Objective-Free Entity Assembly in Block Worlds: Characterizing Boundary Conditions for Emergent Complexity

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Abstract

Artificial life research predominantly relies on fitness functions or selection pressures to drive the emergence of complex structures, potentially biasing which forms of complexity can be discovered. We investigate whether structurally non-trivial entities can arise in an objective-free block world governed by randomly sampled local bonding rules, using Assembly Theory as a bias-free measurement framework. We introduce a two-dimensional toroidal grid world with three block types, stochastic bonding and drift dynamics, and an entity observatory that detects connected components, canonicalizes their graph structure via Weisfeiler–Leman hashing, and computes exact assembly indices through edge-removal dynamic programming. Across 5,000 simulations (1,000 rule tables $\times$ 5 seeds $\times$ 500 steps) yielding over 7 million entity observations and 282 unique entity types, we find that observed assembly indices are entirely explained by entity size: a bond-shuffle null model produces zero significant excess at every size class (1–6 blocks). The entity ecology is dominated by monomers (94.6%) and dimers (4.9%), with the maximum observed assembly index of 6 occurring only 18 times. These results establish a robust negative result: uniform random rule sampling with local bonding does not produce structurally non-trivial assembly, even at scale. We characterize this as a boundary condition for emergent complexity and discuss implications for the design of objective-free ALife systems that might cross this boundary.

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Data/Code available at: https://anonymous.4open.science/

Introduction

A persistent challenge in artificial life (ALife) research is that the complexity of emergent structures is often shaped—and potentially limited—by the objectives imposed on the system (Bedau et al., 2003; Taylor et al., 2016). Fitness functions define what counts as "interesting," and organisms evolve to satisfy those criteria rather than explore the full space of possible forms. Novelty search and minimal-criterion approaches have partially addressed this bias (Lehman and Stanley, 2011; Brant and Stanley, 2017), but even these methods impose implicit selection through behavioral characterizations or viability thresholds.

We ask a more radical question: can structurally complex entities arise in a system with no objective function—not even a novelty metric—when governed solely by randomly sampled local interaction rules? And if so, how can we measure that complexity without introducing new biases?

Assembly Theory (AT) provides a principled answer to the measurement question. Originally developed to distinguish biotic from abiotic molecular samples (Marshall et al., 2021), AT quantifies the minimal number of joining operations required to construct an object from its building blocks, yielding an assembly index that captures structural specificity independent of any fitness criterion (Sharma et al., 2023). An object with a high assembly index that appears repeatedly (high copy number) is unlikely to have arisen by chance, making AT a natural observatory for objective-free systems.

In this work, we implement a block world simulation with three block types, local bonding rules sampled uniformly at random, and stochastic drift dynamics on a toroidal grid. We detect entities as connected components of bonded blocks, canonicalize their graph structure, and compute exact assembly indices via edge-removal dynamic programming. We then apply a bond-shuffle null model to test whether observed assembly exceeds what would be expected from entity size alone.

Our central finding is a robust negative result: across 5,000 simulations producing over 7 million entity observations, the assembly index is entirely size-driven. No entity exhibits statistically significant excess assembly beyond what random bonding topology predicts. This result is itself a contribution: it establishes a con-

crete boundary condition for emergent complexity in objective-free systems and constrains the design space for future work seeking to cross that boundary.

Methods

Block World Model

The simulation takes place on a two-dimensional toroidal grid of size 20×20. The world is populated with $N = 30$ blocks, each assigned one of three types: M (membrane), C (cytosol), or K (catalyst). Block types are drawn uniformly at random at initialization.

At each time step, blocks undergo two phases: bonding and drift. During bonding, each block observes its von Neumann neighbors (Manhattan distance ≤ 1) and may form a bond with an adjacent block according to a shared rule table. During drift, each block moves to a random adjacent cell; bonds between blocks that become non-adjacent after drift are pruned, implementing a bond-motion invariant where bonds break on separation rather than constraining movement.

Rule Table

Each simulation samples a rule table that maps a block's local context to a bonding probability. The context is defined by a triple $(\text{self\_type}, \text{neighbor\_count}, \text{dominant\_type})$, where neighbor_count is the number of occupied von Neumann neighbors (0–4) and dominant_type is the most common block type among those neighbors (with ties broken deterministically). This yields $3 \times 5 \times 4 = 60$ entries (the factor of 4 for dominant_type includes a "none" category when no neighbors are present). Each entry's bonding probability is drawn independently from $\text{Uniform}(0, 1)$.

Entity Detection and Canonicalization

At each time step, entities are detected as connected components in the graph induced by active bonds. Each entity is represented as an undirected graph $G = (V, E)$ where vertices are blocks (labeled by type) and edges are bonds. Entity types are canonicalized using the Weisfeiler–Leman graph hash (Weisfeiler and Leman, 1968) with block type as a node attribute, implemented via NetworkX (Hagberg et al., 2008). The SHA-256 digest of this hash serves as a unique type identifier, enabling efficient deduplication across simulations.

Assembly Index Computation

For each unique entity type, we compute the assembly index a_i. Given an entity graph G with $|E|$ edges, the assembly index is defined as the minimum number of edge-addition steps required to construct G from isolated vertices, where each step adds one edge. For a
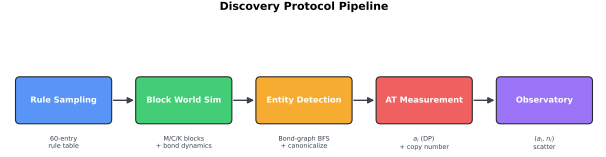
Figure 1: Experimental pipeline. Random rule tables govern block bonding on a toroidal grid. Connected components are detected as entities, canonicalized via graph hashing, and measured by assembly index and copy number. A bond-shuffle null model tests for excess assembly.

complete graph K_n, this equals $\binom{n}{2}$; for a tree on n vertices, $a_i = n - 1$.

We compute a_i exactly via edge-removal dynamic programming—the dual of the construction definition. The algorithm enumerates all subsets of edges via bitmask DP. For each subset $S \subseteq E$, it checks whether the induced subgraph is connected and whether it can be decomposed into two connected subgraphs that share at least one edge. The assembly index is the minimum over all valid decompositions of the maximum depth of the decomposition tree. This is exact for the entity sizes observed in our experiments (up to 6 blocks).

Null Model

To test whether observed assembly indices reflect structural specificity beyond what entity size alone predicts, we implement a bond-shuffle null model (Gotelli and Graves, 2013). For each entity graph G, we generate $n_{\text{shuffle}} = 20$ randomized graphs by applying double-edge swaps (Hagberg et al., 2008) that preserve the degree sequence. We then compute the assembly index of each shuffled graph and report the null distribution $(\mu_{\text{null}}, \sigma_{\text{null}})$.

An entity exhibits significant excess assembly if its observed a_i exceeds $\mu_{\text{null}} + 2\sigma_{\text{null}}$. This threshold corresponds to a one-sided $p < 0.023$ under normality.

Experimental Protocol

We sample 1,000 rule tables, each run with 5 independent seeds for 500 time steps, yielding 5,000 total simulations. Entity observations are logged at every step, producing a combined dataset of over 7 million observations. The full pipeline is illustrated in Figure 1.

Results

Discovery Baseline

Across all 5,000 simulations, we observe 7,079,166 entity instances comprising 282 unique entity types. The vast majority of observations are monomers: 94.6% of entities consist of a single block ($a_i = 0$), 4.9% are
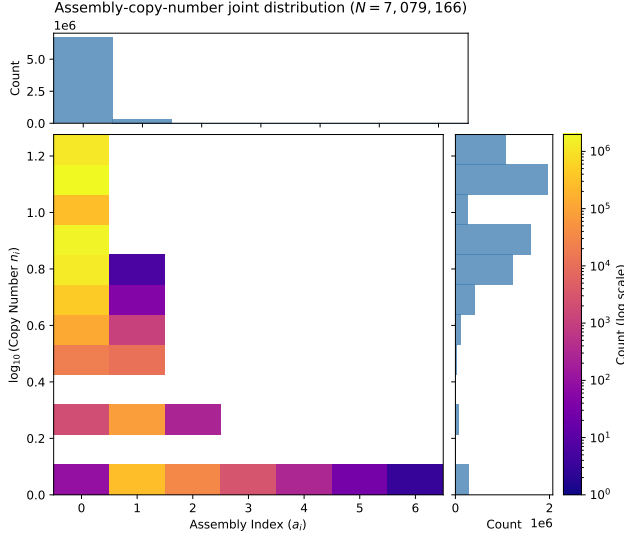
Figure 2: Joint distribution of assembly index (a_i) and copy number (n_i) across 7M entity observations. Color encodes log-frequency. The distribution is dominated by monomers ($a_i = 0$) with high copy numbers.

dimers (2 blocks, $a_i = 1$), and only 0.5% have 3 or more blocks. The maximum observed entity size is 6 blocks (18 instances out of 7M), with a corresponding maximum assembly index of 6.

Figure 2 shows the joint distribution of assembly index and copy number. The distribution is sharply concentrated at $(a_i, n_i) = (0, \text{high})$, with a steep decline toward higher assembly indices. The mean assembly index across all observations is 0.060, reflecting the dominance of trivial structures.

Entity Size Distribution

Figure 3 shows the entity size distribution on a logarithmic scale. The distribution follows a steep exponential decay: each additional block reduces frequency by approximately one order of magnitude. This indicates that the bonding dynamics under uniform random rules strongly favor small entities, with multi-block structures being rare transient configurations rather than stable persistent objects.

Entity Gallery

Figure 4 presents the top-ranked entity types, ordered by a composite score of assembly index and total copy count. The highest-ranked entities are all dimers ($a_i = 1$) with very high copy counts (up to 108,352 across all simulations). Trimers with $a_i = 2$ appear in the top 10, but no entity with $a_i \geq 3$ reaches high copy numbers. The entity ranking is stable across experimental scales: the same entity types dominate at both 100 and
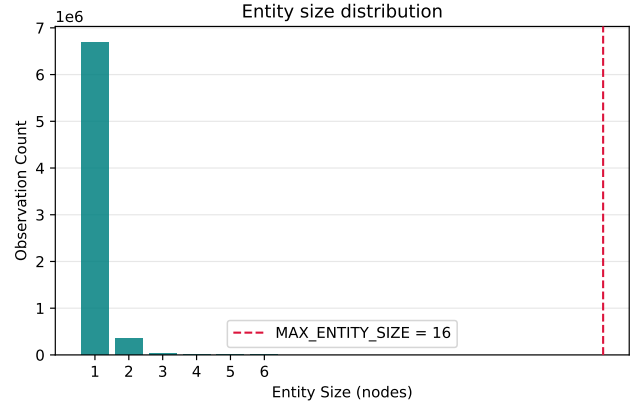

Figure 3: Entity size distribution across all observations (log scale). Each additional block reduces frequency by $\sim 10 \times$. Size-1 entities account for 94.6% of all observations.
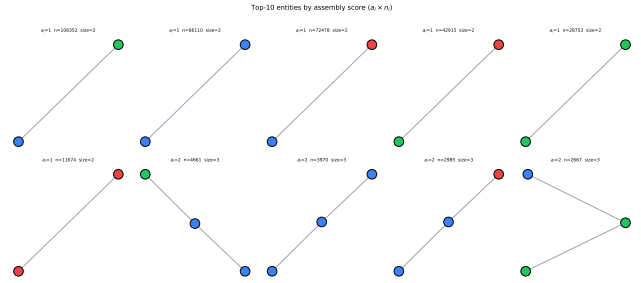

Figure 4: Gallery of top-ranked entity types by $a_i \times n_i$ score. Node colors indicate block type (M: blue, C: green, K: red). The top entities are all dimers; larger structures are rare and low-copy.

1,000 rule samples, suggesting that the emergent entity ecology is deterministic and convergent under uniform random rule sampling.

Assembly Audit: Null Model Comparison

The bond-shuffle null model reveals that observed assembly indices are entirely explained by entity size. Figure 5 shows the distribution of observed versus null assembly indices. Across all 7,079,166 observations, zero entities exhibit significant excess assembly ($a_i > \mu_{\text{null}} + 2\sigma_{\text{null}}$). The mean excess is exactly 0.000 at every entity size class (1–6 blocks).

This result is robust across scales. A smaller pilot experiment (100 rules × 3 seeds, 170,192 observations) produced the same 0% excess, and the 10× scale-up confirms the finding with no change in the null model gap. Table 1 summarizes the comparison.
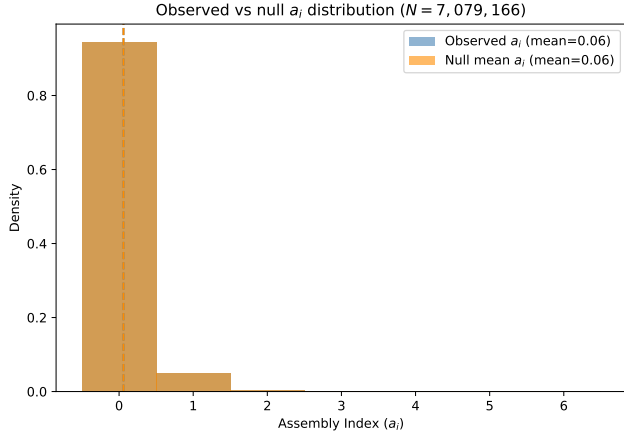
Figure 5: Assembly audit: observed a_i versus null model expectation. Zero entities (0 of 7M) show significant excess assembly. The observed assembly is fully explained by the number of edges in each entity graph.

Metric	Small scale	Large scale
Rule samples	100	1,000
Seeds per rule	3	5
Total simulations	300	5,000
Entity observations	170,192	7,079,166
Unique types	72	282
Max entity size	6	6
Max a_i	6	6
Mean a_i	0.058	0.060
Significant excess	0.0%	0.0%

Table 1: Comparison of small-scale and large-scale experiments. The negative result (0% excess assembly) is stable across a $41\times$ increase in observations.

Discussion

Why Assembly is Size-Driven

The central finding—that assembly index is entirely predicted by entity size under uniform random bonding rules—has a clear mechanistic explanation. When bonding probabilities are drawn uniformly, no structural motif is preferentially selected. The topology of each entity graph is effectively random given its size, and the assembly index of a random graph is determined by its edge count (which scales with size). The null model, which preserves edge count while randomizing topology, therefore matches observed assembly exactly.

This result does not mean that Assembly Theory is unsuitable for ALife systems. Rather, it identifies a necessary condition for non-trivial assembly: the bonding rules must introduce structural bias—preferential for-

mation of specific motifs over random topologies. Uniform random rule sampling, by construction, does not provide such bias.

Implications for Objective-Free ALife

The negative result constrains the design space for objective-free systems seeking emergent complexity:

1. Rule structure matters. Uniformly random rules produce entities but not complex ones. To cross the complexity boundary, rule sampling must be biased toward structural specificity—for example, by conditioning bond formation on multi-hop neighborhood patterns or by introducing catalytic mechanisms where specific block configurations promote bonding.

2. Scale does not substitute for structure. A $41\times$ increase in observations produces $3.9\times$ more entity types but no increase in structural complexity (maximum a_i remains 6, excess remains 0%). More computation yields more copies, not more complex entities.

3. The entity ecology is convergent. The same entity types dominate across independent rule samples, suggesting that the system's emergent ecology is a fixed point of the uniform random sampling distribution rather than a sample-dependent phenomenon.

Boundary Conditions for Emergent Complexity

We interpret these results as characterizing a boundary condition for emergent complexity in objective-free systems. Below this boundary, defined by uniform random local bonding rules on a small grid with few block types, entity assembly is fully explained by size. Crossing this boundary likely requires one or more of: (1) biased rule sampling that favors specific structural motifs, (2) larger grids or higher block densities that increase collision rates, (3) explicit catalytic mechanisms where existing entities promote the formation of specific structures, or (4) environmental gradients that create spatial heterogeneity in bonding conditions.

Each of these represents a departure from the fully objective-free, uniformly random baseline—but they need not introduce fitness functions. Catalytic rules, for example, can be sampled from a biased distribution without defining what constitutes a "good" entity. This suggests a continuum between fully random and fully optimized systems, with non-trivial assembly emerging somewhere along this continuum.

Relation to Prior Work

The observation that random dynamics produce trivial structures resonates with classical results in cellular

automata, where most random rules produce either homogeneous or chaotic behavior, with complex dynamics concentrated at the "edge of chaos" (Langton, 1990; Wolfram, 2002). Our work extends this observation to the domain of compositional objects measured by Assembly Theory, showing that the analogous "edge" for assembly complexity has not been reached under uniform random bonding rules.

The negative-result framing aligns with recent calls for publishing null findings in computational science (Fanelli, 2012). Understanding where complexity does not emerge is as informative as finding where it does, particularly for constraining the design space of future experiments.

Limitations

Several limitations should be noted. First, the grid size (20×20) and block count (30) are modest; larger systems may exhibit qualitatively different dynamics. Second, the rule table conditions on only the immediate von Neumann neighborhood; richer observation ranges could enable more structured bonding. Third, our assembly index computation uses exact edge-removal DP, which does not allow sub-object reuse—a property that Assembly Theory in its full formulation permits. Finally, the three block types may be insufficient to support the combinatorial diversity needed for non-trivial assembly.

Conclusion

We have presented the first systematic application of Assembly Theory to an objective-free artificial life system. Across 5,000 simulations and 7 million entity observations, we find that uniform random bonding rules produce a stable entity ecology but no structurally nontrivial assembly: observed assembly indices are entirely explained by entity size, with zero significant excess over a bond-shuffle null model.

This robust negative result is itself a contribution. It establishes that emergent structural complexity requires more than random local interactions—it requires structural bias in the rules, even in the absence of explicit fitness functions. By characterizing this boundary condition, we constrain the design space for future objective-free ALife systems and provide a concrete experimental baseline against which interventions (catalytic rules, biased sampling, environmental gradients) can be measured.

Acknowledgements

References

Bedau, M. A., McCaskill, J. S., Packard, N. H., Rasmussen, S., Adami, C., Green, D. G., Ikegami, T., Kaneko, K., and Ray, T. S. (2003). Open problems in artificial life. Artificial Life, 9(3):241–252.

Brant, J. C. and Stanley, K. O. (2017). Minimal criterion coevolution: A new approach to open-ended search. In Proceedings of the Genetic and Evolutionary Computation Conference (GECCO), pages 67–74. ACM.

Fanelli, D. (2012). Negative results are disappearing from most disciplines and countries. Scientometrics, 90(3):891–904.

Gotelli, N. J. and Graves, G. R. (2013). Null Models in Ecology. Smithsonian Institution Press.

Hagberg, A. A., Schult, D. A., and Swart, P. J. (2008). Exploring network structure, dynamics, and function using NetworkX. In Proceedings of the 7th Python in Science Conference (SciPy), pages 11–15.

Langton, C. G. (1990). Computation at the edge of chaos: Phase transitions and emergent computation. Physica D, 42:12–37.

Lehman, J. and Stanley, K. O. (2011). Abandoning objectives: Evolution through the search for novelty alone. Evolutionary Computation, 19(2):189–223.

Marshall, S. M., Mathis, C., Carber, E., Keenan, G., Cooper, G. J. T., Graham, H., Craven, M., Gromski, P. S., Moore, D. G., Walker, S. I., and Cronin, L. (2021). Identifying molecules as biosignatures with assembly theory and mass spectrometry. Nature Chemistry, 13:692–698.

Sharma, A., Czegel, D., Lachmann, M., Kempes, C. P., Walker, S. I., and Cronin, L. (2023). Assembly theory explains and quantifies selection and evolution. Nature, 622:321–328.

Taylor, T., Bedau, M., Channon, A., Ackley, D., Banzhaf, W., Beslon, G., Dolson, E., Froese, T., Hickinbotham, S., Ikegami, T., McMullin, B., Packard, N., Rasmussen, S., Virgo, N., Agmon, E., Clark, E., McGregor, S., Ofria, C., Ropella, G., Spector, L., Stanley, K. O., Stanton, A., Timperley, C., Vostinar, A., and Wiser, M. (2016). Open-ended evolution: Perspectives from the OEE workshop in York. Artificial Life, 22(3):408–423.

Weisfeiler, B. and Leman, A. (1968). The reduction of a graph to canonical form and the algebra which appears therein. NTI, Series 2, 9:12–16.

Wolfram, S. (2002). A New Kind of Science. Wolfram Media.