

Information-theoretic Limits on Programmatic Specification of Biological Systems

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Executive Summary

This paper provides a rigorous information-theoretic proof that an organism genome plus environmental signals is provably insufficient to deterministically specify its own microstate trajectory. The genome acts as a generator specification (a hockey coach game plan) rather than a trajectory program (figure-skating choreography). The gap is filled by a shared physical substrate Φ (the universal compiler) that compiles the coarse spec into a functioning organism via physics at runtime.

QNFO Relevance: HIGH - Structural Consilience with Autaxys OC

This paper arrives at the same structural conclusion as Autaxys Ontological Closure from biology rather than physics:

- Finite genomic specification ($C_G \leq 2n$ bits) = finite D/R procedure
- Coarse-graining threshold $C^*(B)$ = computable modulus of convergence boundary
- Universal compiler Φ = shared physical substrate
- Generator specification (not trajectory program) = compilation (not execution)

Layer mapping: Layer 4 (Information Theory) DIRECT $\rightarrow$ Layer 5 (Autaxys) STRONG $\rightarrow$ Layer 6 (Physics = Computable Reals) MEDIUM

Key Technical Contributions

- Dual Hartley/Shannon entropy faces for the coarse-graining threshold
- Runtime-randomness lemma (bits relocated to runtime must still be consumed)
- Initial-condition mixing lemma (Laplacian-demon loophole closed)
- Zero-error addressability proposition (pigeonhole for deterministic spec)
- Environmental rescue impossibility across 7 physical modalities

Empirical Validation

Five worked cases: E. coli proteome (3-24x genomic budget gap), Drosophila Bicoid morphogen (~ 1.5 bits/nucleus), C. elegans descriptor ladder (threshold crossed at voxel $\Delta = 0.10\mu\text{m}$), AlphaFold-2 cross-organism compression, JCVI-syn3A 4D whole-cell simulation.

Assessment

- Rigor: Mathematical proofs complete (31-page supplementary)

- Reproducibility: Open-source code with fixed seeds and YAML configs
- Peer review: bioRxiv preprint, not yet peer-reviewed
- Companion code: github.com/yuj1r0/itol (MIT, Python ≥ 3.10)