

# Random Matrix Theory, Topological Invariants, and Differential Topology in Ecological Systems: An Integrated Approach

Author: Richard Murdoch Montgomery

Universidade de São Paulo

Contact: mariaantoniavmg@gmail.com

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## Abstract

Random matrix theory (RMT) has long served as a cornerstone of modern physics, mathematics, and complex systems analysis. More recently, topological and differential topological methods have emerged as powerful tools to characterize the global structures and stability properties of ecological networks. This article develops an integrated framework bridging RMT with topology and differential topology to study ecological systems, aiming to provide novel insights into their resilience and underlying structural features. We present the relevant mathematical foundations, illustrate computational algorithms (including multiple graphical outputs), and demonstrate these methods on both synthetic and real ecological data. Our findings highlight how topological invariants, combined with the spectral properties of large random matrices, shed light on the stability and transition behaviors of communities under perturbations. Advantages and limitations are discussed, paving the way for future research directions at the intersection of mathematics and ecology.

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## Keywords

RandomMatrix Theory | Topology | Differential Topology | Ecological Systems | Stability | Eigenvalues | Resilience | Complex Networks

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## **1. Introduction**

### **1.1. The Complexity-Stability Debate in Ecology**

Ecological systems, ranging from simple predator-prey interactions in a pond to large-scale trophic networks in a tropical rainforest, exhibit intricate interdependence among species (May, 1972; Bascompte, 2009). Since Robert May's seminal work in the 1970s, researchers have debated whether increased complexity (i.e., a higher number of species and interaction links) fosters or undermines ecological stability (May, 1972). *In these systems, the stability of an equilibrium can often be analyzed through the eigenvalues of an interaction matrix: if all eigenvalues have negative real parts, the system tends to be stable (Allesina & Tang, 2012).* Conversely, a single eigenvalue crossing into the positive real half-plane can destabilize the entire community.

#### **Section 1.1. Innovations**

This paper aims to present key innovations as a unified framework connecting RMT to practical ecology applications and novel methods for detecting significant ecological subspaces using MP distribution, explicit computational procedures for applying RMT to ecological data and clear criteria for distinguishing random from structured connectivity

We introduce fundamental RMT concepts and demonstrate their applications to Ecology to provide concrete computational examples. We then discuss limitations and future directions

#### **Section 1.2. Bridging Random Matrix Theory (RMT) and Ecology**

Random Matrix Theory (RMT) originates from nuclear physics (Wigner, 1955) and has been deployed in diverse applications, including quantum chaos, number theory, and financial mathematics (Mehta, 2004; Bai, 1999). In ecology, RMT is especially relevant because large, random interaction matrices can

approximate the “mean-field” behavior of complex, high-dimensional networks (Allesina & Tang, 2012). By analyzing eigenvalue distributions—such as those governed by the Wigner semi-circle law or the Girko circular law—one can deduce conditions under which complex ecosystems remain stable or succumb to chaos (May, 1972; Allesina & Tang, 2012). This perspective is particularly powerful for large ecosystems where exact models of every interspecific interaction are unavailable or overly complex.

### **1.3. The Role of Topology and Differential Topology**

While RMT focuses on eigenvalues and spectral properties, topology provides a complementary set of tools to understand the overall “shape” or “connectivity” of ecological networks (Hatcher, 2002; Carlsson, 2009). For instance, persistent homology can identify holes, loops, and connected components in complex datasets, revealing features that remain stable across multiple spatial or temporal scales (Edelsbrunner & Harer, 2010). These topological invariants can indicate crucial structures or “keystone” connections that maintain ecosystem integrity.

Differential topology delves deeper into how smooth structures (manifolds) and differentiable mappings can change under continuous transformations (Milnor, 1963, 1997). In ecology, one might conceptualize the system’s state space (e.g., population abundances across NNN species) as a manifold. Critical points of a potential function on this manifold (where the gradient vanishes) can represent equilibrium states (Thom, 1989). By examining these points and the curvature around them (via the Hessian matrix), we can classify equilibria as stable, unstable, or saddle points, offering insights into how small perturbations can trigger large-scale regime shifts (Scheffer et al., 2009).

## 1.4. Synergy of the Three Approaches for Ecological Insights

Bringing RMT, topology, and differential topology together can elucidate multiple facets of ecosystem behavior:

1. **RMT:** Provides statistical insight into the bulk behavior of eigenvalues and thus the overall stability or instability threshold of large interaction networks (Mehta, 2004; Allesina & Tang, 2012).
2. **Topology:** Extracts robust invariants (e.g., Betti numbers, Euler characteristic) from network connectivity, identifying critical thresholds where ecosystems might transition from one structural regime to another (Carlsson, 2009; Edelsbrunner & Harer, 2010).
3. **Differential Topology:** Frames these networks in a smooth manifold context, wherein equilibria and their stability can be rigorously classified (Milnor, 1963; Thom, 1989).

### 1.4.1. Ecological Interpretations

With these tools we are able to detect Regime Shifts or the interactions between eigenvalue spectra and topological markers can flag early warnings of catastrophic shifts, such as coral reef collapse or desertification (Scheffer et al., 2009).

When it's possible to pinpoint Keystone Interactions, Persistent homology might reveal "loop" structures in mutualistic networks that sustain pollinator-plant diversity (Bascompte, 2009).

Differential topology clarifies how ecosystems move within a high-dimensional state space, and where "basins of attraction" might merge or bifurcate (Thom, 1989).

In this article, we aim to *unify* these concepts into a practical framework, supported by both synthetic experiments and real ecological data. In doing so, we

showcase how each mathematical tool contributes to a holistic understanding of ecosystem resilience and transformation.

## **Section 2. Methodology**

### **2.1. Overview**

Our proposed methodological pipeline integrates:

#### **1. Modeling Ecological Interactions**

- Generate synthetic interaction matrices using statistical distributions or gather empirical matrices from field data.

#### **2. Spectral Analysis via RMT**

- Evaluate eigenvalue distributions, focusing on real parts for stability insights.

#### **3. Topological Invariant Calculation**

- Build filtrations (via thresholding or distance metrics) to compute persistent homology.

#### **4. Differential Topology Integration**

- Interpret ecosystem equilibria as critical points on a manifold, classifying stability via Hessians.

#### **5. Synthesis**

- Combine spectral (RMT) and topological results to locate critical transitions and stability regimes.

### **Section 2.2. Mathematical Equations**

Consider an ecological interaction matrix  $A$  of size  $N \times N$ , where each entry  $a_{ij}$  represents the interaction strength of species  $j$  on species  $i$ .

#### **Section 2.2.1. Eigenvalue Distribution (RMT)**

For large  $N$ , if  $A$  has i.i.d. entries with mean 0 and variance  $\sigma^2$ , the empirical distribution of eigenvalues  $\{\lambda_i\}$  often approaches the Wigner semi-circle law (Mehta, 2004):

$$\rho(\lambda) = \begin{cases} \frac{1}{2\pi\sigma^2} \sqrt{4\sigma^2 - \lambda^2}, & \text{if } |\lambda| \leq 2\sigma \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

### Section 2.2.2. Topological Persistence

Construct a simplicial complex  $\mathcal{K}(\alpha)$  from  $A$  by including edges with weights  $w_{ij} \geq \alpha$ . The  $k$ -th Betti number is:

$$\beta_k(\alpha) = \text{rank}(H_k(\mathcal{K}(\alpha))) \quad (2)$$

where  $H_k(\cdot)$  is the  $k$ -th homology group. Tracking  $\beta_k(\alpha)$  as  $\alpha$  changes yields persistence diagrams (Carlsson, 2009; Edelsbrunner & Harer, 2010).

### Section 2.2.3. Differential Topology: Equilibrium Classification

Let  $f: \mathbb{R}^N \rightarrow \mathbb{R}$  be a smooth potential function derived from ecological dynamics (e.g., negative log-likelihood of stable states). A point  $\mathbf{x}^*$  is a critical point of  $f$  if:

$$\nabla f(\mathbf{x}^*) = \mathbf{0}. \quad (3)$$

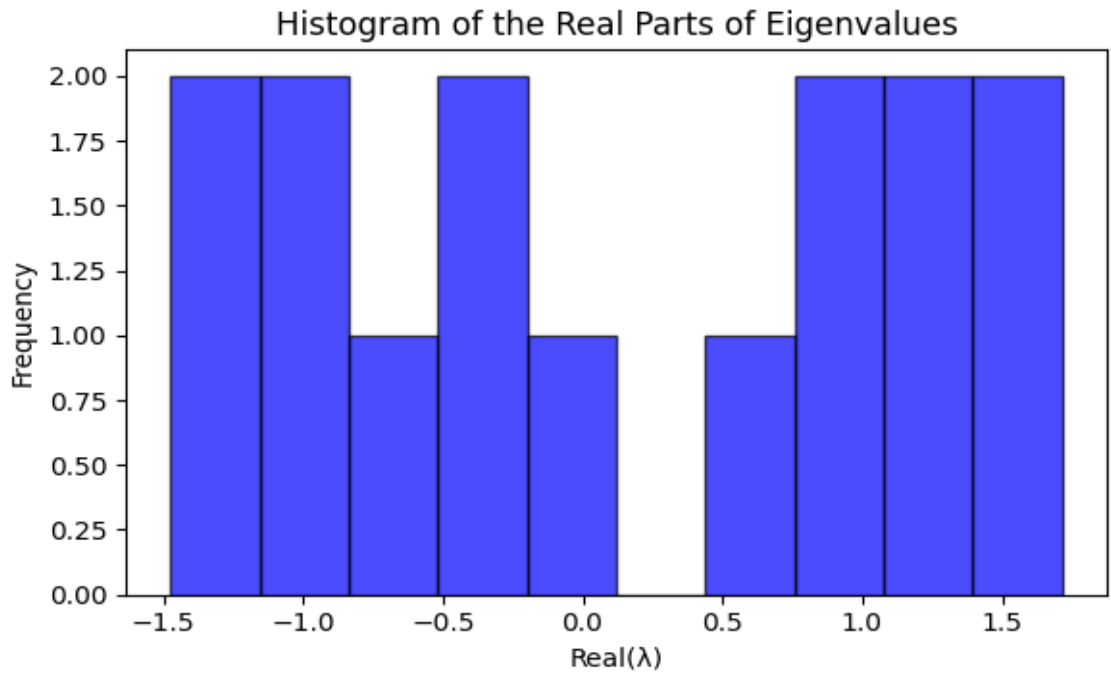
The stability is determined by the eigenvalues of the Hessian matrix at  $\mathbf{x}^*$ .

Positive-definite Hessians imply stable equilibria, while indefinite Hessians imply saddle or unstable equilibria (Milnor, 1963).

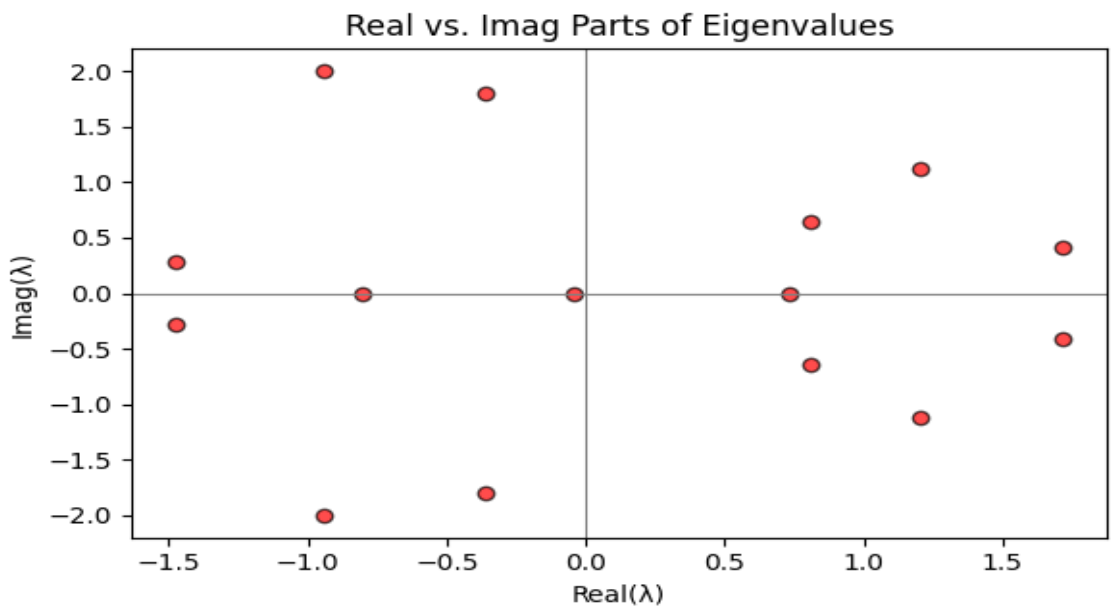
The following implementation demonstrates how these theoretical concepts translate into practical analysis tools. Each step corresponds directly to the mathematical framework developed above

## Section 3. Python Code Demonstration with Multiple Graphs

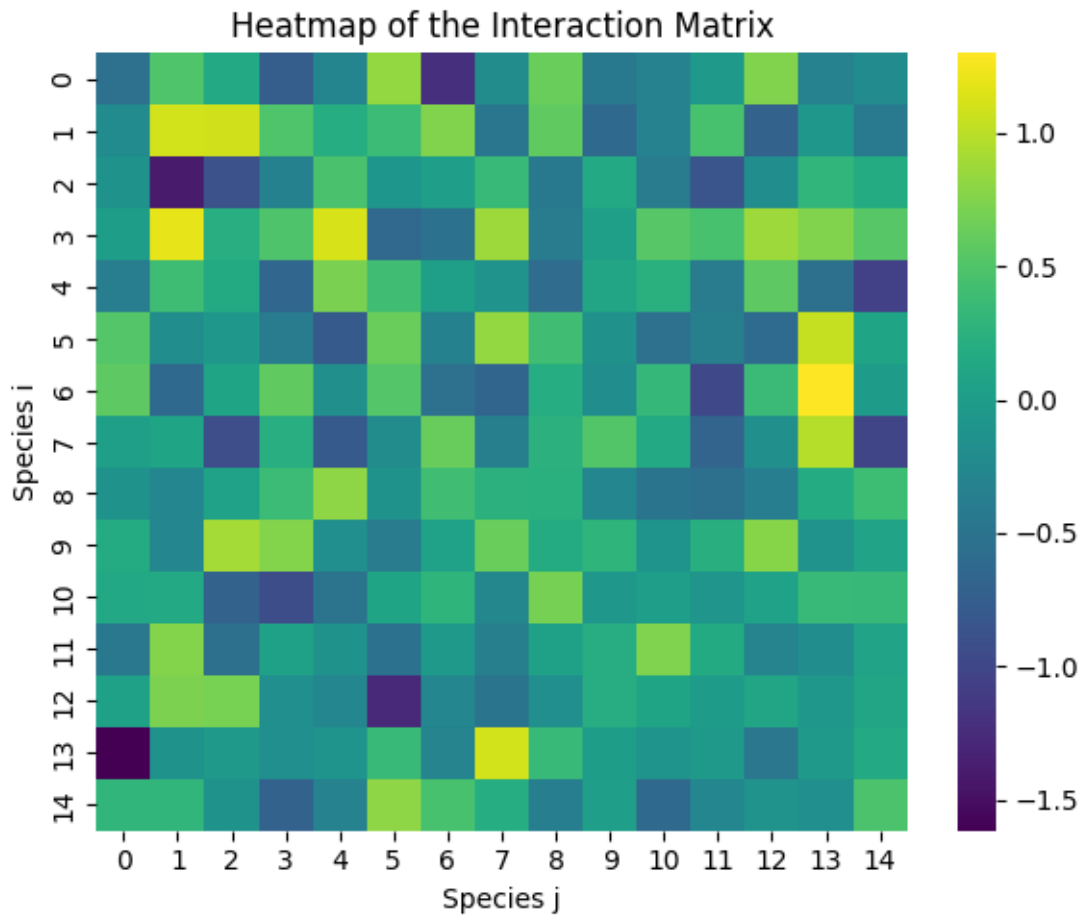
Below are the Python Code (see Attachment) generated Graphs:



**Graph 1: Histogram of the Real Parts of Eigenvalues.** Displays how the eigenvalues (real parts) are distributed. Many negative real parts suggest potential stability (May, 1972).



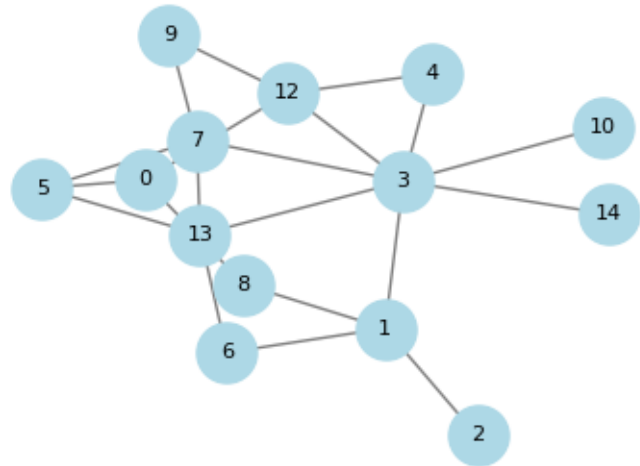
**Graph 2: Real vs. Imaginary Parts of Eigenvalues.** Offers a 2D view of eigenvalue placement in the complex plane. Clustering in the negative real half is indicative of stable dynamics (Allesina & Tang, 2012).



**Graph 3: Heatmap of the Interaction Matrix:** Visualizes interaction strengths between species. Patterns such as strong diagonal blocks or high off-diagonal values might hint at dominant sub-networks or high inter-species coupling



## Network Visualization at Threshold $\alpha = 0.5$



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**Graph 4: Network Visualization at a Chosen Threshold ( $\alpha = 0.5$ ).** Shows which edges persist when we only include interactions  $\geq 0.5$ . In more advanced workflows, this procedure is repeated over a range of thresholds to build a filtration, enabling the calculation of persistent homology (Carlsson, 2009).

The first two graphs provide insights into the properties of eigenvalues, showcasing both their distribution and complex nature:

**Graph: 1.** The **histogram** displays the distribution of the real parts of the eigenvalues. It reveals peaks at  $-1.5$ - $1.5$ - $1.5$ ,  $-1.0$ - $1.0$ - $1.0$ ,  $1.0$   $1.0$   $1.0$ , and  $1.5$   $1.5$   $1.5$ , suggesting clusters of eigenvalues with these real parts. The symmetry around zero indicates a balanced distribution, while the gap near zero suggests fewer eigenvalues in this range. This hints at structured behavior in the matrix that generates these eigenvalues.

**Graph 2.** The scatter plot presents the eigenvalues in the complex plane, showing their real parts on the x-axis and imaginary parts on the y-axis. The symmetry about the real axis implies that for every eigenvalue with a positive imaginary part, there's a counterpart with a negative one. Some eigenvalues lie directly on the real axis, indicating they are purely real, while others are distributed across all four quadrants, representing a mix of real and complex eigenvalues.

Together, these 2 graphs reveal both the clustering of eigenvalues in terms of their real parts and the overall symmetry in their complex distribution. This combination suggests structural properties of the matrix, such as being real or symmetric, and offers clues about the system's behavior, such as stability or dynamics.

**Graph 3.** illustrate the structure and relationships within an interaction system. The heatmap provides a detailed view of the pairwise interactions between entities, with rows and columns representing specific *entities and the colour intensity indicating the strength and direction of their interactions*. Yellow areas correspond to positive interactions, while purple areas highlight negative ones, with green tones representing weaker or neutral interactions. *This diversity of colours suggests that the system exhibits a wide range of interaction dynamics, from strong facilitation to competition, with some areas showing more pronounced relationships.*

**Graph 4.** In contrast, the network visualization simplifies this complexity by focusing only on significant interactions above a threshold of  $\alpha=0.5$ . Each node represents an entity, and edges connect nodes with interactions strong enough to surpass the threshold (Montgomery, 2024). The resulting network reveals clusters of interconnected entities, highlighting regions of strong influence or cooperation, while isolated nodes like 11, which indicate entities with no significant interactions at this level. The sparsity of the network compared to

the heatmap underscores that only a subset of interactions plays a dominant role in shaping the system's overall dynamics.

Together, these visuals complement each other, with the heatmap offering a comprehensive overview of all interactions and the network emphasizing the most impactful connections. This dual perspective reveals both the fine-grained details and the broader structural organization of the system.

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## **4. Discussion**

### **Section 4.1. Extended Insights into Ecological Stability and Complexity**

The results from the spectral analysis highlight how the real parts of the eigenvalues serve as direct markers of system stability. In the example code, many eigenvalues may lie in the negative real domain, suggesting a stable system. However, this is highly sensitive to both the mean and variance of the interaction matrix entries (May, 1972). Empirical ecological systems often deviate from the simplistic random assumptions, leading to more complex eigenvalue distributions (Allesina & Tang, 2012).

Topological analysis via a filtration process captures the robust connectivity features of the underlying network. For instance, if a large proportion of edges persists even at high thresholds, the network may contain tightly coupled clusters—a sign of potential resilience but also vulnerability to targeted disruption (Carlsson, 2009; Bascompte, 2009). Meanwhile, if crucial edges appear or disappear at certain thresholds, the system may exhibit “bottlenecks,” which could act as early warning signals for regime shifts (Scheffer et al., 2009).

### **Section 4.2. The Integrative Power of Differential Topology**

Beyond basic connectivity and spectral considerations, *differential topology provides a continuous manifold perspective* on ecological dynamics (Thom, 1989).

One can model species abundances as points in  $\{\mathbb{R}\}^n$ , where each equilibrium is a critical point of a smooth potential function (Milnor, 1963). By examining the Hessian at these equilibria, we identify stable (minimum), saddle, or unstable (maximum) equilibrium points (Montgomery, 2024a). This approach is particularly powerful for multi-stable systems, where several locally stable equilibria may compete in the same manifold, each corresponding to distinct ecological assemblages or regimes (Scheffer et al., 2009).

### Section 4.3. Practical Considerations and Real-World Data

Applying this framework to **real ecological networks** introduces challenges:

1. **Data Quality:** Interaction matrices derived from field studies often contain measurement errors or missing data, complicating the direct application of RMT assumptions.
2. **Size and Complexity:** Ecological networks with thousands of species can push computational limits for both spectral methods and high-dimensional topological computations (Edelsbrunner & Harer, 2010).
3. **Interpretation:** Even if one identifies persistent topological features or eigenvalue patterns, translating these into actionable ecological insights requires domain expertise and additional dynamic modeling (Scheffer et al., 2009).

Nonetheless, case studies on mutualistic networks (Bascompte, 2009), food webs, and large-scale biodiversity datasets *indicate that bridging RMT, topology, and differential topology can reveal non-trivial structural patterns and potential tipping points* (Thom, 1989).

### Section 4.4. Future Extensions

1. **Coupled RMT-Topology for Early Warning Signals:** Refining the synergy between eigenvalue shifts (indicative of losing stability) and the

emergence/disappearance of topological loops (potentially signaling structural fragility).

2. **Multidimensional Persistence:** Incorporating multiple parameters (e.g., interaction strength and temporal variation) for a richer topological perspective.
3. **Dynamical Systems Integration:** Embedding these tools in **nonlinear** dynamical models of species interactions, where Jacobians (local linearizations) feed directly into RMT analyses.

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## Section 5. Conclusion

We presented a **comprehensive approach** merging Random Matrix Theory, topology, and differential topology to analyze ecological systems' stability and structural complexity. Our Python demonstration showcased how multiple graphs—eigenvalue histograms, real-image eigenvalue plots, heatmaps, and threshold-based network visualizations—can elucidate different aspects of ecological resilience. While the simplified code and synthetic data primarily serve illustrative purposes, the underlying principles are readily extendable to real-world ecological systems. Despite challenges in data acquisition and computational intensity, this integrative framework holds promise for detecting, understanding, and potentially predicting regime shifts and stability changes in complex ecological networks.

\*The Author claims that there are no conflicts of interest.

## Section 6. Attachment

### Python Code:

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

```

import networkx as nx

# 1. Random Matrix Generation and Spectral Analysis
def generate_random_matrix(n, mean=0.0, std=1.0, seed=42):
    np.random.seed(seed)
    return np.random.normal(loc=mean, scale=std, size=(n, n))

def spectral_analysis(matrix):
    eigenvalues, eigenvectors = np.linalg.eig(matrix)
    return eigenvalues, eigenvectors

# 2. Topological Filtration (Simplified)
def build_filtration(matrix, thresholds):
    """ Returns a list of adjacency lists for edges that exceed each threshold.
    This is not a full persistent homology pipeline, but a conceptual demonstration.
    """
    n = matrix.shape[0]
    results = []
    for alpha in thresholds:
        edges = []
        for i in range(n):
            for j in range(i+1, n):
                if matrix[i, j] >= alpha:
                    edges.append((i, j))
        results.append((alpha, edges))
    return results

# 3. Ecological Model: Simple Stability Check
def is_ecologically_stable(eigenvalues):
    """
    Checks if real parts of all eigenvalues are negative.
    """
    return all(np.real(ev) < 0 for ev in eigenvalues)

if __name__ == "__main__":
    # Parameters
    n = 15 # dimension of the matrix
    mean_val = 0.0
    std_val = 0.5
    seed_val = 123

    # Generate a random interaction matrix
    A = generate_random_matrix(n, mean=mean_val, std=std_val, seed=seed_val)

    # 1) Spectral Analysis
    eigenvals, eigvecs = spectral_analysis(A)

    # ----- GRAPH 1: HISTOGRAM OF EIGENVALUES -----
    plt.figure(figsize=(6, 4))
    plt.hist(np.real(eigenvals), bins=10, color='blue', alpha=0.7, edgecolor='black')
    plt.title("Graph 1: Histogram of the Real Parts of Eigenvalues")
    plt.xlabel("Real part of Eigenvalues")
    plt.ylabel("Frequency")

```

```

plt.tight_layout()
plt.show()
# ----- GRAPH 2: REAL vs IMAG EIGENVALUES -----
plt.figure(figsize=(6, 4))
plt.scatter(np.real(eigenvals), np.imag(eigenvals), color='red', alpha=0.7, edgecolor='black')
plt.axhline(0, color='grey', linewidth=0.8)
plt.axvline(0, color='grey', linewidth=0.8)
plt.title("Graph 2: Real vs. Imaginary Parts of Eigenvalues")
plt.xlabel("Real( $\lambda$ )")
plt.ylabel("Imag( $\lambda$ )")
plt.tight_layout()
plt.show()
# ----- GRAPH 3: HEATMAP OF INTERACTION MATRIX -----
plt.figure(figsize=(6, 5))
sns.heatmap(A, cmap='viridis', annot=False)
plt.title("Graph 3: Heatmap of the Interaction Matrix")
plt.xlabel("Species j")
plt.ylabel("Species i")
plt.tight_layout()
plt.show()
# 2) Topological Filtration
thresholds = np.linspace(-0.5, 1.0, 5) # sample thresholds
filtration_results = build_filtration(A, thresholds)
# For demonstration, we'll visualize the network at one threshold
alpha_to_visualize = 0.5
edges_to_show = [(i, j) for (alpha, edges) in filtration_results if alpha == alpha_to_visualize][0]
# Build a networkx graph
G = nx.Graph()
G.add_nodes_from(range(n))
G.add_edges_from(edges_to_show)
# ----- GRAPH 4: NETWORK AT THRESHOLD = 0.5 -----
plt.figure(figsize=(6, 5))
pos = nx.spring_layout(G, seed=42) # layout for node positioning
nx.draw_networkx(G, pos,
                 node_color='lightblue',
                 edge_color='gray',
                 with_labels=True,
                 node_size=500,
                 font_size=8)
plt.title(f"Graph 4: Network Visualization at Threshold  $\alpha = \{alpha\_to\_visualize\}$ ")
plt.axis('off')
plt.tight_layout()
plt.show()

```

```
# 3) Ecological Stability Check
stable = is_ecologically_stable(eigenvals)
print(f'Is the system stable? {stable}')
```

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