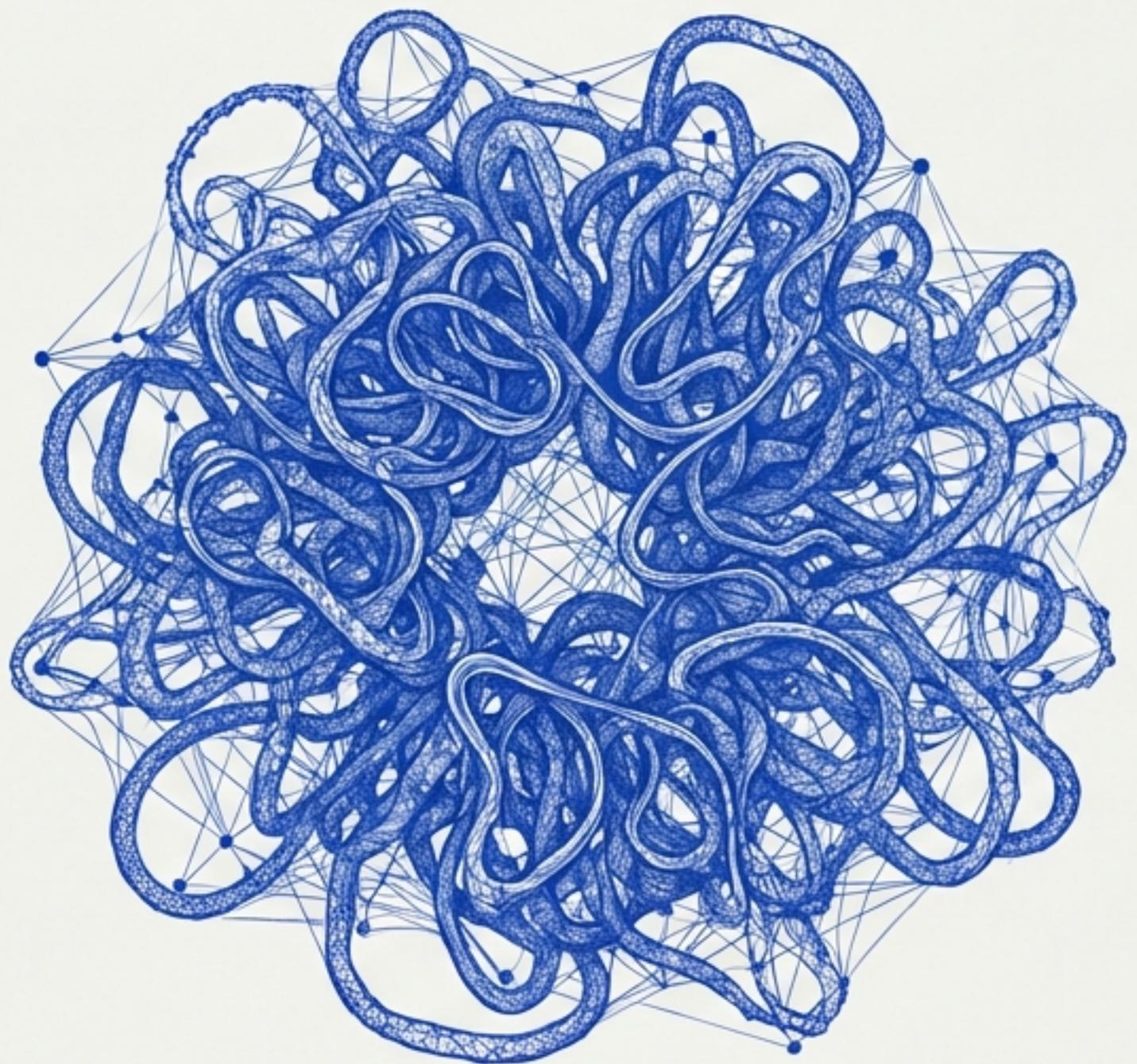


The Genomic Weight Thesis: A Rigorous Post-Mortem

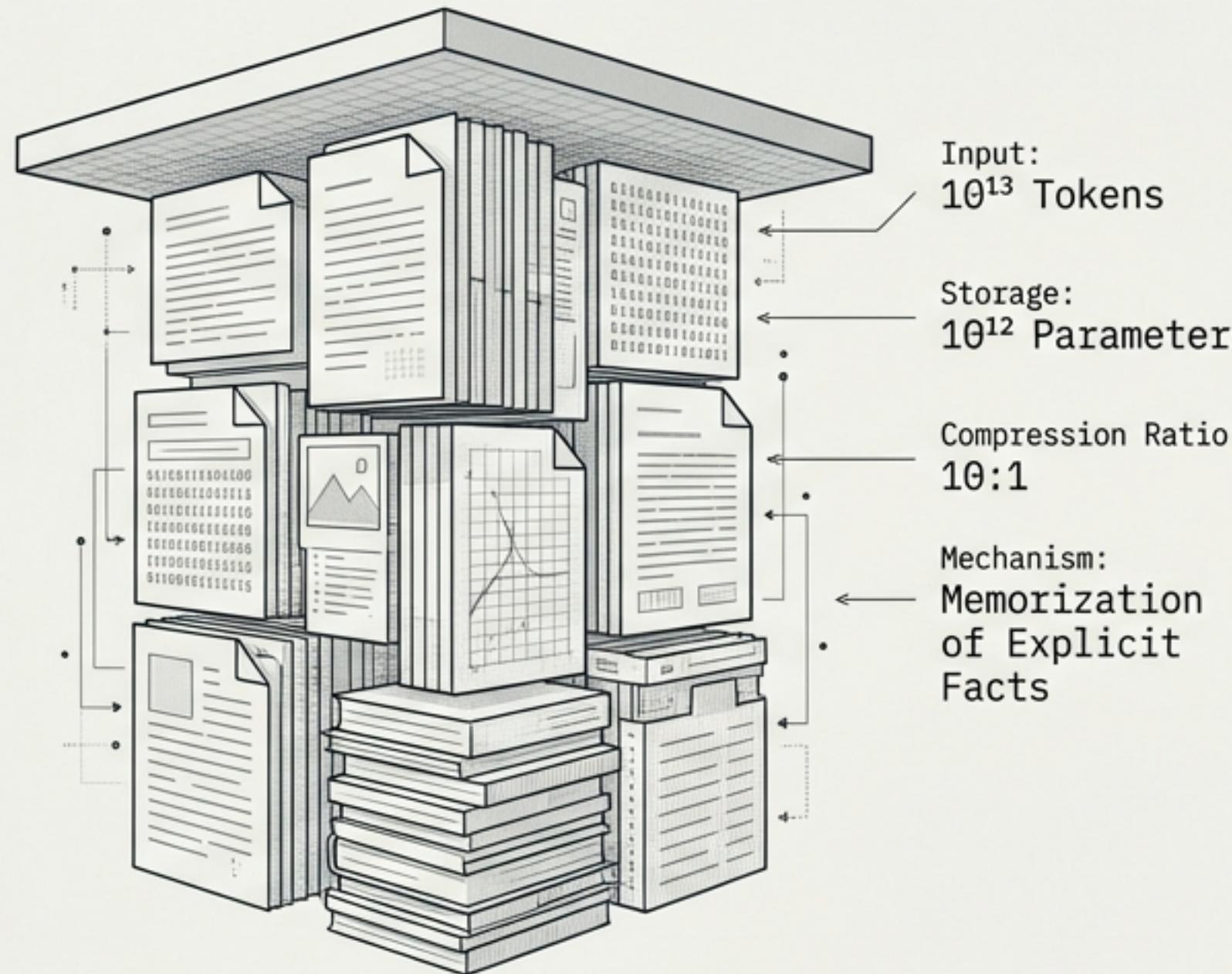
Testing DNA-Inspired Relational Compression
as an Inductive Bias for Neuroevolution.



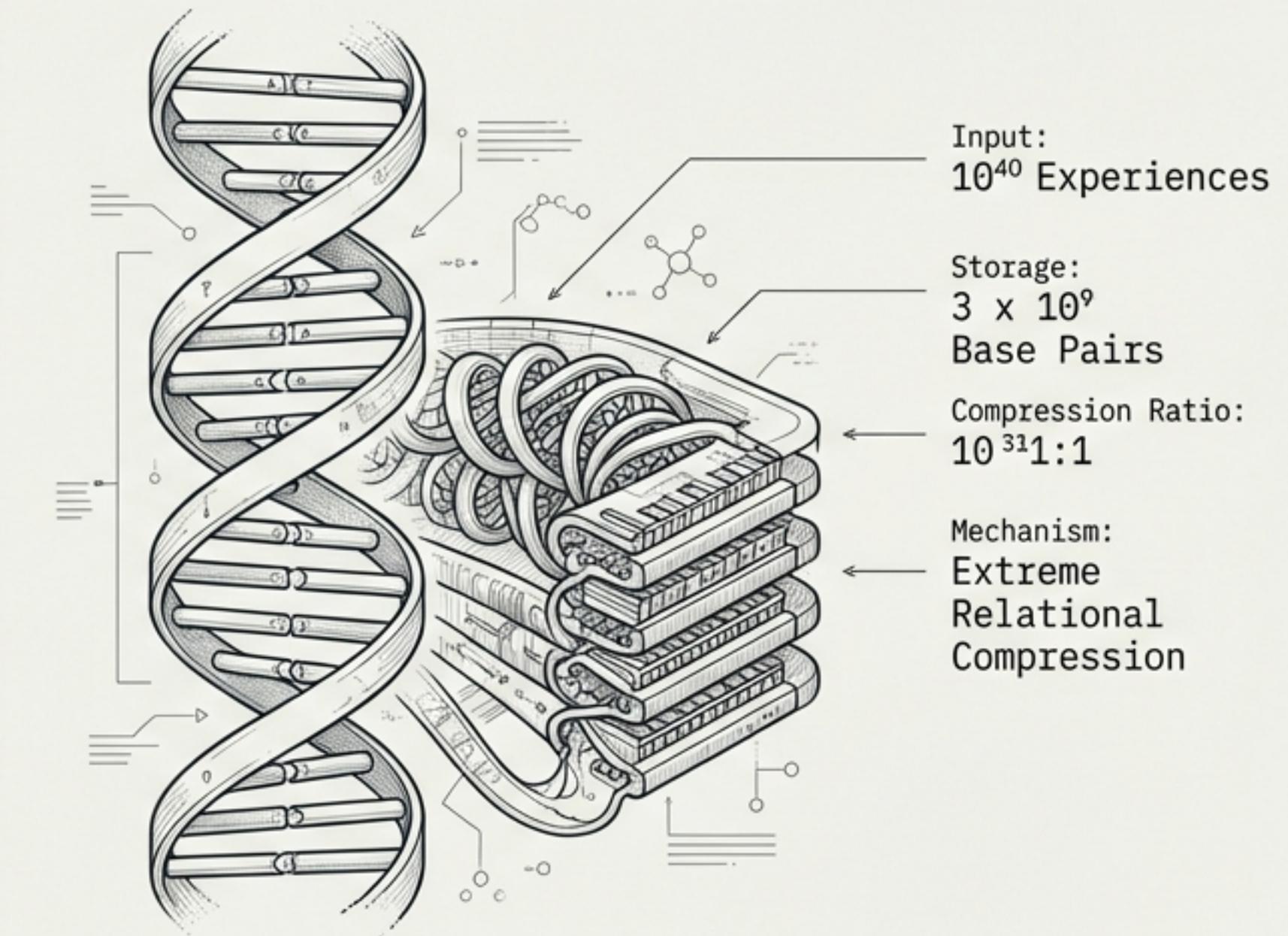
0.45	-0.21	1.02	0.00	-0.88	0.33
0.67	-0.15	0.99	0.12	-0.45	-0.33
0.67	-0.33	0.28	-0.11	0.12	0.58
0.76	0.05	-0.92	0.44	-0.61	0.19
0.25	0.42	-0.39	0.33	1.03	-0.33
0.56	-0.32	0.11	0.06	-0.34	-0.25
0.76	0.05	-0.92	0.44	-0.61	0.19
0.43	0.25	-0.92	0.44	-0.61	0.19
0.45	0.05	-0.92	0.44	-0.61	0.19
0.33	0.67	0.12	0.50	0.33	0.67
0.99	-0.45	-0.33	0.34	0.84	-0.11
0.28	0.12	0.11	0.34	0.16	0.05
0.76	0.05	-0.33	0.11	0.72	0.11
0.05	0.05	-0.92	0.44	-0.61	0.19

The Context: The Data Horizon

Digital Intelligence



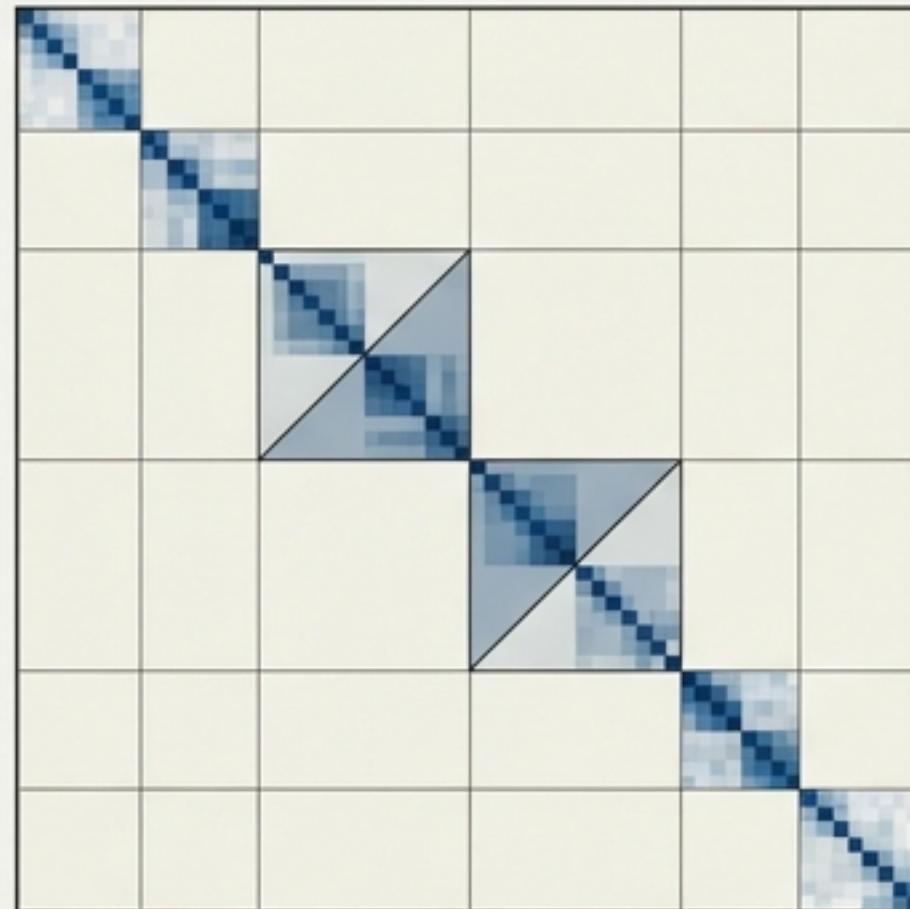
Biological Intelligence



The Zador Paradox: The genome (3GB) cannot specify the connectome (10^{14} synapses). It must be an algorithmic generator, not a blueprint.

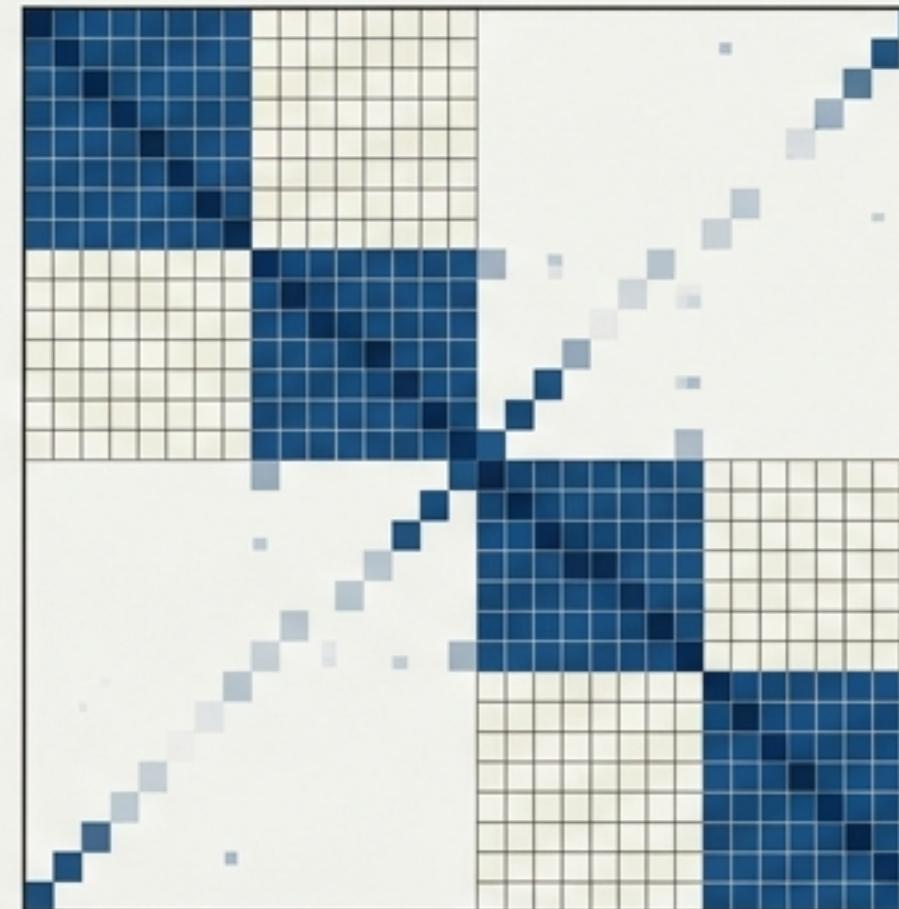
The Hypothesis: DNA as Algorithm

**Stage 1.
Biological Source**



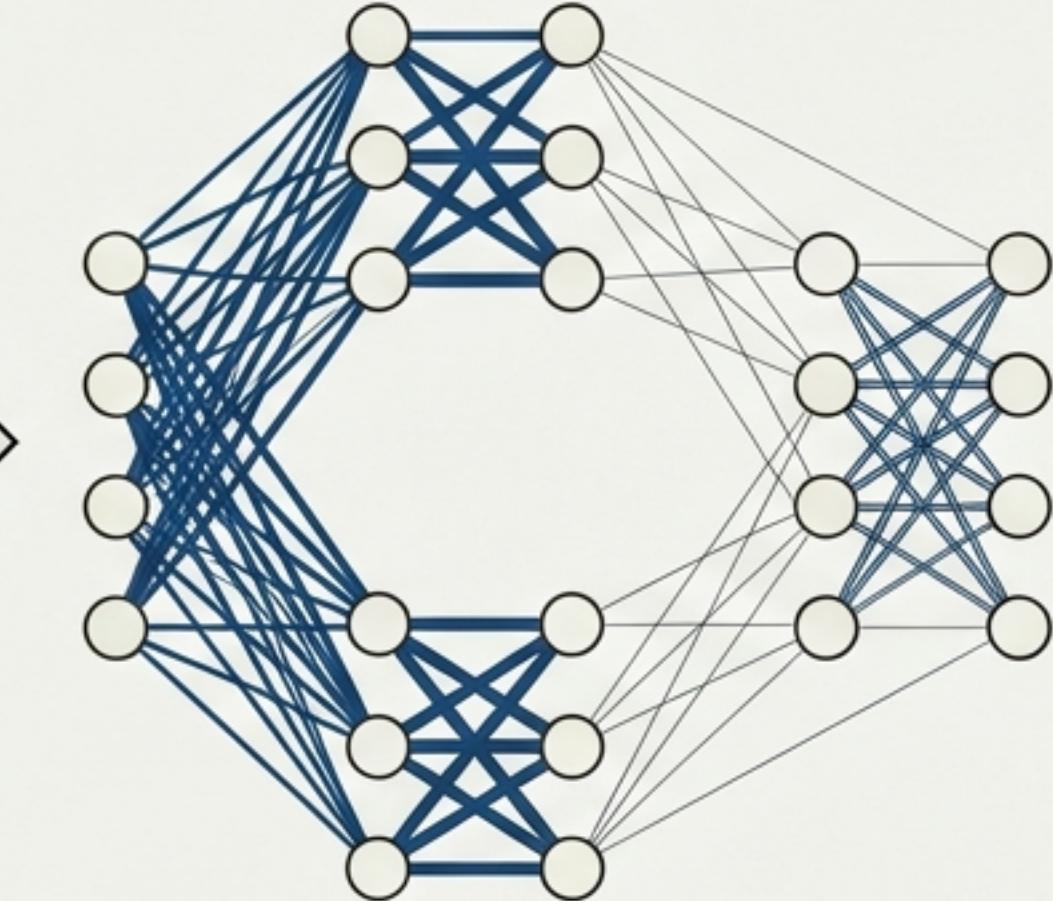
Chromatin Folding
(Proximity = Function).

**Stage 2.
Mathematical Translation**



Adjacency Matrix &
Distance Penalty

**Stage 3.
Computational Prediction**

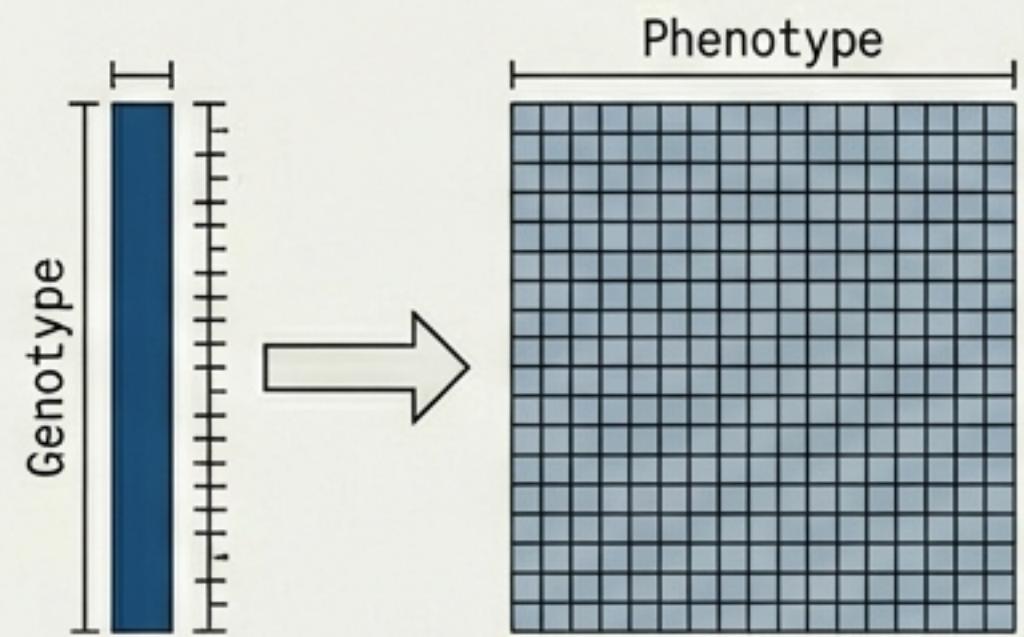


Topological Weights

Prediction: Constraining networks with chromatin-like topology (bottlenecks + distance costs) forces the learning of generalized solutions.

Methodology: Three Compression Strategies

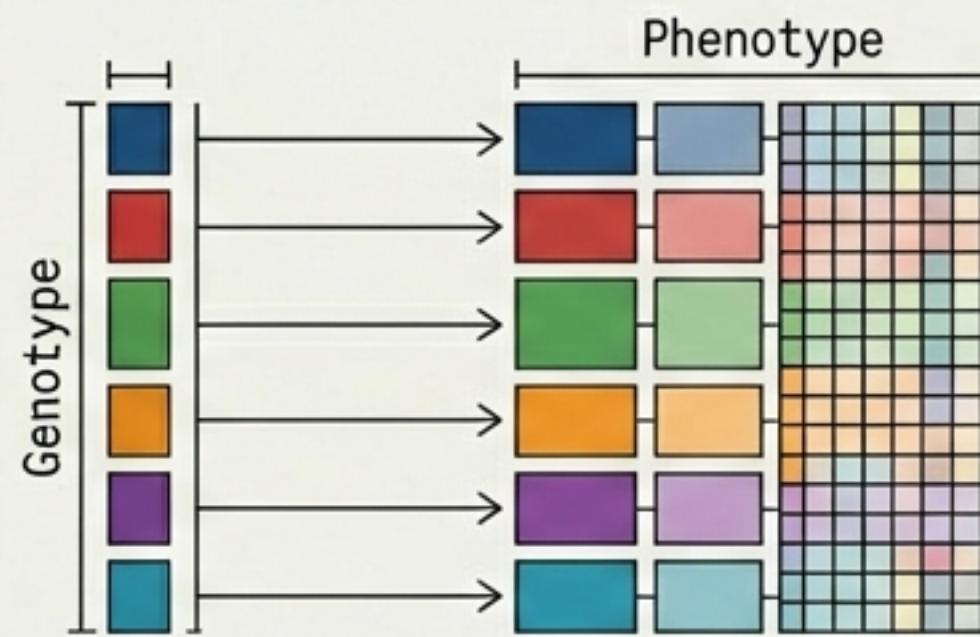
Flat (Control)



Direct Encoding.
No Constraints.
Zador Baseline.

5.2M

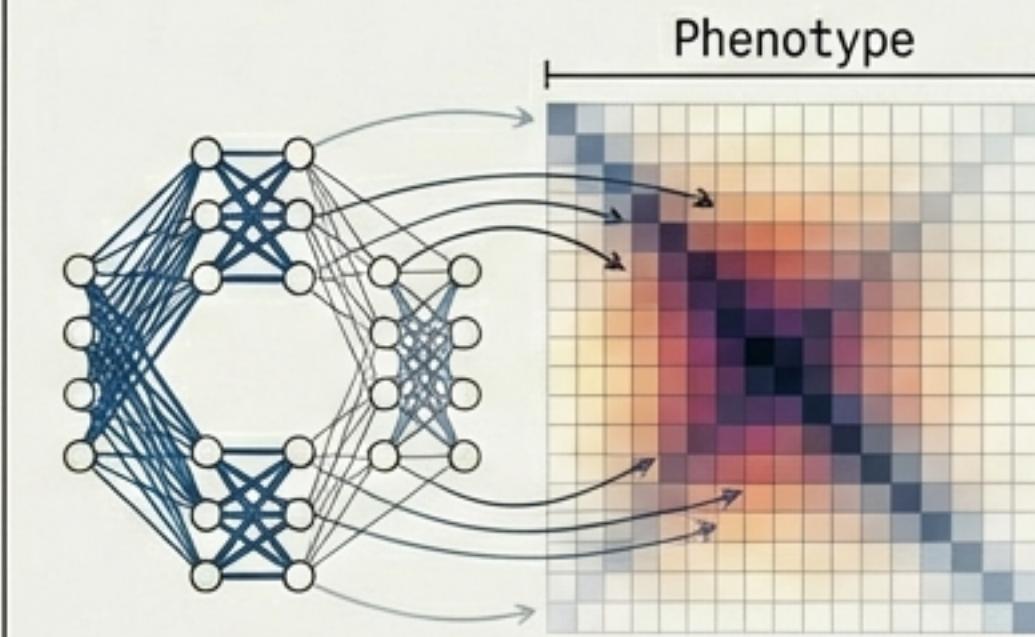
Hierarchical (TAD-Inspired)



Modular Blocks (8x128).
Mimics TADs.

1.2M (4.4x Compression)

Topological (Chromatin-Inspired)

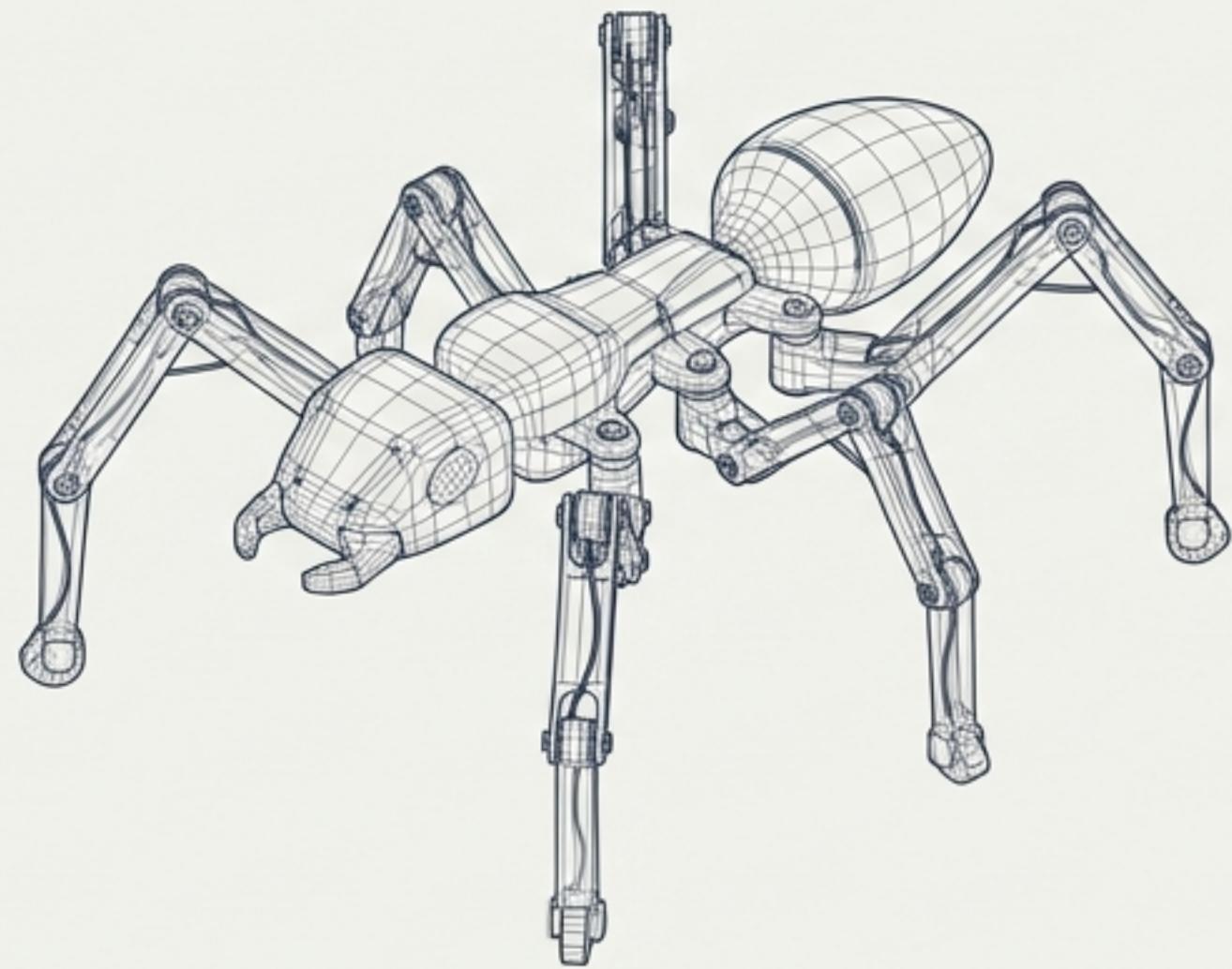


Distance-Based Cost.
Mimics Chromatin Physics.

0.6M (8.7x Compression)

The Testbed: Physics Environments

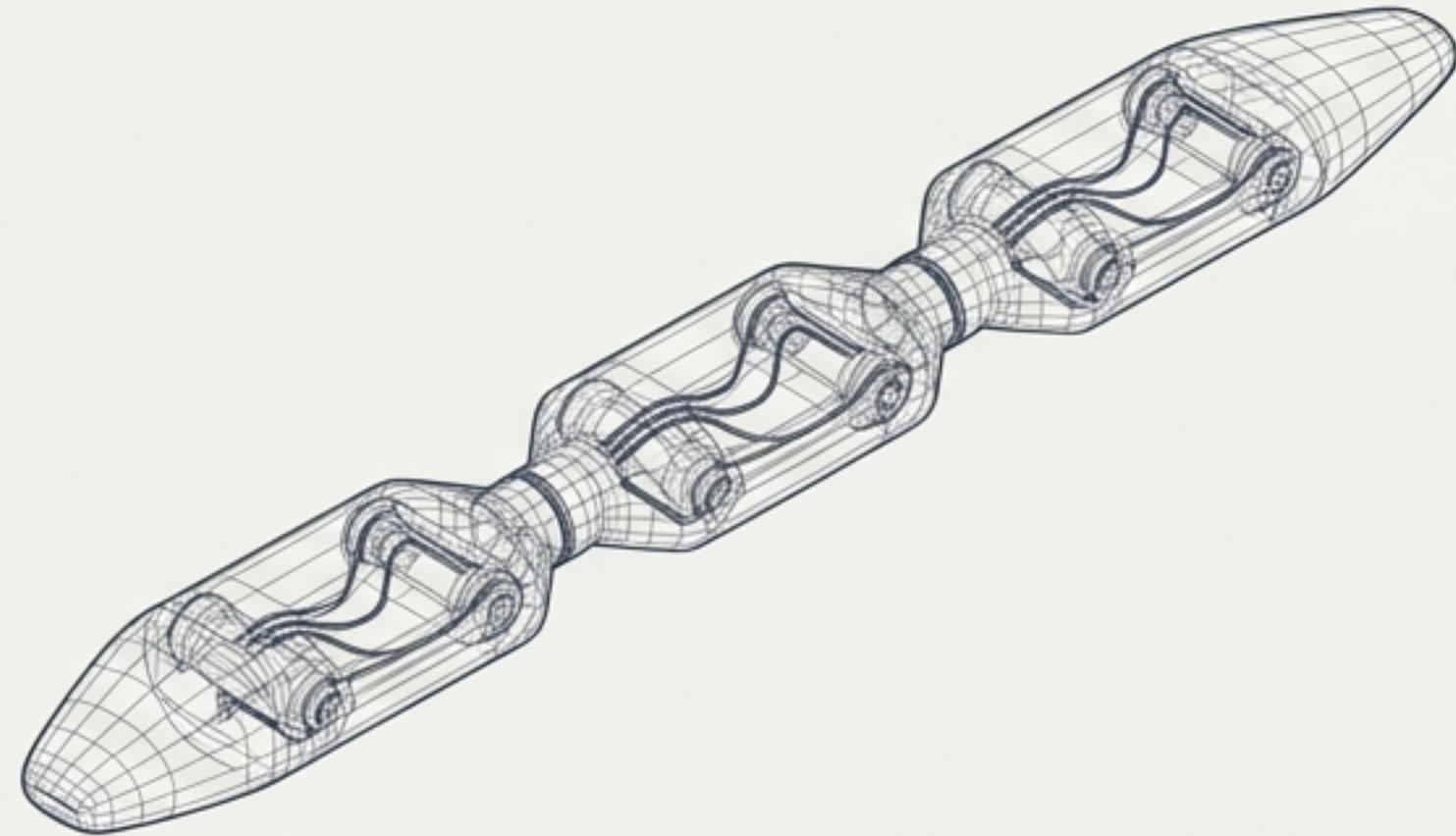
The Baseline: Brax Ant



Standard Locomotion. No obvious modular structure.

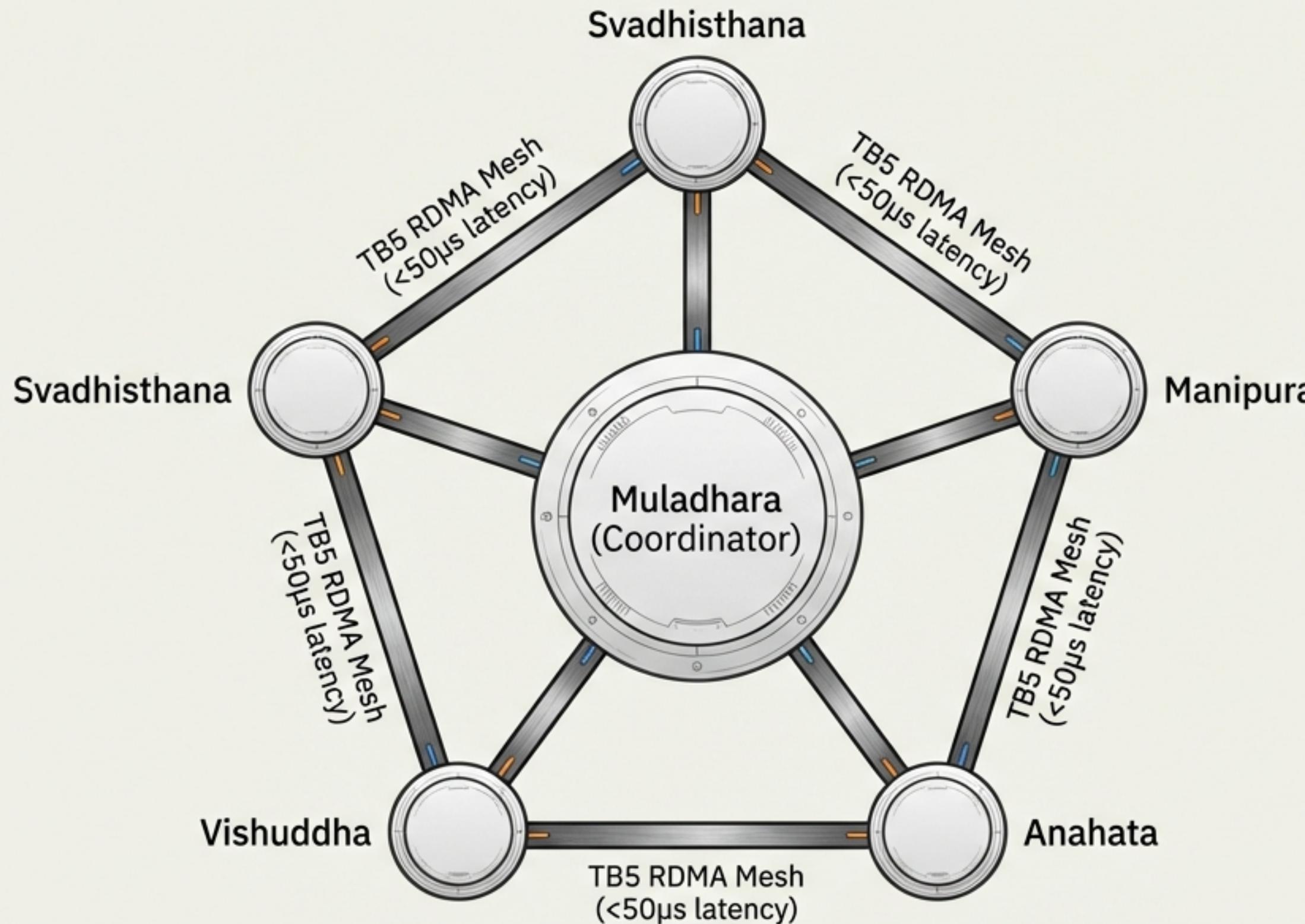
Task 3: Multi-Task Ant. Single genotype must solve 4 directional objectives ($+x$, $-x$, $+y$, $-y$) simultaneously.

The Modularity Trap: Brax Swimmer



Repeated Segment Structure. Theory predicts Hierarchical encoding should dominate here.

The Engine: ‘Chakra’ Cluster Architecture



- Hardware: 5x Apple M3 Ultra
- Memory: 128GB Unified per Node (Zero-Copy)
- Stack: JAX + EvoTorch + MJX
- Throughput: 6,500+ env steps/sec/node

Primary Result: Hypothesis Failed

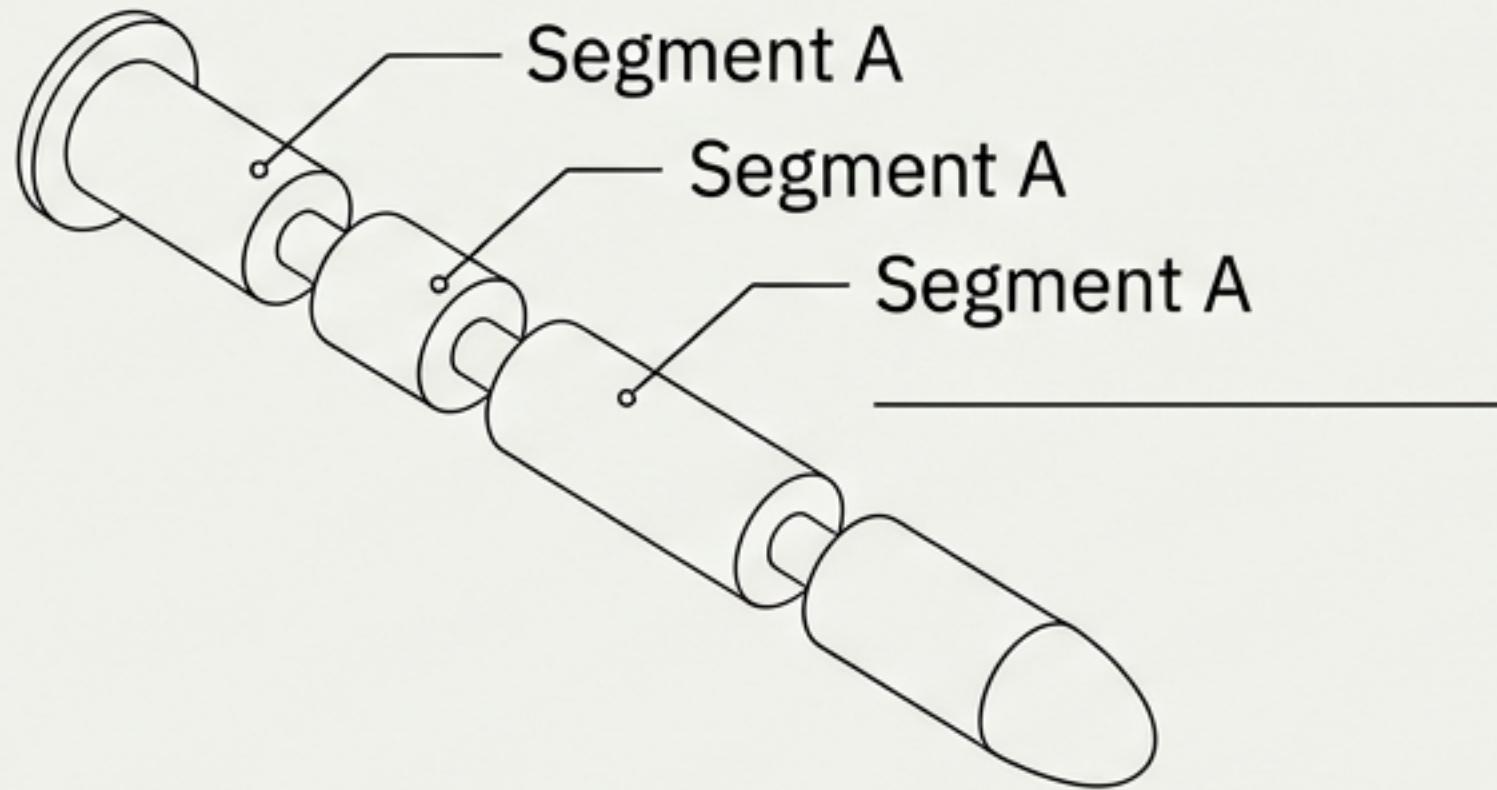
Flat Encoding Dominates Mean Fitness Across All Benchmarks.

Benchmark	Flat (Control)	Hierarchical	Topological
Ant Locomotion	407.9 +9.4	378.0	366.4
Swimmer		36.8	31.7
Multi-Task	265.0	239.5	231.8

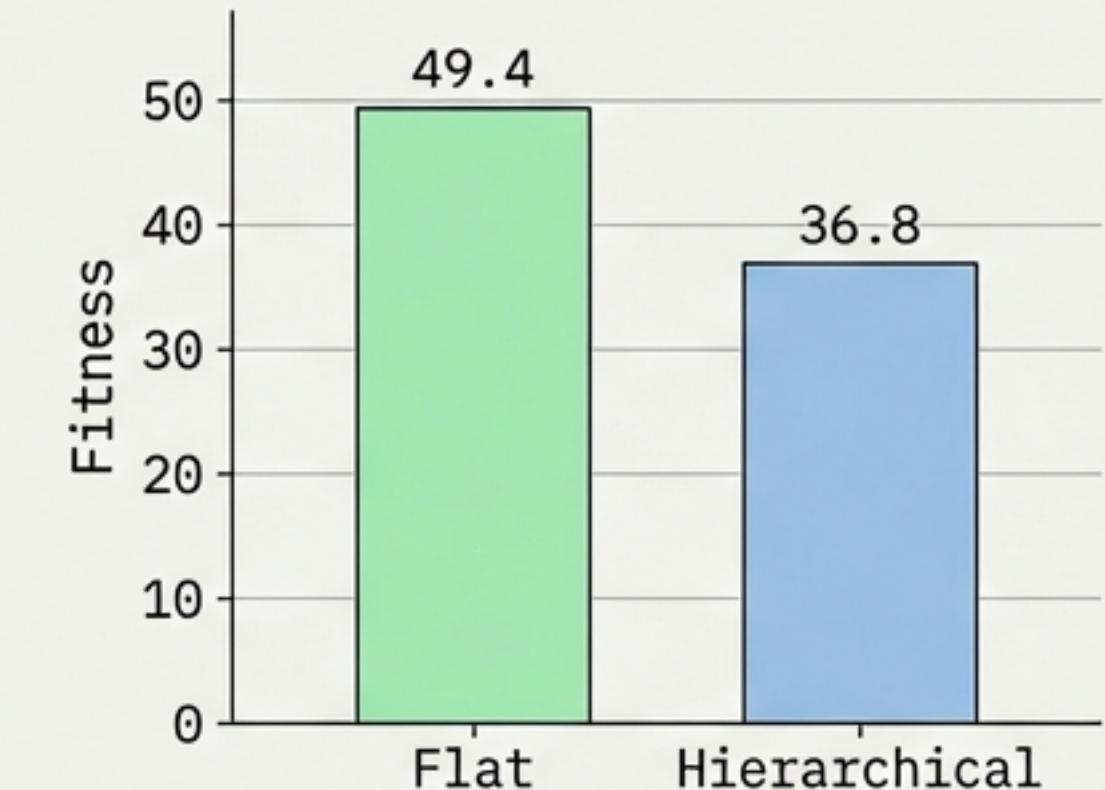
REFUTED

Genomic-inspired constraints hindered rather than helped the evolutionary search.

The Modularity Paradox



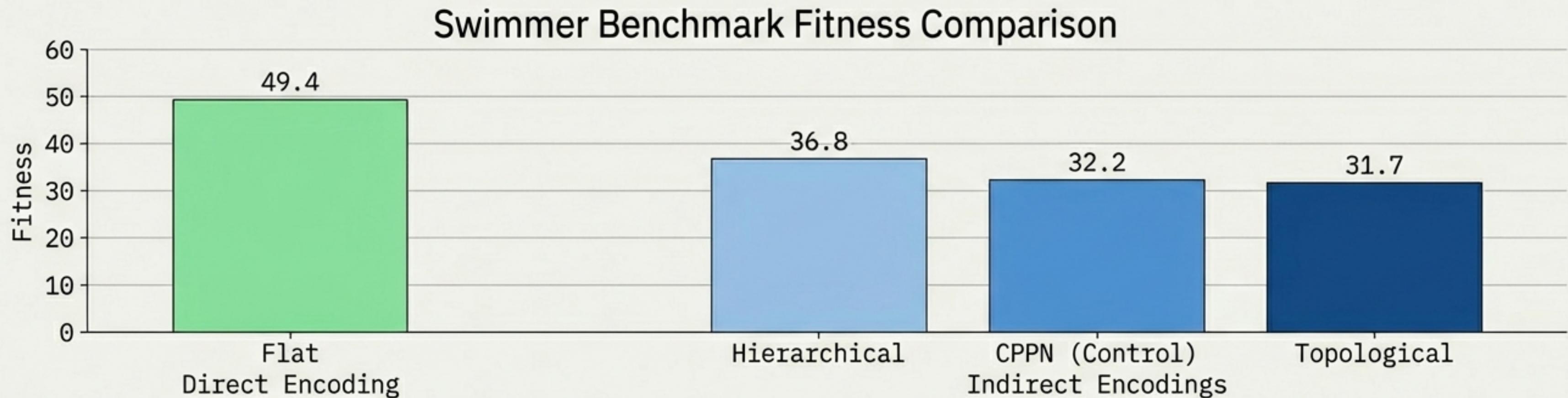
Perfect
candidate for
Modular
Encoding.



“Even with obvious physical modularity, the unconstrained search found better solutions. Inductive bias proved to be a shackle, not a ladder.”

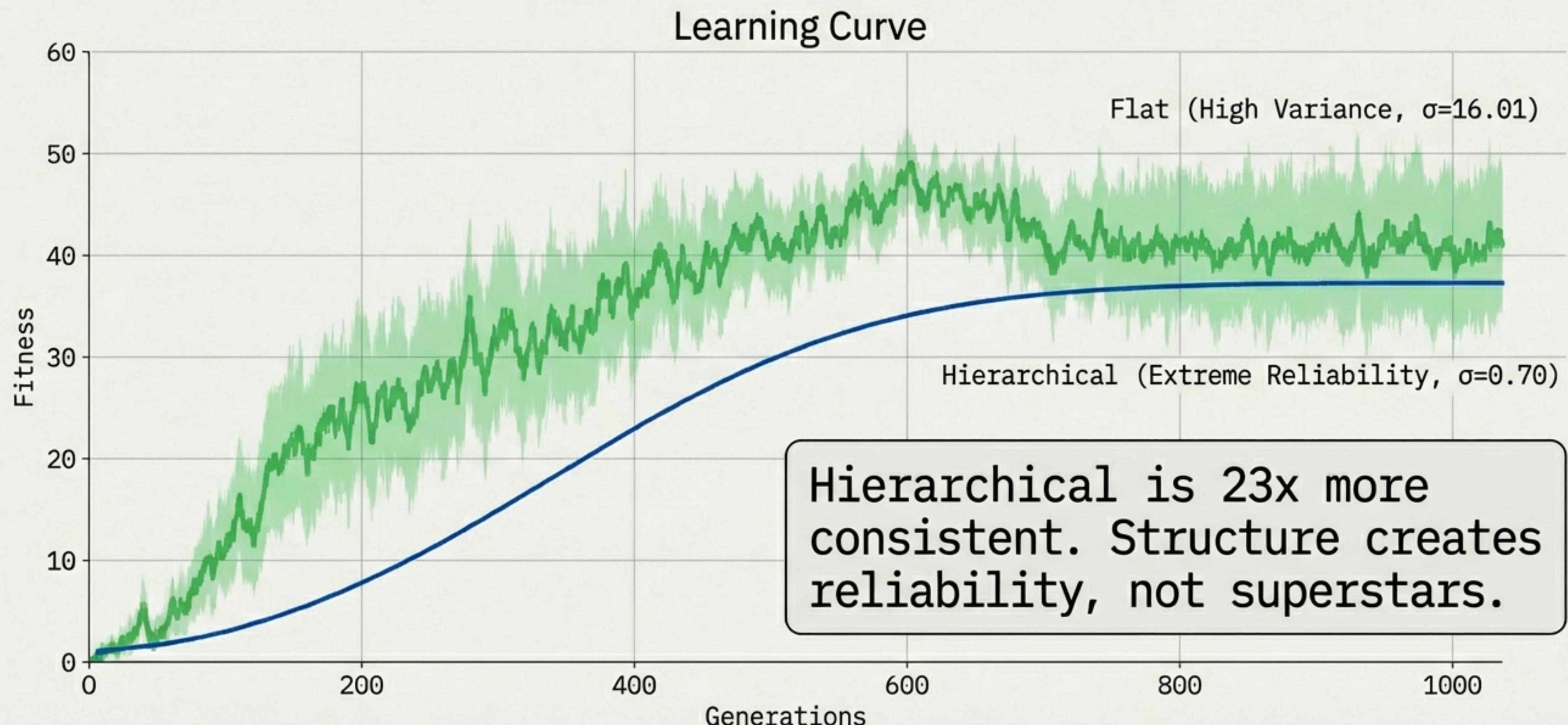
Validation: The CPPN Control

Was our implementation flawed? We compared against CPPN, the industry gold standard for indirect encoding.



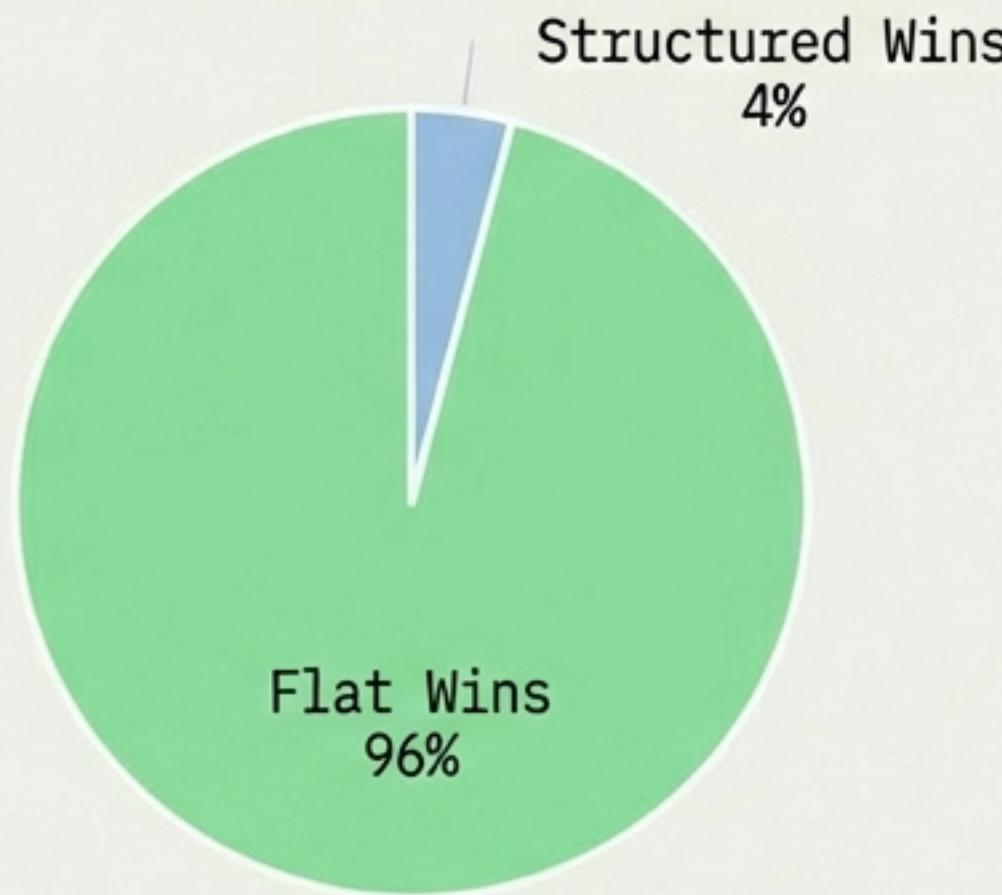
CPPN performs identically to our genomic models.
The failure is fundamental to indirect encoding on
these tasks.

The Pivot: Discovery of Variance Collapse



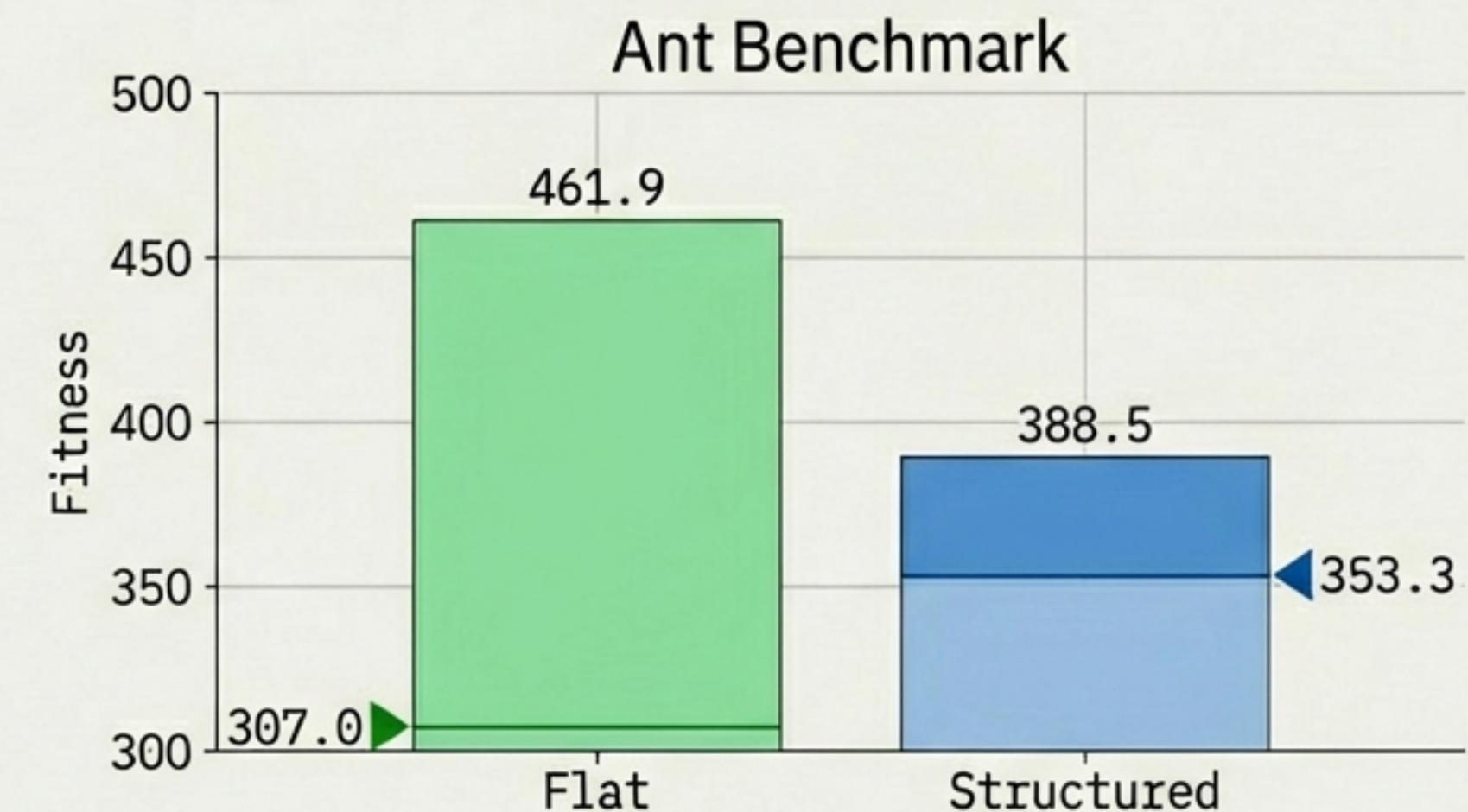
Risk vs. Reward Analysis

Pairwise Dominance



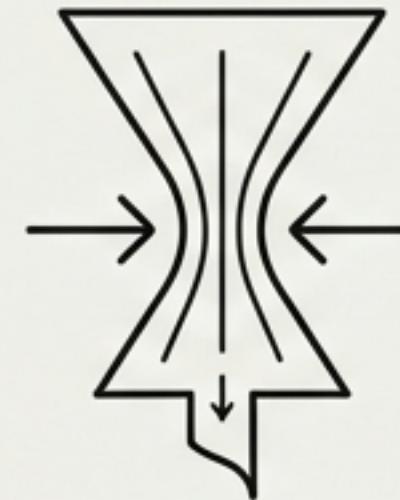
A random Flat seed beats a random Structured seed 96% of the time.

Worst-Case Floor



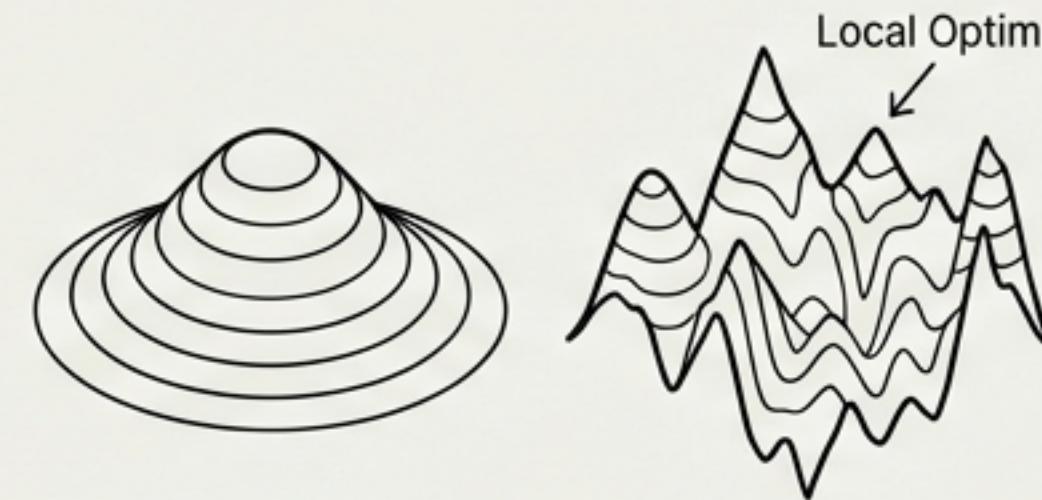
Structure acts as a regularizer. It prevents total failure but caps peak brilliance.

Post-Mortem: Why Did It Fail?



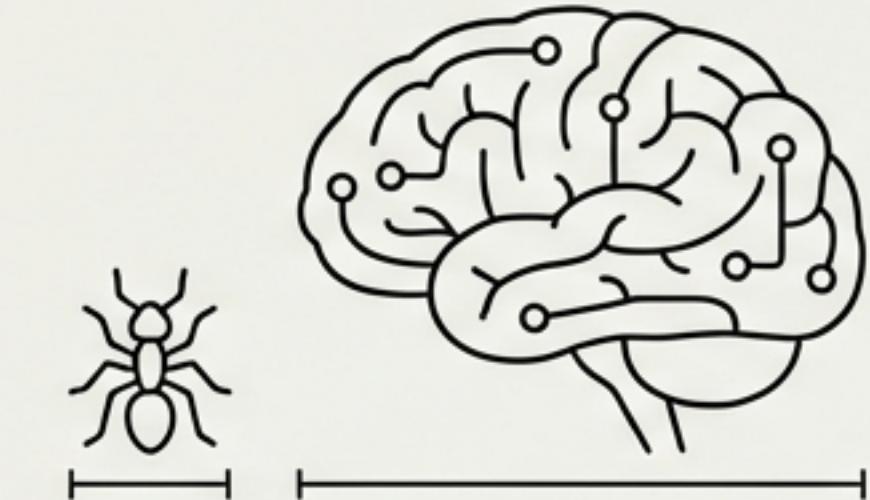
Expressivity Loss

Compression ratio ($10^5:1$) blocked access to unstructured but high-performing regions of the weight space.



Optimization Landscape

Constraints created a rugged landscape with local optima that the SNES algorithm couldn't escape.



Scale Mismatch

At ~10k parameters, compression is unnecessary. Biological advantages likely only emerge at billions of parameters.

Technical Integrity & Validation

Code Audits

- [PASS] Bottleneck Compression ($5.2M \rightarrow 0.6M$ verified)
- [PASS] Physics Cost (Distance penalties applied)
- [PASS] Reproducibility (All seeds logged to JSON)

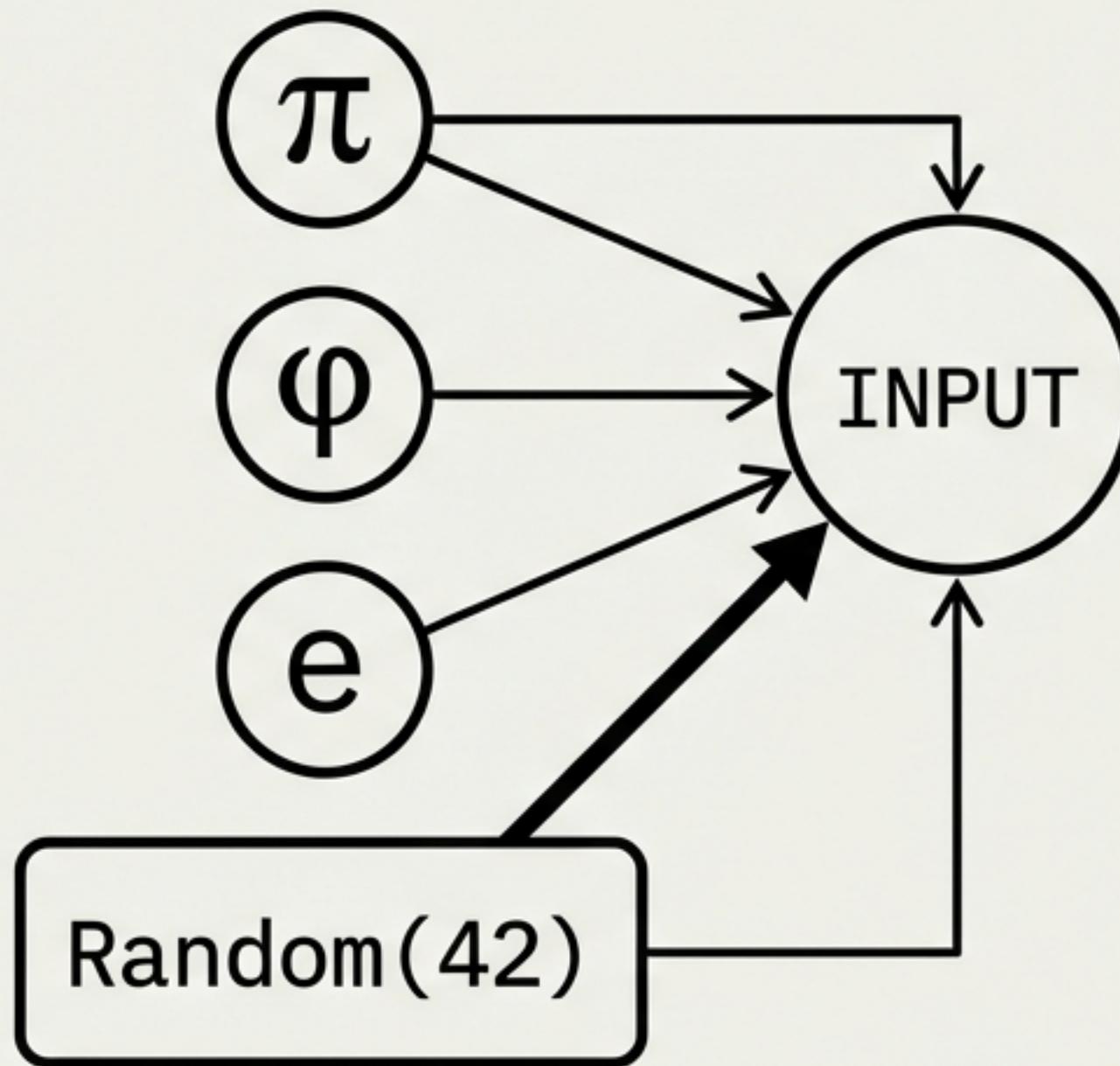
Performance Optimization

Brax Legacy: 2 hours compile time

 MJX (MuJoCo XLA): 3 seconds compile time

We tested an analogy to biology. The failure of the analogy refutes the utility of the approach, not biology itself.

Future Frontier: The Seed Hypothesis



Observation: Pairwise dominance implies “lucky” seeds exist.

Question: Do seeds derived from universal constants interact with the exponential decay of chromatin physics?

Status: Early pilot data suggests high Seed Dependence.

Conclusion: Negative Results Are Valuable Science

1. We operationalized the Genomic Weight Thesis on high-performance hardware.
2. We comprehensively rejected the hypothesis that chromatin-like constraints improve fitness on standard RL tasks.
3. We discovered a Variance-Fitness Tradeoff: Structure creates reliability, not performance.

“The adjacency matrices revealed the truth: on these scales, simple baselines are incredibly strong. We must look for the advantage of genomic compression not in raw performance, but in robustness and evolvability at scale.”