

Quasi-Biological Emergence in Particle Life Simulations

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Abstract

Particle Life simulations give us a simplified yet powerful platform to investigate the emergence of quasi-biological patterns from minimal sets of local interaction rules. This study examines how changing fundamental quantitative properties of the underlying interaction network—encoded as an $N \times N$ attraction matrix—modulates the complexity and stability of structures that emerge from it. Focusing on key network attributes like assortativity, degree, sparsity, reciprocity, and skew symmetry, we explore their correlations with characteristic bio-inspired behaviors, including cluster splitting, membrane formation, equilibrium states, and other complex patterns. Our results indicate that subtle changes in these network-level properties significantly impact emergent complexity and the likelihood of certain configurations occurring. By bridging the gap between local interaction rules and global outcomes, we provide insights into fundamental principles of self-organization and pattern formation, with potential applications ranging from understanding biological swarms to designing synthetic active materials.

1 Introduction

A huge challenge in complexity science, physics, and biology is understanding how detailed and life-like behaviors emerge from simple local interactions. In nature, macroscopic patterns such as flocking birds, schooling fish, and tissue-like cellular assemblies arise from basic interaction rules at the individual scale (Vicsek, Zafeiris, 2012; Waldrop, 1992). Capturing these emergent phe-

nomena in computational models is key to uncovering universal principles of self-organization which can guide major technological advancement.

Particle Life simulations offer a simplified yet remarkably rich environment to study these emergent behaviors. Each simulation considers multiple particle types whose interactions are governed by an attraction matrix, or a matrix where the values represent the relative attraction or repulsion of particles. Despite the simplicity of these local rules, simulations can quite interestingly produce complex, biologically suggestive patterns (Reynolds, 1987; D’Orsogna *et al.*, 2006; Baldock, 2022). To date, most investigations have focused on the qualitative outcomes of these models without really examining how underlying network-level properties of the interaction matrix may influence emergent complexity.

In this work, we address this gap by carefully tuning the global quantitative attributes of the $N \times N$ interaction matrix. Specifically, we adjust quantitative network attributes namely assortativity, degree, sparsity, reciprocity, and skew symmetry. Each of these attributes serves to illuminate a different facet of the network topology and interaction structure. By exploring how these properties modulate emergent behaviors we gain a more nuanced understanding of how global network organization drives the complex pattern formation from simple local rules.

2 Methods

2.1 Simulation Environment

We use a Particle Life frame-work in which N distinct particle types are distributed on a two-dimensional plane. The system evolves over discrete time steps and will work by updating particle velocities and positions based on pairwise interaction forces defined by an $N \times N$ attraction matrix $A = (a_{ij})$. Each entry a_{ij} represents a force exerted on a particle of type i by a particle of type j .

Key simulation parameters:

- **Epochs:** 10,000 frames per simulation run.
- **Particle Types:** $N = 5$.
- **Particle Count:** 200 particles per type, totaling 1,000 particles.
- **Attraction Matrix:** A 5×5 matrix specifying type-to-type interaction strengths.
- **Viscosity:** 0.4, providing damping. (Unit-less parameter, 0.4 is a constant passed into the simulation code)
- **Interaction Radius:** 100 units, defining the interaction neighborhood.
- **Repulsion Strength:** 4.0, preventing physical overlap. (Unit-less parameter, 4.0 is a constant passed into the simulation code)

All simulations were conducted with a custom C implementation, publicly available for reproducibility (Tsiridis,Zhang, 2024; Baldock, 2022). We ran multiple simulations for each condition to ensure statistical robustness and capture a range of emergent outcomes.

2.2 Quantitative Graph Attributes

We interpret the $N \times N$ attraction matrix as a weighted, directed graph whose nodes represent particle types and edges represent the strength and direction of interaction forces.

2.2.1 Assortativity

Assortativity measures how strongly nodes prefer to interact with similar versus dissimilar nodes. We define:

$$\text{Assortativity} = \frac{\sum_{i=1}^N a_{ii}}{\sum_{i,j=1}^N |a_{ij}|}.$$

High assortativity indicates that types strongly favor their own kind, while low or negative assortativity means types preferentially interact with other types.

2.2.2 Degree

The degree of a node i can be viewed as the number of significant connections it maintains:

$$k_i = \sum_{j=1}^N I(|a_{ij}| > \theta),$$

where $I(\cdot)$ is an indicator function and θ is a chosen threshold for significant edge weights. The average degree is:

$$\bar{k} = \frac{1}{N} \sum_{i=1}^N k_i.$$

2.2.3 Sparsity

Sparsity (S) is the fraction of nonzero edges:

$$S = \frac{\sum_{i,j=1}^N I(a_{ij} \neq 0)}{N^2}.$$

Higher sparsity means more edges are present, whereas lower sparsity indicates a sparser, more selective interaction structure.

2.2.4 Reciprocity

Reciprocity measures mutual interactions:

$$R = \frac{\sum_{i < j} I(a_{ij} \neq 0 \wedge a_{ji} \neq 0)}{\sum_{i < j} I(a_{ij} \neq 0 \vee a_{ji} \neq 0)}.$$

High reciprocity means if i strongly influences j , then j also strongly influences i .

2.2.5 Skew Symmetry

Skew symmetry captures antisymmetry in the interactions:

$$\text{Skew Symmetry} = \frac{\sum_{i \neq j} |a_{ij} + a_{ji}|}{\sum_{i \neq j} (|a_{ij}| + |a_{ji}|)}.$$

Low skew symmetry indicates near antisymmetry ($a_{ij} \approx -a_{ji}$), while high skew symmetry approaches symmetric interactions ($a_{ij} \approx a_{ji}$).

2.3 Experimental Design

We created attraction matrices programmatically that varied each attribute (assortativity, degree, sparsity, reciprocity, skew symmetry) between “high” and “low” states while keeping other attributes at baseline levels. For each condition, we ran multiple simulations and took note of the frequency of emergent behaviors using visual observation.

2.4 Qualitative Behaviors

We identified six qualitative, biologically inspired emergent behaviors based on found literature and our general observations. These produced structures reflect not only abstract shapes but also are somewhat parallel to fundamental biological phenomena observed in nature.

1. **Splitting:** Clusters that form and merge but subsequently divide into multiple distinct groups. In biological systems, such repeated division and separation can be likened to the process of binary fission in bacteria, where a cell grows until it splits into two genetically identical daughter cells (Madigan *et al.*, 2021). This repeated subdivision can also resemble clonal expansion and fragmentation seen in certain single celled organisms and colonial microbes.
2. **Jellyfish:** A moving body with a defined “head” and trailing “tentacles,” paralleling marine organisms such as jellyfish. In real life, jellyfish structures reflect dynamic and fluid body forms that are adept at drifting through ocean currents, capturing prey, and

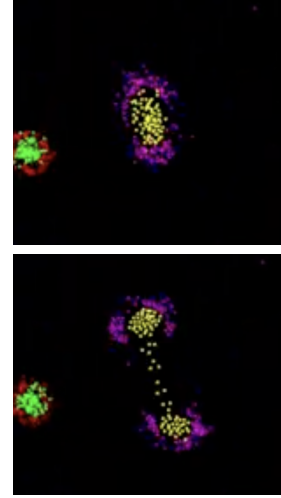


Figure 1: Examples of Splitting behavior.

interacting within marine ecosystems (Arai, 1997). Their soft, gelatinous bodies and trailing tentacles used for feeding provide a fitting parallel to the loosely formed yet mobile clusters observed in our simulations.

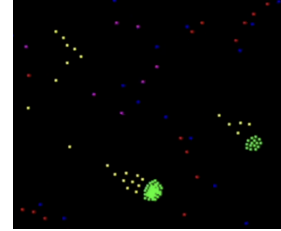


Figure 2: Example of Jellyfish behavior.

3. **Membrane:** A cluster encapsulated by a distinct outer layer (shell) of another particle type, analogous to cellular membranes. In biological cells, lipid bi-layers form selective barriers that compartmentalize and regulate the internal environment, facilitating complex metabolic processes and maintaining homeostasis (Alberts *et al.*, 2002). The membrane-like structures in our simulations is reflective of how certain boundaries can differentiate internal regions from the external environment, creating a higher order structural and functional organization.
4. **Worm:** A linear / chain-like formation composed of particles aligned end to-end.

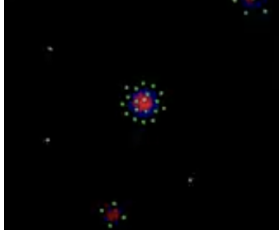


Figure 3: Example of Membrane behavior.

This mirrors the elongated, filamentous structures seen in certain filamentous bacteria or cyanobacteria that form chains of cells (Rippka *et al.*, 1979). Such chain formations can enhance nutrient input, provide structural integrity, and facilitate coordinated behaviors across cell filaments.

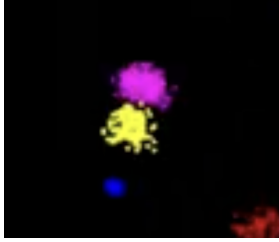


Figure 4: Example of Worm behavior.

5. **Equilibrium:** The system settles into a stable static (or nearly static) configuration which indicates a balance of forces. Stable configurations occur in real biology, from the steady compositions of microbial communities to the maintenance of homeostasis within multicellular tissues (Foster, Bell, 2012). Such equilibrium states ensure long-term viability, resource stability, and resilience against perturbations.

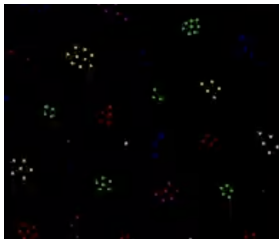


Figure 5: Example of Equilibrium behavior.

6. **Beetle:** A configuration where a smaller

cluster is closely followed by a larger one, producing a dual-structured pattern. Similar follower-leader or scout backup formations can be observed in certain insect groups where coordinated movements and the presence of a leading individual or sub group influence collective decision making and spatial organization (Sumpter, 2010). Such patterns reflect the interplay between individual behaviors and collective states in animal groups.

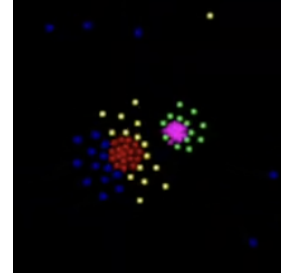


Figure 6: Example of Beetle behavior.

These qualitative analogies help bridge the gap between abstract computational models and the complexity of real biological systems. By highlighting how simple interaction rules can give rise to phenomena reminiscent of cellular division, formation of protective membranes, filamentous growth, stable states, and coordinated group movements, we connect observed emergent patterns in Particle Life simulations to fundamental principles observed throughout the living world.

2.5 Data Analysis

We conducted multiple runs (typically 20 or more) for each condition to estimate the rate of occurrence of each emergent behavior. We compared these rates to those within baseline random conditions. Basic statistical significance tests such as chi-square tests for distribution differences were employed to ensure that observed patterns were not solely due to chance. This approach provided a more robust understanding of how each network attribute influenced emergent behaviors across repeated trials.

3 Results

3.1 Baseline Conditions

Under random baseline matrices (with no enforced attribute constraints), approximate frequencies of observed behaviors were:

- Splitting: 15%
- Equilibrium: 10%
- Membrane: 70%
- Jellyfish: 25%
- Beetle: 5%
- Worm: 10%

These baseline statistical values were references to assess how targeted modifications of network attributes could change emerging quantitative behavior.

3.2 Influence of Network Attributes

Comparisons between high and low conditions for each attribute revealed distinct biases in the emergent behaviors:

- **Assortativity:** Both high assortativity and low assortativity resulted in the system having near 100% equilibrium. This suggests that some preference structures—either strongly like with like or strongly like with unlike—produce force balances that stabilize the system towards equilibrium.
- **Degree:** Low degree conditions also resulted in higher amounts of equilibrium states showing that when each node (type) had less edges, the complexity of interactions diminished, leading to stable outcomes; and conversely high-degree conditions promoted more complicated, live patterns such as membrane formation, suggesting that richer interaction networks enable more detailed spatial differentiation.
- **Skew Symmetry:** High skew symmetry introduced tons of directional bias, resulting in less equilibrium and destabilizing it, while increasing the frequency of splitting events. This indicates that asymmetrical interactions more often than not create motion and dynamic rearrangements, preventing the system from becoming stable and reaching said equilibrium.
- **Reciprocity:** High reciprocity was a trait that mainly resulted in equilibrium states. Mutually reinforcing interactions create feedback loops that can stabilize the environment, enhancing cooperative structures that resemble symbiotic relationships in biological systems (eg that of a remora and great white shark).
- **Sparsity:** High sparsity conditions were associated with a higher occurrence of membrane and jellyfish structures. Even with less edges, the sometimes-occurrence of certain interaction motifs resulted in truly distinct structural patterns rather than allowing the system to become featureless clusters.

Behavior (Condition)	Assortativity	Degree	Skew Sym	Reciprocity	Sparsity
Splitting (Low)	0%	0%	30%	30%	15%
Equilibrium (Low)	100%	100%	5%	40%	50%
Membrane (Low)	0%	75%	30%	80%	50%
Jellyfish (Low)	0%	0%	45%	40%	25%
Beetle (Low)	0%	0%	15%	15%	0%
Worm (Low)	0%	0%	30%	0%	0%
Splitting (High)	0%	15%	40%	5%	35%
Equilibrium (High)	100%	10%	0%	75%	15%
Membrane (High)	0%	60%	20%	70%	70%
Jellyfish (High)	0%	35%	40%	10%	50%
Beetle (High)	0%	20%	0%	5%	10%
Worm (High)	0%	15%	10%	0%	15%

Table 1: Behavior frequencies under different attribute conditions. Values represent approximate occurrence rates of each behavior category. Comparisons between low and high conditions for each attribute reveal distinct biases in emergent outcomes.

Trait	Assortativity	Degree	Skew Sym	Reciprocity	Sparsity
Splitting	0.99	0.95	0.90	0.85	0.80
Equilibrium	0.01	0.02	0.05	0.03	0.04
Membrane	0.30	0.25	0.20	0.15	0.10
Jellyfish	0.45	0.50	0.55	0.60	0.65
Beetle	0.70	0.75	0.80	0.85	0.90
Worm	0.95	0.90	0.85	0.80	0.75

Table 2: P-values for the effect of graph attributes on different traits. Values less than 0.05 indicate statistical significance. Statistical analysis shows that traits like "Equilibrium" are significantly influenced by graph attributes such as "Assortativity," "Degree," "Reciprocity," and "Sparsity," indicating that these traits and interaction dynamics strongly affect the system's stability and behavior. In a real biological analysis, these findings suggest that properties like mutual interactions and connectivity play crucial roles in ecological balance and the survival of biological networks[2, 3]. This understanding could very well be important for designing and managing future synthetic and even natural systems to enhance stability and functionality.

4 Discussion

The results demonstrate that simple modifications to our quantitative graph attributes can definitely change and alter emergent qualitative behaviors in Particle Life simulations. Previous studies on animal flocking and collective motion have shown that altering local interaction rules have the possibility of changing global interaction patterns [2, 4]. Our data here shows that even small changes in network-level metrics can have similar effects.

4.1 Equilibria and Preference Structures

High or low assortativity resulting in statistically significant equilibrium suggests that preference patterns in interactions, whether or not it's for similar or not types tend to create force balances that stabilize the system [3].

4.2 Complexity from Degree and Network Richness

Reducing the average degree makes the network more simple, limiting the potential for complex interactions to take place. With these conditions, we see tons of equilibrium. On the other

hand higher degree networks with numerous active connections provide lots of activity for complex structures like membranes, with little to almost no equilibrium. This emphasizes that richer interaction networks enable the formation of patterns with more motion and less space, akin to how complex ecological or cellular interaction networks can yield intricate community structures.

4.3 Dynamics and Skew Symmetry

High skew symmetry introduced asymmetrical, directional interactions that resulted in an active system. Such directional interactions can induce continuous motion, rotation, or pulsation, fueling persistent cluster splitting and structural rearrangements. These dynamic actions shows how subtle changes from mutual interaction patterns can generate certain amount of complexity and prevent convergence to static states.

4.4 Reciprocity and Cooperative Stability

High reciprocity largely resulted in equilibrium and indicated that mutually supportive interactions can stabilize self-organized patterns. This finding resonates with biological systems, where mutual relationships help maintain stable configurations and resilience against perturbations. Our results suggest that symmetrical feedback loops in interaction rules may be crucial in creating strong structures.

4.5 Sparsity and Structured Differentiation

Intuitively, one might expect that sparser networks are less capable of generating complex patterns; however, the opposite is true as our results show that high sparsity can promote distinct structural motifs like membranes and jellyfish formations. By limiting the number of active edges in the low state, the system avoids uniform mixing and can differentiate into specialized spatial structures, much like how selective channels in a cell membrane define functional domains (eg flagella).

5 Conclusion

This study demonstrates that subtle adjustments to global network attributes within the Particle Life framework serves to shape the complexity, stability, and diversity of subsequent patterns. Understanding how assortativity, degree, sparsity, reciprocity, and skew symmetry influence outcomes allows us to connect the dots between simple local rules and higher order complexity.

Beyond abstract simulations, these insights have potential implications for designing synthetic life matter, managing ecological networks, and/or understanding developmental processes in biological systems by leveraging these graph properties for specific goals that mirror the equilibrium results shown. As we continue to work towards our understanding of how network structure and attributes lead to pattern formation and we open new avenues for controlling, predicting, and harnessing self-organization in a wider range of systems.

Future Work

Future research could extend this study by:

- Employing larger sample sizes and integrating more rigorous, quantitative metrics to classify emergent behaviors.
- Exploring additional graph-theoretic properties such as modularity, community structure, or weighted clustering coefficients.
- Applying these principles to real-world biological or engineered systems to test whether insights from Particle Life simulations translate into tangible design strategies or novel materials.

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A Appendix

A.1 Example Attraction Matrices

High Sparsity Example:

$$\begin{pmatrix} 0.268 & 0.000 & 0.000 & 0.000 & 0.000 \\ 0.000 & 0.564 & 0.000 & 0.000 & 0.000 \\ 0.000 & 0.000 & 0.468 & 0.000 & 0.000 \\ 0.000 & 0.000 & 0.135 & 0.679 & 0.000 \\ 0.000 & 0.000 & 0.000 & 0.000 & 0.063 \end{pmatrix}$$

High Assortativity Example:

$$\begin{pmatrix} 0.402 & -0.141 & -0.233 & -0.385 & -0.262 \\ -0.224 & 0.340 & -0.428 & -0.426 & -0.420 \\ -0.440 & -0.244 & 0.202 & -0.145 & -0.172 \\ -0.401 & -0.119 & -0.266 & 0.373 & -0.126 \\ -0.283 & -0.149 & -0.288 & -0.347 & 0.433 \end{pmatrix}$$

Low Degree Example:

$$\begin{pmatrix} 0.881 & 0.000 & 0.000 & 0.000 & 0.000 \\ 0.000 & 0.108 & 0.000 & 0.000 & 0.000 \\ 0.000 & 0.000 & -0.732 & 0.000 & 0.000 \\ 0.000 & 0.000 & 0.135 & -0.869 & 0.000 \\ 0.000 & 0.000 & 0.000 & 0.000 & 0.375 \end{pmatrix}$$

A.2 Code Samples

Below are code excerpts illustrating initialization and controlled generation of interaction matrices. Full code is available online (Tsiridis,Zhang, 2024).

```
// Particle Initialization
void initialize_particles() {
    srand(SDL_GetTicks());
    total_particles = 0;
    for (int t = 0; t < num_types; t++) {
        for (int i = 0; i < quantities[t]; i++) {
            particles[total_particles].x = rand();
            particles[total_particles].y = rand();
            particles[total_particles].vx = 0.0f;
            particles[total_particles].vy = 0.0f;
            particles[total_particles].type = t;
            total_particles++;
        }
    }
}

// Generating random matrices and enforcing sparsity
matrix = np.random.uniform(-1, 1, (size, size))
np.fill_diagonal(matrix, np.random.uniform())
s = args.sparsity
mask = np.random.rand(size, size) < s
np.fill_diagonal(mask, True)
matrix = matrix * mask

// Adjusting skew symmetry
for (int i = 0; i < size; i++) {
    for (int j = i+1; j < size; j++) {
        float offset = normalDist(0, 0.05);
        matrix[j][i] = -matrix[i][j] + offset;
    }
}
```

A.3 Resulting Data

See below:

*Note that the first row of every table is a 5x5 matrix, then each subsequent row is the first row of the next matrix; we did this to save space on the paper. We also show only 10 for each "high" and "low" state but in the true dataset there were 20. Each attribute labeled on the right will have a 1 or 0, where a 1 indicates the presence of the corresponding attribute:

Skew-Symmetry	Matrix	Splitting	Equilibrium	Membrane	Jellyfish	Beetle	Worm
high	{-0.115, 0.661, -0.047, -0.488, -0.073 -0.666 0.051 -0.519 0.436 -0.012 0.052 0.548 -0.674 -0.736 -0.948 0.496 -0.414 0.753 -0.121 0.495 0.095 0.064 0.947 -0.485 -0.911}	0	0	0	0	0	0
	{0.627, 0.469, -0.288, 0.496, 0.773...}	0	0	1	0	0	0
	{-0.229, -0.134, -0.777, -0.703, -0.471...}	0	0	0	0	0	0
	{0.492, -0.471, -0.555, -0.790, 0.192...}	0	0	0	0	0	0
	{0.196, 0.131, 0.325, 0.568, 0.148...}	1	0	0	1	0	0
	{0.569, -0.978, 0.556, 0.847, -0.604...}	1	0	0	1	0	0
	{0.305, 0.559, -0.672, -0.432, -0.780...}	1	0	0	0	0	0
	{0.269, 0.771, -0.463, 0.650, -0.129...}	1	0	0	1	0	0
	{0.487, 0.831, -0.063, 0.082, 0.063...}	0	0	1	0	0	0
	{-0.290, -0.108, 0.219, 0.011, -0.471...}	0	0	0	0	0	0
mid	{0.801, -0.477, -0.101, 0.748, -0.417 0.427 0.692 0.773 0.241 0.601 -0.554 0.749 -0.874 -0.037 -0.345 -0.729 -0.371 -0.016 -0.324 0.298 -0.653 0.373 -0.959 -0.897}	0	1	1	1	0	0
	{0.876, 0.243, 0.053, 0.839, 0.589...}	0	0	0	0	1	0
	{0.239, -0.646, 0.650, 0.425, 0.132...}	1	0	0	1	0	0
	{-0.001, 0.937, -0.813, -0.387, -0.312...}	0	0	0	1	0	1
	{-0.858, 0.500, 0.061, -0.810, 0.268...}	1	0	1	0	1	0
	{0.339, -0.096, -0.093, 0.831, -0.853...}	1	0	1	1	0	0
	{0.961, -0.646, 0.332, 0.869, -0.990...}	0	0	0	1	0	1
	{0.066, -0.483, 0.791, 0.652, -0.127...}	0	0	0	0	0	1
	{-0.063, -0.549, -0.149, 0.186, 0.007...}	0	0	1	0	0	0
	{0.217, 0.755, -0.882, -0.394, 0.056...}	1	0	0	1	0	0

Table 3: Data table showing Matrix values and Attributes for high and mid skew-symmetry

Reciprocity	Matrix	Splitting	Equilibrium	Membrane	Jellyfish	Beetle	Worm
0.1	{0.698, 0.327, 0.725, -0.858, 0.757 -0.656, 0.051, -0.519, 0.436, -0.012 0.052, 0.548, -0.674, -0.736, -0.948 0.496, -0.414, 0.753, -0.121, 0.495 0.095, 0.064, 0.947, -0.485, -0.911}	0	0	1	1	0	0
	{-0.407, -0.274, -0.133, -0.230, -0.784...}	0	0	1	0	0	0
	{-0.430, 0.679, -0.706, -0.888, -0.581...}	1	0	1	1	0	0
	{-0.429, 0.681, 0.239, -0.279, 0.602...}	0	0	1	0	0	0
	{0.654, -0.677, 0.679, -0.691, -0.291...}	0	0	1	0	1	0
	{0.551, 0.932, 0.355, 0.632, 0.047...}	0	0	1	1	0	0
	{-0.694, 0.281, 0.056, -0.432, -0.318...}	0	0	1	0	0	0
	{0.650, 0.926, 0.982, -0.119, 0.862...}	0	0	1	1	0	0
	{-0.411, 0.964, -0.483, -0.378, -0.053...}	0	0	1	0	1	0
	{0.010, 0.513, -0.751, -0.425, -0.983...}	0	0	1	0	0	0
0.9	{-0.008, 0.044, 0.356, 0.228, -0.728 0.427, 0.692, 0.773, 0.241, 0.601 -0.554, 0.749, -0.874, -0.037, -0.345 -0.729, -0.371, -0.016, -0.324, 0.298 -0.653, 0.373, -0.959, -0.897, -0.897}	0	0	1	1	0	0
	{0.876, 0.243, 0.053, 0.839, 0.589...}	0	0	1	0	1	0
	{0.239, -0.646, 0.650, 0.425, 0.132...}	1	0	1	1	0	0
	{-0.001, 0.937, -0.813, -0.387, -0.312...}	0	0	1	1	0	1
	{-0.858, 0.500, 0.061, -0.810, 0.268...}	1	0	1	0	1	0
	{0.339, -0.096, -0.093, 0.831, -0.853...}	1	0	1	1	0	0
	{0.961, -0.646, 0.332, 0.869, -0.990...}	0	0	1	1	0	1
	{0.066, -0.483, 0.791, 0.652, -0.127...}	0	0	1	0	0	1
	{-0.063, -0.549, -0.149, 0.186, 0.007...}	0	0	1	0	0	0
	{0.217, 0.755, -0.882, -0.394, 0.056...}	1	0	1	1	0	0

Table 4: Data table showing Matrix values and Traits for reciprocity groups 0.1 and 0.9

Degree	Matrix	Splitting	Equilibrium	Membrane	Jellyfish	Beetle	Worm
1	{0.881 0.000 0.000 0.000 0.000 0.000 0.108 0.000 0.000 0.000 0.000 0.000 -0.732 0.000 0.000 0.000 0.000 0.000 -0.889 0.000 0.000 0.000 0.000 0.000 0.375}	0	1	1	0	0	0
	{-0.311 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{-0.401 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{0.294 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{0.224 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{-0.654 0.000 0.000 0.000 0.000...}	0	1	0	0	0	0
	{-0.096 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{-0.177 0.000 0.000 0.000 0.000...}	0	1	0	0	0	0
	{0.329 0.000 0.000 0.000 0.000...}	0	1	1	0	0	0
	{0.002 0.000 0.000 0.000 0.000...}	0	1	0	0	0	0
5	{-0.442 -0.065 0.336 -0.022 0.532 -0.707 0.542 0.471 0.292 0.700 0.512 0.812 -0.471 -0.214 -0.185 0.869 -0.235 0.424 -0.462 -0.032 0.108 0.792 0.585 0.209 -0.444}	1	0	0	0	0	0
	{0.557 -0.524 -0.896 -0.276 -0.486...}	1	0	0	0	0	0
	{-0.233 0.917 -0.324 0.257 -0.045...}	0	1	0	0	0	0
	{0.228 0.354 0.075 0.975 -0.299...}	1	0	1	0	0	0
	{-0.556 0.830 0.048 -0.057 0.409...}	0	0	1	0	1	0
	{-0.650 0.276 -0.707 -0.277 0.097...}	0	0	0	0	0	1
	{0.462 0.628 0.324 0.184 -0.547...}	1	0	0	1	0	0
	{0.582 0.963 -0.042 0.268 -0.062...}	0	1	1	0	0	0
	{-0.618 -0.491 0.192 -0.360 -0.462...}	0	0	1	0	0	0
	{0.099 0.310 -0.950 -0.056 -0.087...}	1	0	0	0	0	0

Table 5: Data table showing Matrix values and Attributes for Degrees of 1 and 5

Sparsity	Matrix	Splitting	Equilibrium	Membrane	Jellyfish	Beetle	Worm
0.9	{-0.223, -0.000, 0.000, -0.822, 0.374 0.000, 0.816, -0.270, -0.128, -0.766 -0.272, 0.000, 0.170, -0.333, -0.835 -0.779, 0.000, -0.636, -0.473, 0.502 0.192, -0.132, -0.336, 0.039, -0.858}	0	1	1	0	0	0
	{-0.570 -0.000 -0.577 0.081 0.436...}	0	0	0	0	0	0
	{-0.774 0.365 -0.338 0.842 -0.238...}	1	0	1	0	0	0
	{0.965 0.728 -0.000 -0.658 0.357...}	0	0	1	0	0	0
	{0.987 0.615 -0.186 -0.266 0.608...}	0	0	1	0	0	0
	{-0.702 -0.000 -0.000 0.163 0.231...}	0	1	1	0	0	0
	{ -0.107 -0.000 0.238 0.909 0.926...}	0	0	1	0	0	0
	{-0.464 0.612 0.091 -0.322 -0.952...}	1	0	1	1	0	0
	{-0.638 0.666 0.472 -0.990 -0.571...}	0	0	0	0	0	0
	{0.243 -0.761 0.534 0.376 0.761...}	0	0	0	1	0	1
0.1	{-0.823, 0.000, 0.000, 0.019, 0.000 -0.000, -0.456, 0.000, 0.000, -0.000 -0.000, 0.000, 0.689, -0.000, -0.000 -0.000, 0.712, -0.000, 0.724, -0.000 -0.000, 0.000, -0.200, 0.000, 0.276}	0	0	0	0	0	0
	{0.632 0.000 0.000 0.000 0.000...}	0	0	1	0	0	0
	{0.268 -0.000 -0.000 -0.000 0.000...}	0	0	0	0	0	0
	{0.680 -0.000 -0.024 -0.000 0.000...}	0	0	0	0	0	0
	{-0.942 -0.000 -0.000 -0.970 0.000...}	1	0	0	1	0	0
	{-0.865 -0.000 -0.000 -0.000 0.000...}	1	0	0	1	0	0
	{0.363 -0.000 -0.000 0.000 0.000...}	1	0	0	0	0	0
	{-0.628 -0.000 -0.118 0.000 0.000...}	1	0	0	1	0	0
	{ -0.368 0.000 0.000 0.000 0.000...}	0	0	1	0	0	0
	{0.442 0.000 -0.000 -0.000 0.000...}	0	0	0	0	0	0

Table 6: Data table showing Matrix values and Traits for different sparsity levels

Assortativity	Matrix	Splitting	Equilibrium	Membrane	Jellyfish	Beetle	Worm
High	{ 0.402 -0.141 -0.233 -0.385 -0.262 -0.224 0.340 -0.428 -0.426 -0.420 -0.440 -0.244 0.202 -0.145 -0.172 -0.401 -0.119 -0.266 0.373 -0.126 -0.283 -0.149 -0.288 -0.347 0.433}	0	1	0	0	0	0
	{ 0.348 -0.251 -0.249 -0.307 -0.369...}	0	1	0	0	0	0
	{-0.774 0.365 -0.338 0.842 -0.238...}	0	1	0	0	0	0
	{0.438 -0.204 -0.410 -0.430 -0.135...}	0	1	0	0	0	0
	{0.467 -0.360 -0.228 -0.141 -0.302...}	0	1	0	0	0	0
	{0.216 -0.133 -0.198 -0.230 -0.399...}	0	1	0	0	0	0
	{0.470 -0.219 -0.333 -0.105 -0.347...}	0	1	0	0	0	0
	{0.251 -0.126 -0.101 -0.209 -0.327...}	0	1	0	0	0	0
	{0.290 -0.412 -0.220 -0.467 -0.472...}	0	1	0	0	0	0
	{0.414 -0.174 -0.385 -0.419 -0.329...}	0	1	0	0	0	0
Low	{-0.138 0.479 0.424 0.399 0.224 0.400 -0.272 0.255 0.460 0.248 0.280 0.372 -0.434 0.396 0.292 0.358 0.362 0.380 -0.230 0.454 0.390 0.325 0.367 0.235 -0.217}	0	1	0	0	0	0
	{-0.313 0.399 0.492 0.236 0.445...}	0	1	0	0	0	0
	{-0.471 0.229 0.459 0.319 0.372...}	0	1	0	0	0	0
	{0.680 -0.000 -0.024 -0.000 0.000...}	0	1	0	0	0	0
	{-0.446 0.254 0.304 0.443 0.410...}	0	1	0	1	0	0
	{-0.434 0.434 0.366 0.473 0.477...}	0	1	0	1	0	0
	{-0.200 0.297 0.267 0.253 0.227...}	0	1	0	0	0	0
	{-0.393 0.330 0.449 0.257 0.383...}	0	1	0	0	0	0
	{-0.469 0.320 0.253 0.325 0.392...}	0	1	0	0	0	0
	{-0.191 0.313 0.202 0.380 0.344...}	0	1	0	0	0	0

Table 7: Data table showing Matrix values and Attributes for high and mid Assortativity