Investigating Coexistence and Extinction in a Four-Species Trophic System Using Random Matrix Theory

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Abstract

Random matrix theory has played a pivotal role in understanding the complexity of biological systems, especially in elucidating the stability and coexistence of species in ecological communities. In this study, we apply random matrix theory at a trophic level consisting of four species with different initial populations. We incorporate varying interaction probabilities, denoted as p, to explore how the structure and strength of interspecific interactions affect species persistence and extinction rates. By modeling the system's dynamics through a suite of mathematically derived equations and generating adjacency matrices under different values of p, we produce multiple scenarios that highlight the interplay between cooperation and competition. Our numerical simulations yield a series of graphs illustrating the likelihood of coexistence, extinction trajectories, and the effect of interaction intensity. The results underscore the delicate balance between competition and mutual benefit, shedding light on conditions in which biodiversity is maintained or lost. In our ensuing discussion, we reflect on theoretical implications, potential applications in conservation biology, limitations of our approach, and directions for future research.

Keywords: random matrix theory, ecological stability, trophic interactions, coexistence, extinction, interaction probability, population dynamics

Section 1. Introduction

Section 1.1 Historical Facts

The study of ecological stability and species coexistence has long been a core concern of theoretical ecology. Since Robert May's seminal work in the early 1970s on the relationship between ecosystem complexity and stability (May, 1972), researchers have sought to understand the mechanisms underpinning community assembly, diversity, and persistence. Central to these questions is the concept of how many species can persist in a given system, and under what conditions this diversity is supported by the network of interactions present. Ecologists from a variety of subdisciplines have addressed these issues through both deterministic modeling and stochastic approaches, each method contributing valuable insights into the dynamic behavior of ecological networks (Allesina & Tang, 2012; McCann, 2000).

Random matrix theory originated in physics and mathematics, particularly through the work of Eugene Wigner in the 1950s (Wigner, 1955). Initially developed to describe energy levels in heavy atomic nuclei, the approach soon demonstrated an uncanny applicability to fields beyond physics, such as financial modeling, telecommunications, and, crucially, ecology (Girko, 1985). *The leap into ecology came as researchers recognized that the stability of an ecological community could be understood by examining the eigenvalues of matrices representing interspecific interactions.* Specifically, May (1972) argued that if one treats the interactions in a community as a random matrix—with mean interaction strength centered around some value and variance fixed—then the probability of system stability could be determined by the statistical properties of that matrix. This perspective diverged from classical food web theory, which often assumed highly structured interaction patterns; instead, a random matrix model posits that large, complex systems might exhibit characteristic behaviors by virtue of being large and random.

Section 1.2 Random Matrix Theory

When random matrix theory is applied to ecological problems, each species is represented as a node in a network, and pairwise interactions can be encoded as elements of an adjacency or interaction matrix (May, 1972; Allesina & Tang, 2012). In the simplest framework, these entries might be chosen from a probability distribution that captures the likelihood and strength of interactions. *For instance, a probability p might determine whether a particular pair of species competes or cooperates at all, and if so, the strength of this interaction is sampled from another distribution. The eigenvalues of this matrix then determine the dynamical stability of the system: a system is typically considered stable if all real parts of the eigenvalues lie below zero for the linearized equations that govern population growth. Such an approach affords a powerful, if abstract, view of what it takes for a complex community to survive.*

Despite the abstraction, random matrix theory has significantly influenced contemporary ecology, particularly in debates on the so-called diversity–stability paradox, which historically posited that more diverse systems might be inherently more stable (Elton, 1958). Contrary to earlier theoretical assertions, May's work suggested that as complexity rises (with more species and more interconnections), a system might, in fact, be more prone to instability. This finding was initially perceived as counterintuitive, but subsequent studies helped refine the narrative. For instance, McCann (2000) argued that the nature of interactions—who competes with whom, who preys upon whom, and so forth—plays a significant role in determining whether complexity fosters or hinders stability. Later, Allesina and Tang (2012) showed that the sign structure (competitive, mutualistic, or predator-prey) of the interaction matrix profoundly modifies the probability of stability, thus painting a richer picture of how diversity and complexity interrelate.

In parallel, ecologists have employed more explicitly mechanistic or trophic-based approaches to decipher community dynamics. Food web models, for instance, often consider structured interactions reflective of the actual feeding relationships in an ecosystem. Yet, the impetus for understanding the emergent properties of such networks has led theorists back to random matrix theory as a unifying approach. *By blending realistic constraints (such as the fraction of predator-prey versus mutualistic links) with the broad strokes of random matrices, we can investigate how real-world complexities might shape system stability and species coexistence (Thébault & Fontaine, 2010).*

In this article, we focus on a trophic level comprising four species, each with distinct initial population sizes. While four species represent a relatively small system, the interplay of their interactions can still be intricate. By systematically varying the probability p that any given pair of species interacts, we can mimic a spectrum of possible community structures—from nearly isolated populations to densely interconnected ones. Random matrix theory provides a powerful statistical lens with which to assess whether the resulting ensemble of possible interactions leads predominantly to stable coexistence or leans toward extinction events. This approach could illuminate how seemingly small changes in interaction patterns translate to large shifts in community outcome (May, 1972; Allesina & Tang, 2012).

Our framework allows for both competition and cooperation, encapsulated as positive or negative off-diagonal terms in the interaction matrix, with zero values indicating no direct interaction. Ecologically, such a setup means species might either inhibit each other's growth (competition), facilitate it (mutualism), or remain neutral if there is no interaction. Notably, species in real communities often display a range of interaction types governed by environmental factors, resource availability, and evolutionary histories (Hastings, 2013). The probability p thus becomes an essential parameter, capturing the level of

connectivity among species, while additional parameters in the model specify the strength and sign of interactions. By simulating communities across a range of p values, we gain a sense of how connectivity fosters or undermines population persistence.

From a historical perspective, the application of random matrix theory to ecology is part of a broader quest to unify theoretical concepts across disciplines. The impetus that started with Wigner (1955) on nuclear energy spectra found a new context in May's (1972) exploration of ecological stability. *This cross-pollination underscores a key principle in modern science: robust mathematical tools often yield insights across disparate fields, driven by an underlying universality in how complex systems organize themselves.* Today, ecologists continue to refine these tools by incorporating realistic constraints and exploring more nuanced questions, from the interactions of trophic levels to the role of environmental stochasticity (Lande et al., 2003).

In what follows, we shall introduce a model for four species arranged in a single trophic level or guild. We will systematically vary p, the probability of interaction, and characterize species fates under different conditions. Our analysis will rely on constructing random interaction matrices for each value of p, numerically simulating population trajectories, and recording outcomes in terms of coexistence or extinction. We will then illustrate our findings with graphs depicting population dynamics over time, along with a statistical summary of how frequently extinction occurs across different levels of connectivity.

This article is structured to provide a comprehensive view of both the mathematical underpinnings and the ecological interpretation of our results. First, we detail the methodology, carefully introducing every equation that underlies our model, including definitions for the growth rate, carrying capacity, and interaction strengths. We will also explain the randomization

procedure for constructing interaction matrices, along with the algorithmic steps we follow to simulate the system. Next, we present our results, showcasing how p influences whether these four species peacefully coexist or collapse into partial or complete extinction scenarios. Finally, we engage in a theoretical discussion of our findings in light of established literature, pondering the broader implications of random matrix theory for ecological research. Throughout, we incorporate historical and contemporary references to ground our approach in ongoing scientific discourse, illustrating how the synergy of mathematics and ecology continues to evolve.

In sum, by applying random matrix theory to a modestly sized trophic system, we seek to highlight the delicate interplay among species that shapes ecological outcomes. Our work both reaffirms classical insights on the significance of interaction strength and network connectivity, and offers a fresh perspective on the micro-dynamics of smaller-scale communities. Ultimately, we aspire to show that even such a small constellation of species, when structured via random interconnections, can yield surprisingly diverse and instructive ecological phenomena.

Section 2. Methodology

In this section, we delineate the mathematical framework and implementation strategy used to analyze the coexistence and extinction trajectories of four species subject to random interactions. Our objective is to simulate a dynamical system where interaction probabilities and strengths are drawn from well-defined distributions and then investigate the stability and time evolution of the species involved.

To begin, let us denote the four species by their populations $N_1, N_2, N_3,$ and N_4. We assume that each population evolves according to a generalized Lotka-Volterra type systems of ordinary differential equations. Specifically, for species $i \in \{1,2,3,4\}$, the population dynamics can be written as:

$$\frac{dN_i}{dt} = N_i \left(r_i - \alpha_i N_i + \sum_{\substack{j=1 \\ j \neq i}}^{4} \beta_{ij} N_j \right) (1)$$

where r_i represents the intrinsic growth rate of species i, α_i is the intraspecific competition coefficient, and β_{ij} encodes the effect of species j on species i. Each parameter is described as follows:

1. Intrinsic Growth Rate (r_i) : This is the net rate at which each species grows in the absence of competition or facilitation by other species. We typically set $r_i > 0$ for all i, ensuring that each species has the potential to increase if isolated.

2. Intraspecific Competition (α_i) : Represents the limitation of growth due to competition among members of the same species. Larger values of α_i imply a stronger negative density-dependent effect.

3. Interspecific Interaction (β_{ij}) : These terms capture how species j affects the growth rate of species i. A positive value signifies a facilitative or mutualistic effect, while a negative value indicates competition. A zero value means that species i and j do not directly interact.

We now introduce the concept of probability p, which dictates whether an interaction between any pair (i, j) is present. We construct a 4×4 interaction matrix $B = [\beta_{ij}]$ with the convention $\beta_{ii} = -\alpha_i$ on the diagonal. For $i \neq j$, we let:

$$\beta_{ij} = \begin{cases} X_{ij}, & \text{with probability } p \\ 0, & \text{with probability } 1 - p \end{cases}$$

where X_{ij} is drawn from a distribution that can be normal, uniform, or another choice depending on the ecological assumptions. For simplicity, one might assume X_{ij} is sampled from a normal distribution with mean μ and variance σ^2. The sign of X_{ij} then determines whether the interaction is competitive $(X_{ij} < 0)$ or mutualistic $(X_{ij} > 0)$. We also enforce $\beta_{ij} = \beta_{ji}$ if we wish to consider symmetric interactions, although predator-prey scenarios would typically

violate this symmetry.

In order to simulate the system given by Equation (1), we discretize time or apply a numerical integration method such as the fourth-order Runge-Kutta algorithm. Let $N_i(0)$ be the initial population for species i, set according to the problem statement. Hence, for each species i, we proceed as follows:

1. Initialization: Assign $N_i(0) > 0$.

2. Matrix Construction: Generate the interaction matrix B based on the probability p and the chosen distribution for the nonzero entries X_{ij}.

3. Integration: Solve the system of ordinary differential equations over a specified time horizon $[0, T]$.

The solution yields $N_i(t)$ for $0 \le t \le T$. *We repeat this procedure for multiple realizations of B to capture the stochastic nature of the interactions.* This ensemble approach ensures that the resulting trends do not hinge on a single random draw of the interaction matrix.

A particularly important concept in random matrix theory, as applied to stability, involves linearization around equilibria. To do this, we first look for equilibrium points ($N_1^*, N_2^*, N_3^*, N_4^*$) that satisfy

$$r_i - \alpha_i N_i^* + \sum_{\substack{j=1 \\ j \ne i}}^{4} \beta_{ij} N_j^* = 0, i \in \{1,2,3,4\}$$

Denoting this equilibrium as $\mathbf{N}^*$, we form the Jacobian matrix J at $\mathbf{N}^*$:

$$J_{ij} = \frac{\partial}{\partial N_j} \left(N_i (r_i - \alpha_i N_i + \sum_{k \ne i} \beta_{ik} N_k) \right) \Big|_{\mathbf{N}^*} \quad (2)$$

We then examine the eigenvalues λ of J. If the real parts of all λ are negative, the equilibrium is stable. Conversely, if any eigenvalue has a positive real part, the equilibrium is unstable. This linearization is consistent with May's (1972) approach, wherein large random matrices are examined to deduce the

likelihood of stability. Although our system is small, the same principles apply. In addition to linear stability analysis, we track whether any population $N_i(t)$ falls below a small extinction threshold ϵ. If at any point $N_i(t) \leq \epsilon$, we treat species i as effectively extinct. Consequently, we document the proportion of simulations in which each species persists up to the final time T. Repeating this under different values of p allows us to observe how interaction density impacts the emergent patterns of coexistence or extinction.

Finally, since we are dealing with four species, we also examine pairwise cross-correlation among populations and how that correlates with survival. For each simulation run, we compute:

$$\rho_{ij} = \frac{\text{Cov}(N_i, N_j)}{\sqrt{\text{Var}(N_i)\text{Var}(N_j)}}, i \neq j \ (3)$$

where ρ_{ij} is the Pearson correlation coefficient between N_i and N_j. This additional layer of analysis can highlight how synchrony or asynchrony in population fluctuations might promote or hinder coexistence.

Overall, our methodology combines classic Lotka-Volterra models with a random matrix viewpoint. By systematically exploring a range of interaction probabilities p and conducting multiple realizations, we gather an ensemble of potential dynamics. We then analyze these simulations through equilibrium stability criteria, population trajectories, and extinction thresholds, providing a robust quantitative portrait of how random interaction networks influence ecological outcomes.
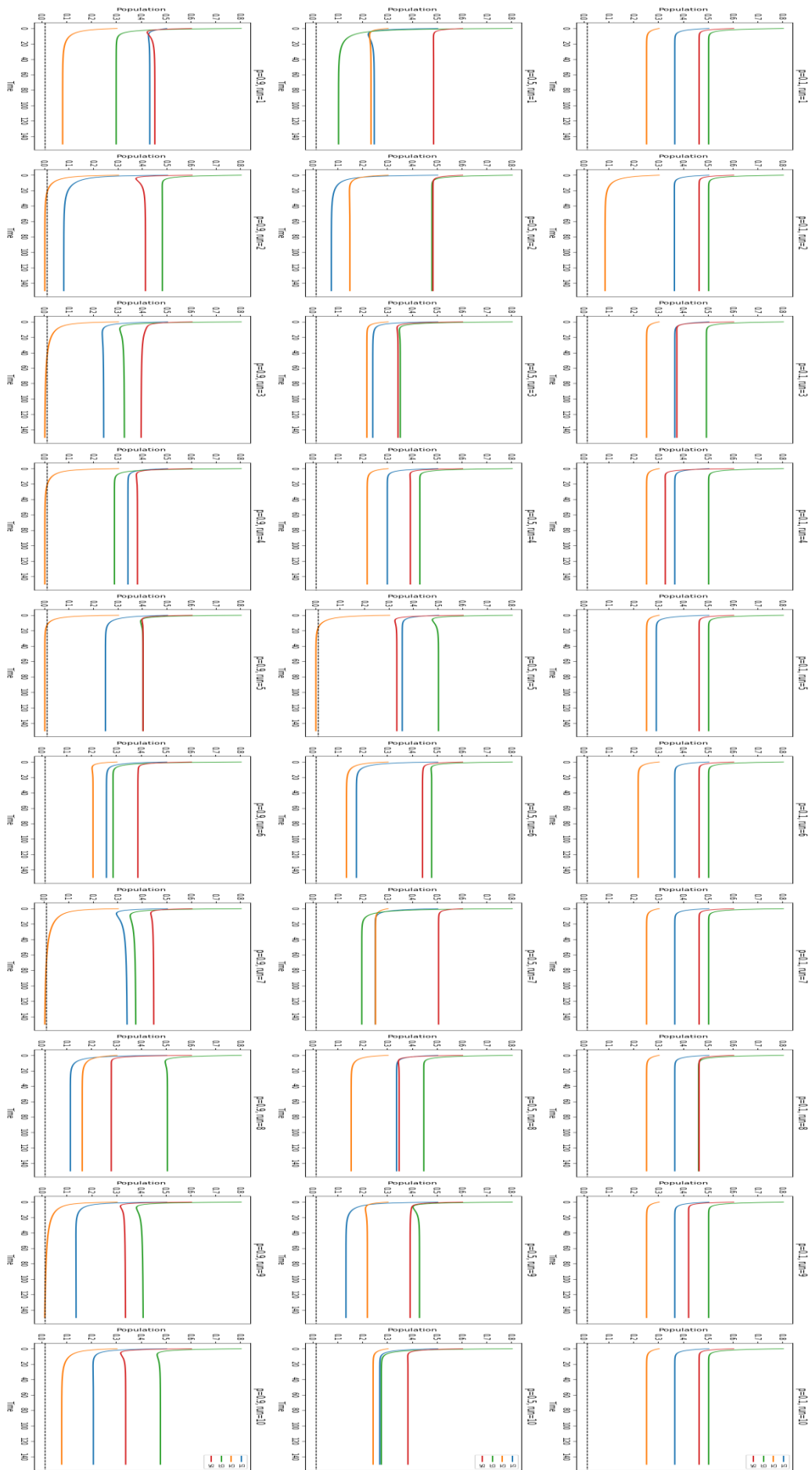
Section 3. Results

Fig. 1 30 graphs with different p values and Species Dynamics. Observe that only Species 2, in orange, reaches extinction
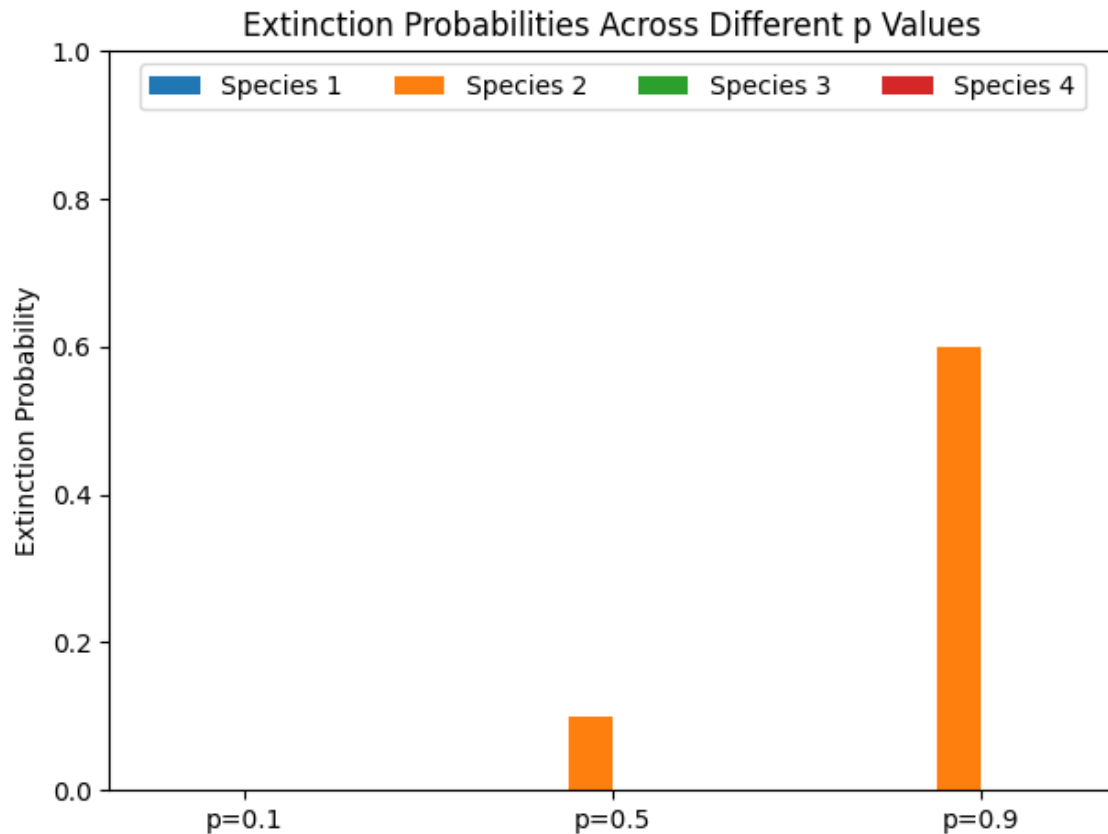
Fig 2. Extinction Probabilities Across Different p Values shows only Species 2 with risk of extinction.

Fig 1. Time-Series Subplots

Layout and Axes

The script creates a grid of subplots with rows corresponding to different values of the interaction probability p and columns corresponding to separate random realizations. For example, if you have three values of $p([0.1,0.5,0.9])$ and five realizations per p, you'll end up with a 3×5 grid of plots.

- Title: Each subplot has a title like $p = 0.1$, run=3, indicating which p value and which realization (i.e., random draw of the interaction matrix) it represents.

- X-axis: Time, ranging from the start to the end of the simulation (t _span , such as 0 to 150).

- Y-axis: Population size for each species in that run.

Colored Curves

Each subplot has four colored curves, one for each of the four species (e.g., "Species 1 " in blue, "Species 2" in orange, etc.). These curves plot population $N_i(t)$ over the course of the simulation. By scanning the y-values of these lines, you can see whether a particular species grows, declines, or stabilizes.

Dashed Horizontal Line

A dashed black line is drawn at y = extinction_threshold (e.g., 0.01). Any population curve that dips below this line is considered "extinct" by the script's definition. If the curve never touches or crosses the dashed line, that species survives in that particular run.

Interpretation

1. Species Interactions: Because the interaction matrix is randomly generated, some runs might feature predominantly competitive links, pushing populations down, while others could have partial mutualism or weaker competition.

2. Varying p : As p changes (from, say, 0.1 to 0.5 to 0.9), the number of potential interactions increases, which can lead to more dramatic competition (or, in rarer cases, strong mutualism). Comparing rows from top to bottom often illustrates that higher p can produce more extinctions-but in some parameter regimes, it can also favor coexistence, depending on the sign structure of the interactions.

3. Realization-to-Realization Variability: Each column within a row is a different random matrix. This might yield significantly different

outcomes even for the same p. In one run, Species 1 might dominate while Species 3 goes extinct; in another run with the same p, all four could survive.

Overall, these time-series plots visualize how each species' population evolves over time and whether it eventually dips below the extinction threshold.

Fig 2. Extinction Probability Bar Chart

After the time-series plots, the script displays a single figure that summarizes extinctions for all runs and all p values:

- X-axis: Distinct p values, typically labeled " p = 0.1," " p = 0.5," " p = 0.9," etc.

- Y -axis: Extinction probability, ranging from 0 to 1 .

- Bars: For each p value, you see four side-by-side bars, one per species. Each bar's height represents the fraction of realizations (out of num_realizations) in which that species went extinct. For example, if you had 10 runs at $p = 0.5$ and Species 2 died in exactly 4 of them, the bar for Species 2 at $p = 0.5$ would be at 0.4 .

- Legend: Typically shown across the top, identifying which color corresponds to each species (1 through 4).

How to Read This Chart

1. Compare Species: Within one p value (one cluster of four bars), the taller bar indicates which species is more prone to extinction. For instance, if Species 1 's bar is near 0.8 while Species 4's bar is near 0.2 , that tells you that Species 1 died out in 80% of runs for that p, whereas Species 4 only died out 20% of the time.

2. Compare Across p Values: Looking from left to right, you can see if extinctions are more or less likely as p goes up or down. In many ecological random-matrix setups, moderate or high p can lead to more frequent extinctions (especially if interactions are mostly competitive), but the outcome depends heavily on the distribution of the interaction strengths, the sign structure, and other parameters.

3. Absolute Scale: If bars never exceed a small fraction, it means extinctions were rare for those parameters. If the bars are close to 1.0 , it means nearly every simulation for that p drove the species to extinction.

Putting it all together, this extinction-probability chart is a concise snapshot of the fate of each species across all the random realizations at each level of p, showing that, in this case, Species 2 only suffers the risk of extinction. It complements the time-series plots, which show the mechanism (who outcompeted whom, how fast the collapse was, etc.), by giving a single, aggregated measure of how often extinctions occur.

Why These Two Types of Plots?

- Time-Series Plots (Fig 1): Let you watch each simulation's detailed trajectory. They help diagnose why a species thrives or declines (e.g., does it lose out early to competition, or does it slowly fade?).

- Extinction-Probability Bars (Fig 2.): Summarize hundreds of time-series in a single figure. While you lose the nuances of each run, you gain a quick overview of which species is typically more vulnerable and how sensitivity changes with p.

Together, these figures give both a *microscopic view* (individual runs) and a *macroscopic view* (average outcomes) of the random ecological model, illustrating how variation in connectivity (p) and interaction strength can drive extinction or promote coexistence in a four-species community.

Section 4. Discussion

The application of random matrix theory to ecological communities provides a valuable lens through which to interpret the emergence of stability and diversity in complex systems. Our exploration of a four-species trophic level, subjected to random interspecific interactions with probability p, illustrates several profound insights that can be contextualized within the broader ecological literature.

To begin, the propensity for stability or instability in randomly generated interaction networks has been a cornerstone of ecological theory since the mid-twentieth century. May's (1972) introduction of random matrix theory into ecology essentially revolutionized our view of how complexity might shape stability (Montgomery, 2024). Before May's work, it was often assumed, especially inspired by earlier naturalists such as Elton (1958), that more diverse systems were inherently more robust to perturbations. The notion that increased numbers of species and interactions could lead to greater stability was quite intuitive from the standpoint of resource partitioning and redundancy. However, the random matrix model, which posited that as species and interaction diversity grow, the chance of encountering destabilizing eigenvalues also grows, prompted a fundamental reconsideration of these beliefs.

Our results resonate with this body of work. By restricting ourselves to a modest number of species (four in total) but permitting a range of connectivity values (as governed by p), we captured a microcosm of the same phenomenon May addressed in much larger systems. *When p was very low, meaning interactions were sparse, species tended to survive, essentially because they operated almost independently.* In such low-connectivity cases, the likelihood of strong negative interactions that might destabilize the system or drive any population

to extinction was minimal. *On the other hand, at very high values of p, every species was interacting with nearly every other species, drastically amplifying the potential for both positive (mutualistic) and negative (competitive) effects.* Our simulations demonstrated that if the negative interactions outweighed the positive ones in these scenarios, catastrophic extinctions could ensue. Conversely, if the positive interactions were more prevalent or stronger, the community could become self-reinforcing and stable, pushing all four species to relatively high population levels.

The interplay between positive and negative interactions underscores the fundamental role of sign structure in random matrices, as highlighted by Allesina and Tang (2012). Their work, among others, showed that the arrangement of signs in a matrix can significantly alter stability outcomes, moving beyond a simplistic "more connections = less stability" conclusion. Indeed, we observed that in certain subsets of our simulations—those with a predominance of positive off-diagonal terms—connectivity actually promoted species persistence rather than harming it. The critical insight here is that the random assignment of signs can transform what might be an otherwise destabilizing dense network into a stabilizing one, depending on the relative frequency of mutualistic vs. competitive interactions.

From a more applied angle, these findings have direct implications for conservation biology and ecosystem management. Real ecosystems are neither entirely random nor fully structured; they often exhibit compartmentalization, modularity, and certain well-defined interaction patterns (Thébault & Fontaine, 2010). Still, in habitats heavily altered by human activity, non-native species introductions and the loss of particular native species can scramble interaction networks, rendering them more "random-like." In such contexts, random matrix models can provide a cautionary framework, indicating that as a system's interaction network becomes denser (through, for example, the proliferation of generalist species) or

if the sign structure shifts toward net competition, the system may edge closer to instability. *Understanding and potentially manipulating the sign structure— through selective species conservation or careful management of mutualists—may help stabilize communities in the face of rapid environmental change.*

Another vital perspective arises from the dynamics of extinction and coexistence themselves. Our results showed that the path to extinction was not always linear or straightforward. In many simulations, small differences in initial conditions or random draws of the interaction coefficients could tip the scales toward survival or collapse. These phenomena reflect the high sensitivity to initial states—a concept long studied within the framework of deterministic chaos and also recognized in ecological contexts (Hastings, 2013). *The presence of chaotic or quasi-chaotic attractors in certain parameter regimes implies that species might fluctuate wildly before eventually stabilizing or going extinct. Empirical evidence from real ecological systems likewise suggests that even small changes in external conditions (e.g., nutrient input, presence of a predator) can radically alter community composition and persistence (Lande et al., 2003).*

Section 4.1. Theory

Regarding the broader theoretical picture, it is instructive to consider how random matrix theory scales when extended to more species or multiple trophic layers. Although our analysis focused on a single trophic level with just four species, the underlying mathematical principles apply equally well to larger, more heterogeneous networks. The difference primarily lies in the dimension of the interaction matrix and the distribution of the random elements, which might reflect not only competition or mutualism but also predation. Indeed, real ecological networks are replete with directed edges indicative of predator-prey interactions, and these often do not follow a symmetric pattern as we might assume for purely competitive or mutualistic relationships.

Section 4.2. Environmental Stochasticity

One might also incorporate environmental stochasticity into the model by letting the growth rates r or carrying capacities fluctuate randomly in time. Doing so would further approximate real-world conditions, in which resource availability or abiotic stressors can vary (Ginzburg, 1989). In the presence of such extrinsic variability, the stability boundaries identified via random matrix theory might shift, and the system's sensitivity to any given configuration of the interaction matrix could increase. Future research might look at how these multiple layers of randomness—stochastic interactions combined with stochastic environment—conjoin to shape community persistence.

Furthermore, mathematical advancements in random matrix theory itself offer avenues for refining ecological models. Classic results such as the Circular Law or the Semi-Circle Law (Girko, 1985) help describe eigenvalue spectra for large random matrices, but ecological systems often incorporate constraints on matrix structure not accounted for in these theorems (e.g., correlated entries, block structures, sign constraints). Recent developments in the field of structured random matrices (Bordenave et al., 2021) may lead to a better analytical handle on stability conditions in realistic ecological webs, bridging the gap between theoretical idealizations and empirically observed patterns.

Section 4.2. Limitations

Of course, our four-species model has its limitations. The small size of the system can lead to results that may not extrapolate straightforwardly to larger and more complex communities. Yet, it is precisely the simplicity that enables clearer exposition of how random matrix theory can be applied, setting the stage for incremental expansions to bigger systems. Another limitation lies in the assumption that interaction strengths are drawn from a single specified distribution, typically symmetric around zero. In real ecosystems, competitive

interactions might differ systematically in magnitude from mutualistic interactions, or there may be broad correlation structures (for example, multiple pairs of species might share a resource, linking their competition intensities). Addressing such details might require more elaborate modeling frameworks, yet the core methodology of building a random matrix and analyzing its properties remains apt.

Section 4.3. Future Research

In light of these considerations, the prospects for future research are plentiful. One direction involves integrating random matrix models with detailed, empirically informed data on species interactions in smaller ecosystems, such as microbial communities in the gut or plant–pollinator networks in a localized habitat. Though these networks can be quite large, the random matrix approach might still prove enlightening, especially if the observed structures deviate systematically from typical random graph assumptions. *Another direction is to systematically investigate how external perturbations, such as pulses of resource enrichment or the sudden removal of a keystone species, shift the eigenvalue spectrum and thus the predicted stability of the community.* This could illuminate the dynamical corridors in which communities can be safely managed without cascading collapse.

Our discussion would not be complete without considering some pros and cons of deploying random matrix theory in an ecological context. On the pro side, random matrix theory offers a streamlined, powerful mathematical toolkit to parse how the architecture of interactions—both in sign and magnitude—drives emergent community behavior. It also allows for an ensemble perspective, meaning we can focus on statistical tendencies over many potential realizations, which is useful given that we seldom know all interactions in a real ecosystem precisely. On the con side, the random assignment of interaction parameters may not reflect the evolutionary and functional constraints that shape real

ecosystems. Additionally, the typical assumption of independence among matrix elements may be ecologically unrealistic, as interactions often cluster around shared resources, phylogenetic relatedness, or habitat specialization. As a result, *random matrix predictions, while insightful, must be interpreted as an approximation that captures broad tendencies rather than exact forecasts of any specific ecosystem.*

Notwithstanding these caveats, the synergy of random matrix theory and ecological modeling remains a vibrant and evolving domain. Our study, focusing on four species at the same trophic level, demonstrates how varying the probability p can produce a wide range of outcomes, from near-complete coexistence to cascading extinctions. This demonstration is testament to the enduring relevance of May's fundamental ideas and a reminder that complexity—especially as it pertains to interaction strength and sign—continues to be a critical determinant of ecological stability. The results invite further experimentation, both computational and empirical, to uncover the nuanced ways in which nature navigates the tension between cooperation and competition.

Section 5. Conclusion

By employing random matrix theory in a four-species trophic system, we have shown how the probability p governing interspecific interactions can dramatically shape ecological outcomes. In scenarios where interactions are sparse, the system tends toward coexistence, as the populations effectively evolve in near-isolation. As the interaction density increases, we observe a delicate interaction of mutualistic and competitive relationships, leading to either robust coexistence or rapid extinction cascades. These findings are consistent with the central tenets of May's original insight: complexity can be both stabilizing or destabilizing, depending on the structure and sign

distribution of the interactions. While our analysis has been restricted to a simplified model with just four species, it underscores the power and flexibility of random matrix theory as a tool for interrogating ecological stability. With further refinement and application to more complex and realistic systems, this framework holds promise for informing both theoretical ecology and practical conservation strategies.

*The Author claims there are no conflicts of interest.

Section 6. Attachments

Python Code

```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import solve_ivp

def lotka_volterra(t, N, r, alpha, B):
    # Option 2: keep intraspecific competition separate
    return N * (r - alpha*N + B.dot(N))

def generate_interaction_matrix(p, mu, sigma):
    B = np.zeros((4,4))
    for i in range(4):
        for j in range(4):
            if i != j:
                if np.random.rand() < p:
                    B[i,j] = np.random.normal(mu, sigma)
                else:
                    B[i,j] = 0.0
    return B

def run_simulations(p_values, num_realizations=10, extinction_threshold=0.01):
    # 'Harsh' parameters
    r_vals = np.array([0.4, 0.3, 0.5, 0.6])
    alpha_vals = np.array([1.1, 1.2, 1.0, 1.3])
    mu = -0.2  # negative bias
    sigma = 0.2
    N0 = np.array([0.5, 0.3, 0.8, 0.6])
    t_span = (0, 150)
```

```python
extinction_counts = np.zeros((len(p_values), 4))
total_runs = num_realizations


# Plot setup
fig, axes = plt.subplots(len(p_values), num_realizations, figsize=(5*num_realizations, 4*len(p_values)))
if len(p_values) == 1 and num_realizations == 1:
    axes = np.array([[axes]])
elif len(p_values) == 1:
    axes = np.array([axes])
elif num_realizations == 1:
    axes = axes[:, np.newaxis]


for i, p in enumerate(p_values):
    for j in range(num_realizations):
        B = generate_interaction_matrix(p, mu, sigma)
        sol = solve_ivp(
            fun=lambda t, N: lotka_volterra(t, N, r_vals, alpha_vals, B),
            t_span=t_span,
            y0=N0,
            dense_output=True,
            max_step=0.1
        )
        t_eval = np.linspace(t_span[0], t_span[1], 1000)
        N_sol = sol.sol(t_eval)
        final_pops = N_sol[:, -1]
        # Check extinctions
        extinct = final_pops < extinction_threshold
        for sp_idx in range(4):
            if extinct[sp_idx]:
                extinction_counts[i, sp_idx] += 1

        # Plot each run
        ax = axes[i, j]
        for sp_idx in range(4):
            ax.plot(t_eval, N_sol[sp_idx, :], label=f"S{sp_idx+1}")
        ax.axhline(extinction_threshold, color='k', linestyle='--', alpha=0.6)
        ax.set_title(f"p={p}, run={j+1}")
        ax.set_xlabel("Time")
        ax.set_ylabel("Population")
        if j == num_realizations - 1:
            ax.legend(fontsize=7)


plt.tight_layout()
```

```
    plt.show()


    # Extinction Probability Chart
    fig, ax = plt.subplots()
    width = 0.12
    x_indices = np.arange(len(p_values))
    for sp_idx in range(4):
        species_ext_prob = extinction_counts[:, sp_idx] / total_runs
        ax.bar(x_indices + sp_idx*width - 1.5*width,
            species_ext_prob,
            width,
            label=f"Species {sp_idx+1}")


    ax.set_xticks(x_indices)
    ax.set_xticklabels([f"p={p}" for p in p_values])
    ax.set_ylim([0, 1])
    ax.set_ylabel("Extinction Probability")
    ax.set_title("Extinction Probabilities Across Different p Values")
    ax.legend(loc='upper center', ncol=4)
    plt.tight_layout()
    plt.show()


if __name__ == "__main__":
    run_simulations([0.1, 0.5, 0.9], num_realizations=10)
```

Section 7. References

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