groups [15], and from isolated economic agents to integrated economies.

By demonstrating robust self-organization through minimal assumptions, our adaptive threshold network model not only sheds light on microbial dynamics but provides a versatile conceptual tool applicable across biological, economic, and social domains. Given enough time, diversity, and interaction potential, the emergence of cooperative structures and new levels of organization appears to be not merely possible but inevitable.

5 Conclusions and Future Work

We have demonstrated that, under minimal assumptions, adaptive threshold networks naturally give rise to communities of support and cooperation, even in the presence of substantial antagonism. The primary insight is that the vast diversity of possible interactions enables complex systems to reliably find paths towards sustained cooperation. The two phase transitions identified in the model suggest that at some point quantity turns into quality. Thus, our results provide support for the conjecture that life inherently "finds a way," tinkering to build cooperative structures despite adverse conditions.

Our current model intentionally excludes stronger forms of evolutionary and co-evolutionary dynamics, setting these aspects as key areas for future development. Integrating evolutionary games — which have been widely explored elsewhere [21, 22, 26] — could enrich our understanding of how cooperation not only emerges but is subsequently refined and stabilized through selective pressures.

Another aspect of our model that remains to be explored is the fact that it can be seen as an example of strong emergence [2, 3, 28, 16] and downward causation [6, 4, 10, 12]. Once communities are formed (at a higher scale), they influence the survivability of nodes (at a lower scale). Thus, it is not possible to reduce the behavior of the system to the properties of its elements. Nevertheless, there are epistemological nuances that should be considered and are beyond the scope of this paper.

Furthermore, the notion of resources is presently implicit in the parameter ‘lifespan,’ which dictates how long a node persists without adequate support. Introducing explicit resource dynamics and spatial constraints would enhance biological realism, enabling the exploration of more nuanced ecological and economic scenarios. Spatial structure, in particular, can affect opportunities for interaction and substantially impact emergent dynamics. [18, 23]

A natural step is to identify biologically and economically realistic parameter ranges, particularly for lifespan and interaction (binding) probabilities. Lifespan can affect the short and long run behaviors of the network, preventing formation if set too low, or inflating the size of the SCC as it increases. We expect these steady-states can be analytically approximated by functions of lifespan and binding probabilities, which is an open avenue for future work. Another investigation would be to what degree lifespan is emphasized here as one of our minimal assumptions. For example, a species’ death may continue to provide an affordance (easier access to food, etc.) but these interactions would be lost in our model.

We can assume that evolution will favor a balanced ρ ratio: too much harm is not sustainable. However, only help might hinder adaptability and evolvability [17]. To explore this hypothesis systematically, we plan to introduce evolutionary feedback explicitly in the next iteration of our model. Edge weights will dynamically evolve, strengthening or weakening interactions probabilistically over time, reflecting real-world processes of mutual adaptation and co-evolution. Preliminary results and theory suggest this enhancement should lead to rich dynamics, potentially revealing other novel phase transitions or critical thresholds that influence community resilience and connection.

Finally, empirical validation remains paramount. We eagerly await the experimental outcomes from Jan Dijksterhuis’ ongoing microbial experiments involving 140 microbial species. These empirical findings may yet validate our model’s assumptions but also inspire refinements. Will we find evidence of persisting networks of support? Will these networks look the same in different soil plots? Whatever daylight exists between our findings and the empirical results will motivate, or afford, more interesting explorations.

Acknowledgements

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