Directing Open-Ended Evolution in Artificial Life via Temporal Multi-Scale Structural Complexity

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Abstract. Open-ended evolution (OEE) in artificial life is typically driven by uninterpretable, non-transferable neural-network metrics that cannot be connected to physical theory—and previously generated complex behaviors have never been characterized quantitatively in terms of their multi-scale dynamical structure. We introduce T-MSSC (Temporal Multi-Scale Structural Complexity), a renormalization-group-inspired scalar that asks: can a single explicit formula simultaneously serve as an evolutionary fitness function *and* reveal the physical signatures underlying life-like complexity? T-MSSC measures how Lagrangian particle trajectory dynamics diversify across timescales via Sliced Wasserstein distances in Flow-Lenia. As a fitness function it generates multi-species ecologies comparable to NN-optimized baselines from a three-line formula; as an analytical lens it enables *causal* diagnosis, revealing that evolved systems spontaneously satisfy two physics-derived life criteria: dynamical scale separation and high frustration. The formula is transferable to any system with trackable particles.

1 Introduction

A central goal of ALife is open-ended evolution—the sustained generation of novel forms and behaviors [3, 5]. Neural-network-based open-endedness metrics drive this effectively but are black boxes: they yield results without principles and cannot be connected to physical theories of complexity. Multi-Scale Structural Complexity (MSSC) offered a physics-grounded alternative for static spatial patterns [1], but life is inherently dynamic. We extend MSSC temporally, replacing the spatial coarse-graining scale λ with observational window W, and ask: can a single explicit scalar simultaneously *optimize* for complexity and *reveal* its physical basis?

We validate T-MSSC in Flow-Lenia [4], a continuous cellular automaton supporting diverse life-like gliders. T-MSSC optimization produces ecologies with co-existing organisms that independently satisfy the scale-separation and frustration criteria of Vanchurin et al. [6]—hallmarks of living systems never optimized for directly.

2 Method

Lagrangian tracking. We inject 8,000 passive tracer particles into the Flow-Lenia mass field at t=0 and track trajectories $\mathbf{x}_i(t)$ for ∼20,000 steps. Lagrangian tracking avoids Eulerian grid noise and yields stable per-particle velocity distributions. For particle i, window W, and lag τ:

$$p_i(W,\tau) = \left\{ \frac{\mathbf{x}_i(t+\tau) - \mathbf{x}_i(t)}{\tau} : t \in W \right\}$$

Diversity metric. Mean pairwise dissimilarity across particles is measured via Sliced Wasserstein-1 (SW_1, pair-subsampled). Subtracting a null baseline $\tilde{H}_0$ (trajectory-label shuffle within each window) isolates intrinsic population heterogeneity:

$$\Delta H(W,\tau) = \mathbb{E}_{i\neq j}[\mathrm{SW}_1(p_i,p_j)] - \tilde{H}_0(W,\tau) \geq 0$$

T-MSSC aggregator. Fixing τ^*≈3,000 steps (glider self-crossing timescale), ΔH is evaluated over logarithmically spaced sub-windows $\{W_k\}$ within the full run:

$$\text{T-MSSC} = \sum_{k<k'} |\Delta H(W_k,\tau^*) - \Delta H(W_{k'},\tau^*)|$$

High T-MSSC indicates that dynamical structure changes substantially across timescales—a signature of hierarchical complexity. A gradient-free evolutionary algorithm optimizes Flow-Lenia kernel parameters to maximize T-MSSC.

3 Results

(C1) Separates complex from random. Optimized systems score significantly higher than random

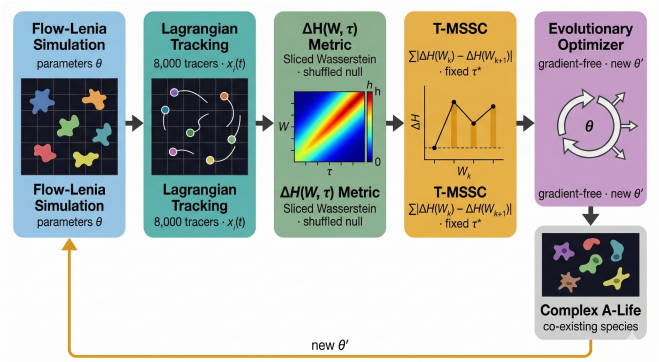

Figure 1: Pipeline: Lagrangian tracking → $\Delta H(W, \tau)$ heatmap → T-MSSC aggregation → evolutionary loop → complex simulation output.

controls in both ΔH magnitude and cross-window variance; random systems yield near-zero T-MSSC.

(C2) ΔH tracks biological events. Spikes in $\Delta H(t)$ correlate temporally with species-turnover events (glider emergence/extinction), confirming the metric captures meaningful system-level dynamics.

(C3) Scale separation at τ^*. Velocity distributions p_i at $\tau^* \approx 3{,}000$ steps split into slow (glider-core) and fast (medium/periphery) clusters—a quantitative signature of the Vanchurin/Katsnelson scale-separation life criterion [6].

(C4) Matches NN-OEE quality. T-MSSC-optimized worlds develop multi-species ecologies (collision, replication, predation) comparable in richness to NN-based OEE [5], arising from a three-line formula instead of a trained network.

(C5) Frustration signature. High-T-MSSC systems show elevated frustration (blockwise vs. global re-optimization gap)—the second Vanchurin/Katsnelson life criterion.

4 Conclusion

T-MSSC is the first interpretable, formula-based metric that both *directs* open-ended evolution and *diagnoses* its physical structure. The systems it selects satisfy scale separation and frustration—two independent life criteria—without being optimized for either. This establishes a principled bridge between ALife and the statistical physics of complexity, opening causal investigations inaccessible to black-box approaches.

References

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