Nonergodic Development: How High-Dimensional Systems with Low-Dimensional Anchors Generate Phenotypes

Ian Todd

Sydney Medical School

University of Sydney

itod2305@uni.sydney.edu.au

Abstract

Biological development is a high-dimensional dynamical process that cannot explore its state space in finite time—it is *nonergodic*. We argue that this nonergodicity, combined with low-dimensional genetic anchors, is the fundamental reason why genotype does not algorithmically determine phenotype. The genome constrains which regions of developmental state space are reachable, but environmental history determines which attractor basin the system occupies. Using a minimal developmental network model, we demonstrate that (1) identical genotypes produce substantially different phenotypes depending on which trajectory the system follows, (2) these trapped states constitute "developmental memory" that is invisible to genetic analysis, and (3) the "dimensional gap" Δ_D between genetic parameters and developmental degrees of freedom quantifies this non-identifiability. We apply this framework to recent findings on cooperative lifestyles and cancer prevalence, showing that the pattern "cooperative species have less cancer" admits both allele-based and trajectory-based interpretations. The mod-

els diverge only under environmental intervention. Allele stories are not wrong but are projections that discard the nonergodic structure of development.

Keywords: nonergodicity, developmental dynamics, genotype-phenotype map, epigenetic memory, attractor basins, dimensional constraints

1 Introduction

Biological development unfolds in a high-dimensional state space. Gene regulatory networks, signaling cascades, and metabolic pathways create a system with vastly more degrees of freedom than the genome that parameterizes it. This dimensionality has a fundamental consequence: the system is *nonergodic*—it cannot explore its state space in biological time. A developing organism follows one trajectory through developmental state space and ends up in one attractor basin, leaving the vast majority of possible states forever unvisited.

This nonergodicity is not a limitation to be overcome but a feature that enables stable phenotypes. The genome acts as a low-dimensional *anchor* that constrains which regions of state space are reachable, while environmental history determines which specific attractor the system occupies within those constraints. The phenotype is not algorithmically determined by the genotype; it is the trapped state of a nonergodic system whose trajectory was shaped by both genetic and environmental inputs.

This framework offers one perspective on a persistent puzzle in genetics: why do genome-wide association studies fail to account for the majority of heritable variation in complex traits [8, 9]? Many explanations have been proposed—rare variants, epistasis, gene-environment interactions. We add another: trajectory information. From a nonergodic developmental perspective, "missing heritability" includes the environmental history that determined which attractor basin each individual occupies. Additive genetic models project a high-dimensional, trajectory-dependent reality onto a low-dimensional genotype space, discarding precisely the information that distinguishes individuals with identical genotypes.

We formalize this via the **Dimensional Gap** (Δ_D), which quantifies the mismatch between genetic parameters and developmental degrees of freedom. When $\Delta_D \gg 0$, the mapping from genotype to phenotype is many-to-one: the same genotype can produce different phenotypes depending on which trajectory the system followed. This creates a fundamental *non-identifiability* between allele-based and trajectory-based explanations for phenotypic patterns.

Application: Cooperative Lifestyles and Cancer

We apply this framework to a recent finding in cancer evolution. Sierra et al. (2025) demonstrated that cooperative mammalian species exhibit lower cancer prevalence than competitive species, and modeled this as selection on "oncogenic variants" [1]. Their allele-based interpretation is compelling—but our framework shows it is not uniquely supported by the data.

The same pattern admits a trajectory-based interpretation:

- **Allele interpretation:** Cooperative lineages have accumulated cancer-suppressing alleles through selection.
- **Trajectory interpretation:** Cooperative environmental cues enable slower, more coordinated development with fewer attractor bifurcations, yielding lower cancer mortality as an emergent property.

These interpretations are *non-identifiable* from cross-species comparative data. They diverge only in predictions for intervention: the allele model predicts that changing an organism's environment will not change its cancer risk; the trajectory model predicts substantial phenotypic shifts.

This connects to Lissek's [19] proposal of "cancer memory"—epigenetic mechanisms that maintain malignant phenotypes once initiated. Our framework situates epigenetics within a larger dynamical picture: the high-dimensional developmental system determines *which*

epigenetic marks get laid down; epigenetic mechanisms then stabilize the resulting attractor. Epigenetics is not a competing explanation but the molecular implementation of nonergodic trapping. The trajectory through developmental state space creates the epigenetic pattern; the pattern then helps maintain the trapped state.

In this paper, we:

1. Develop the theoretical framework of nonergodic development with low-dimensional anchors (Section 2).

2. Formalize a minimal developmental network model that demonstrates these principles (Section 3).

3. Prove a non-identifiability proposition showing that allele-based patterns can always be matched by trajectory-based mechanisms (Section 4).

4. Demonstrate the framework with simulations, including a "Twin Worlds" experiment (Section 5).

5. Discuss implications for evolutionary biology, GWAS, and intervention design (Section 6).

2 Theoretical Framework

2.1 Nonergodicity in High-Dimensional Systems

A dynamical system is *ergodic* if, given sufficient time, its trajectory will visit every accessible region of state space with frequency proportional to the equilibrium measure. Ergodicity underlies much of statistical mechanics: it allows us to equate time averages with ensemble averages, and justifies treating a single long trajectory as representative of the whole system [31].

A subtlety: high dimensionality alone does not guarantee nonergodicity. A liter of air at room temperature is extraordinarily high-dimensional ($\sim 10^{23}$ molecules, each with position and momentum), yet statistical mechanics treats it as ergodic and succeeds. The difference is *structure*. Air molecules are interchangeable; their specific configuration carries no information; the system equilibrates rapidly and forgets its history. Biological systems are different: cells are not interchangeable, specific configurations matter, and developmental history is retained in the system's structure.

The relevant criterion is: **high dimensionality + structured coupling + information retention = nonergodicity**. When the system's state carries information that must be preserved—when configurations are not equivalent—then exploration becomes constrained. State space volume still grows exponentially with dimension (k^D), trajectory length still grows linearly with time, but now the system cannot simply diffuse through phase space. It must maintain coherence. It becomes trapped.

Biological systems satisfy all three conditions. A gene regulatory network with N genes has k^N possible expression states, but these states are not equivalent—they correspond to different cell types, different developmental stages, different functional outcomes. The system is strongly coupled through regulatory feedback; it retains information in its epigenetic state; it cannot equilibrate without losing its identity. Development, behavior, physiology, and cognition all unfold in state spaces too vast to explore and too structured to forget. High-dimensional biological systems are nonergodic by necessity, not by accident.

Definition 1 (Developmental Nonergodicity)**.** A developmental system is **nonergodic** if its trajectory through state space cannot visit a representative sample of accessible states within the organism's lifetime. Formally, let $\mathcal{M}$ be the accessible manifold of developmental states. The system is nonergodic if:

$$\frac{\text{Vol(trajectory)}}{\text{Vol}(\mathcal{M})} \to 0 \tag{1}$$

as the dimensionality of $\mathcal{M}$ increases.

This nonergodicity has a crucial consequence: the developmental trajectory is *trapped*. Once the system enters an attractor basin, it cannot spontaneously explore alternative basins. The final phenotype reflects not the equilibrium distribution over possible states, but the particular basin the trajectory happened to enter.

2.2 Beyond the Computational Metaphor

This continuous dynamical systems perspective differs fundamentally from the dominant metaphor in molecular biology. Since the discovery of the genetic code, biological systems have been described using computational language: genes "encode" proteins, regulatory networks "process" signals, development follows a "program." This framing—treating organisms as discrete-state machines executing algorithms—has been so successful and so pervasive that it is rarely questioned. Network diagrams with nodes and edges are the standard visual vocabulary; information flow through discrete processing steps is the default conceptual framework.

Yet the graph model carries a hidden puzzle: how do discrete signals get routed precisely through the molecular chaos of a living cell? The network diagram shows an edge from node A to node B, but physically there is no edge—only molecules diffusing in crowded cytoplasm.

We propose a complementary perspective grounded in continuous physics. Instead of discrete nodes and edges, we have continuous state spaces and smooth trajectories. Instead of algorithms that map inputs to outputs, we have dynamical systems that *flow* through high-dimensional landscapes. The genome does not "compute" the phenotype—it shapes the landscape through which the developmental trajectory flows. The routing puzzle dissolves: there are no discrete signals being routed, only continuous trajectories constrained by the physics of the substrate.

This shift matters because computational metaphors implicitly assume something like ergodicity. Here is why: algorithms are *time-abstract*. A Turing machine will eventually

halt with its output; we analyze what it computes, not how long it takes. This abstraction implies that given any input, the system can "find" the corresponding output—it can reach the correct state. When we model the genotype-phenotype map as a computation, we inherit this assumption: the genome specifies an algorithm; development executes it; the phenotype is the output. The system is assumed capable of reaching whatever state the algorithm specifies.

But physical systems embedded in time cannot do this. Continuous high-dimensional dynamics reveals why: the state space is too vast; trajectories are trapped. A developing organism does not "find" its phenotype the way an algorithm finds its output. It falls into an attractor basin determined by its trajectory. The phenotype is not the output of a computation but the basin into which a physical system settled.

The distinction is not merely philosophical. Algorithms are abstractions that can, in principle, explore any computable state space given sufficient steps. Physical dynamical systems cannot. When dimensionality is high, state space volume grows exponentially while trajectory length grows only linearly with time [27]. This is the "curse of dimensionality"—not a computational inconvenience but a fundamental barrier. Bayesian inference becomes intractable as posteriors concentrate on measure-zero manifolds [28]; MCMC samplers fail to mix as dimension increases [29]; even exhaustive search becomes impossible. Levinthal's paradox [30] made this vivid for protein folding: a polypeptide cannot explore all conformations, so folding must follow constrained trajectories through funnel-shaped landscapes. The same logic applies to development, at a vastly larger scale.

2.3 Low-Dimensional Anchors

If developmental state space is vast and trajectories are trapped, what prevents phenotypic chaos? The answer is *anchoring* by low-dimensional constraints.

Definition 2 (Developmental Anchor)**.** An **anchor** is a low-dimensional structure that constrains which regions of developmental state space are reachable. The genome is the

primary anchor, specifying regulatory network topology, protein sequences, and signaling pathways. The epigenome provides secondary anchoring, modulating which regions of the genome-defined landscape are accessible at any given time.

Together, genetic and epigenetic anchors define the "landscape" of possible developmental trajectories. They do not specify which attractor basin the system will occupy—that depends on the trajectory, which depends on environmental history. But the anchors constrain *which basins exist* and *which are reachable* from a given starting point.

Crucially, the epigenome is not independent of the trajectory—it is *shaped by* it. The high-dimensional developmental dynamics determine which epigenetic modifications occur; these modifications then feed back to constrain future trajectories. This creates a hierarchy: genome → developmental dynamics → epigenome → stabilized attractor. Epigenetic marks are the molecular record of where the trajectory has been, not an independent source of phenotypic variation.

This is precisely Waddington's [10] epigenetic landscape, reframed in dynamical systems terms: the genome shapes the hills and valleys; the developmental trajectory is a ball rolling down one particular path. Different environmental perturbations can push the ball into different valleys—but not into valleys that the landscape doesn't contain. As Noble [11] argues, there is no privileged level of causation in biological systems; the genome anchors the dynamics, but environmental boundary conditions constrain them just as fundamentally.

2.4 The Dimensional Gap

We quantify the relationship between anchor dimensionality and state space dimensionality:

Definition 3 (Dimensional Gap)**.** Let L be the dimension of the genotype (anchor) space and k the dimension of measured phenotypic traits. Let the developmental system evolve on a manifold $\mathcal{M}$ with **effective dimension** m_{eff}. The **dimensional gap** is:

$$\Delta_D = m_{\text{eff}} - (L + k) \tag{2}$$

When $\Delta_D \gg 0$, the developmental system has far more degrees of freedom than can be specified by the genome or captured by phenotypic measurement. This creates a fundamental ambiguity:

- The same genotype can produce different phenotypes (depending on which trajectory/attractor)
- The same phenotype can arise from different mechanisms (genotype-determined vs. trajectory-determined)

The dimensional gap is the source of non-identifiability. Projecting from the high-dimensional developmental reality to the low-dimensional genotype-phenotype pair destroys the trajectory information that distinguishes otherwise identical outcomes [6, 7].

2.5 Epigenetic Memory as Trapped States

The connection to epigenetic memory is now clear. "Epigenetic memory" refers to heritable cellular states that are not encoded in the DNA sequence—persistent patterns of gene expression, chromatin modification, or cellular identity that are maintained across cell divisions.

In our framework, epigenetic memory is simply a *trapped state* in a nonergodic developmental system. The genome (anchor) constrains which states are stable, while environmental history determines which stable state the system entered. Once entered, the state persists because the system cannot spontaneously explore alternatives.

This provides the information-theoretic foundation for Lissek's [19] "cancer memory" hypothesis: oncogenic changes may push the developmental system into a new attractor basin, where the nonergodic dynamics maintain the malignant phenotype without requiring continued mutation accumulation.

2.6 Application Context: Cancer and Cooperation

Sierra et al. (2025) found that cooperative mammalian species have lower cancer prevalence than competitive species [1]. Their model explains this via allele frequency differences: selection favors cancer-suppressing alleles in cooperative lineages where older individuals contribute as helpers.

Our framework suggests an alternative: cooperative environmental cues may enable slower, more coordinated developmental trajectories with fewer cellular bifurcations. The genome constrains which trajectories are possible; the social environment determines how coherently development proceeds. Species that consistently experience cooperative environments would consistently develop with higher coherence—producing the same aggregate pattern (lower cancer) as allele-based selection, but via a different mechanism.

More generally, any species experiencing variable environments across generations would be expected to evolve genomes that anchor multiple attractor basins—allowing environment-dependent phenotype determination rather than fixed strategies. Singh and Glowacki [2] documented such environmental variability in human evolutionary history, but the principle applies broadly: when environments vary, selection favors trajectory-responsive developmental systems over rigidly canalized ones.

3 Model

We construct a minimal developmental network that instantiates the theoretical framework: the genotype serves as a low-dimensional anchor, the developmental state evolves in a high-dimensional space, and environmental history shapes the trajectory through that space.

3.1 The Developmental System

Let $g \in \mathbb{R}^L$ be the genotype (the *anchor*, with L small), $e_t \in \mathbb{R}^p$ be the environmental input at time t, and $h_t \in \mathbb{R}^m$ be the developmental state (with $m \gg L$).

The developmental dynamics follow a recurrent network:

$$h_{t+1} = \sigma\left(W_h h_t + W_e e_t + W_g g\right) \tag{3}$$

where W_h, W_e, W_g are weight matrices and $\sigma = \tanh$ provides nonlinearity.

The key features of this model:

- **Nonergodicity:** The state space $\mathbb{R}^m$ is high-dimensional; any single trajectory visits a negligible fraction of it.
- **Anchoring:** The genotype g enters at every timestep, constraining which regions of state space are accessible.
- **Trajectory-dependence:** The environmental history $\{e_0, e_1, \ldots, e_T\}$ determines which specific trajectory is followed within the anchor's constraints.
- **Attractor dynamics:** The recurrent structure creates attractor basins; different trajectories can converge to different attractors.

3.2 Phenotype as Trapped State

The phenotype $x \in \mathbb{R}^n$ is a readout of the final developmental state:

$$x = W_{out} h_T \tag{4}$$

This final state h_T is a *trapped state*—the endpoint of a nonergodic trajectory. The same genotype g can produce different h_T (and thus different x) depending on which trajectory was followed.

We extract a "developmental coherence" variable $c \in [0, 1]$ from the phenotype, representing how well-coordinated the developmental trajectory was—how consistently all cells followed the same attractor. Cancer, in this framing, is attractor bifurcation: cells that

diverge from the organismal trajectory into a different basin. The emergent cancer mortality is:

$$\mu_S(x) = \mu_0(1 - \alpha \cdot c(x)) \tag{5}$$

where μ_0 is baseline mortality and $\alpha \in (0, 1)$ is the efficacy of coherence in preventing bifurcation.

3.3 Environmental Regimes

We define two environmental regimes that guide trajectories into different attractor basins:

- **Cooperative:** Low variance, high social support, low conflict → slower, more coordinated development → high coherence.
- **Competitive:** High variance, low support, high conflict → faster, less coordinated development → low coherence.

Parameter values: We use $L = 5$ (anchor dimension), $m = 20$ (developmental state dimension), $n = 10$ (phenotype dimension), and $p = 3$ (environmental input dimension). This gives $\Delta_D = m - (L + 1) = 14$ when measuring a single trait (μ_S). Cancer parameters: $\mu_0 = 0.1$, $\alpha = 0.8$. See code for implementation details.

Note on model scope: The developmental network is intentionally minimal and not fitted to any species. Its role is illustrative: to instantiate the dimensional and identifiability arguments with a concrete dynamical system, not to make quantitative predictions about specific organisms.

3.4 Contrasting Interpretations

Figure 3 illustrates how the same outcome admits two causal interpretations:

- **Allele model:** $G \to \mu_S \to$ Cancer. The genotype algorithmically determines mortality; environment only modulates selection pressure over evolutionary time.

- **Trajectory model:** $G \to \text{Dev} \to \pi(E) \to r_t \to \mu_S$. The genotype anchors a developmental system; environment shapes the trajectory; the trapped state determines mortality.

Both produce the same aggregate correlation (Environment $\leftrightarrow \mu_S$) when projected to observables—this is the non-identifiability created by $\Delta_D > 0$.

4 Non-Identifiability Result

Proposition 4 (Non-identifiability of allele vs. policy mechanisms)**.** *Let Model A be any allele-based system where late-life mortality takes values* $\{\mu, \mu + \delta\}$ *across two ecological regimes, with* $0 \leq \mu < \mu + \delta \leq \mu_0$*. Let Model B be any trajectory-based developmental system* ***capable of realizing any coherence level*** $c \in [0, 1]$ ***via some environmental history****, and where* $\mu_S = \mu_0(1-\alpha c)$ *as in Equation 5. Then for any pair* $(\mu, \mu+\delta)$ *satisfying these constraints, there exists an environment pair* (E_{coop}, E_{comp}) *such that the induced* μ_S *distributions in Model B match those in Model A for all species-level summary statistics.*

Proof. Take any $(\mu, \mu + \delta)$ from Model A. We construct environments that induce matching μ_S distributions in Model B.

Choose c_{coop} and c_{comp} such that:

$$\mu_0(1 - \alpha c_{\text{coop}}) = \mu \tag{6}$$

$$\mu_0(1 - \alpha c_{\text{comp}}) = \mu + \delta \tag{7}$$

Solving: $c_{\text{coop}} = (1 - \mu/\mu_0)/\alpha$ and $c_{\text{comp}} = (1 - (\mu + \delta)/\mu_0)/\alpha$.

For sufficiently expressive dynamics (e.g., the recurrent network of Equation 3), there exists a mapping from environmental histories to any desired c; this is empirically illustrated in Figure 1D. Thus there exist environments E_{coop} and E_{comp} that induce these coherence levels.

Therefore, any species-level summary (mean μ_S, variance, etc.) that Model A produces can be exactly matched by Model B with appropriate environment choice. The models are observationally equivalent at this level. □

Remark 5. This result formalizes the sense in which allele models are "incomplete": they are not wrong, but they are *non-identifiable* from aggregate data. The models become distinguishable only through interventions that change environment while holding genotype fixed.

5 Results

All figures show simulated outputs from the developmental network model; no empirical data are used. The simulations demonstrate the core theoretical claims: trajectory-dependence, attractor dynamics, and non-identifiability.

5.1 Trajectory Divergence: Same Anchor, Different Attractors

Figure 1 demonstrates the fundamental prediction of nonergodic development: identical genotypes (anchors) produce different phenotypes when developmental trajectories follow different paths through state space.

Panel (B) is the key visualization: the two trajectories diverge in state space despite sharing the same anchor constraints. The endpoints represent different attractor basins—trapped states that persist because the system cannot spontaneously explore alternatives. Panel (D) shows the phenotypic consequence: different developmental coherence and thus different cancer mortality from identical genotypes.

5.2 Population-Level Non-Identifiability

Figure 2 shows that aggregate population patterns cannot distinguish between allele-based and trajectory-based mechanisms.

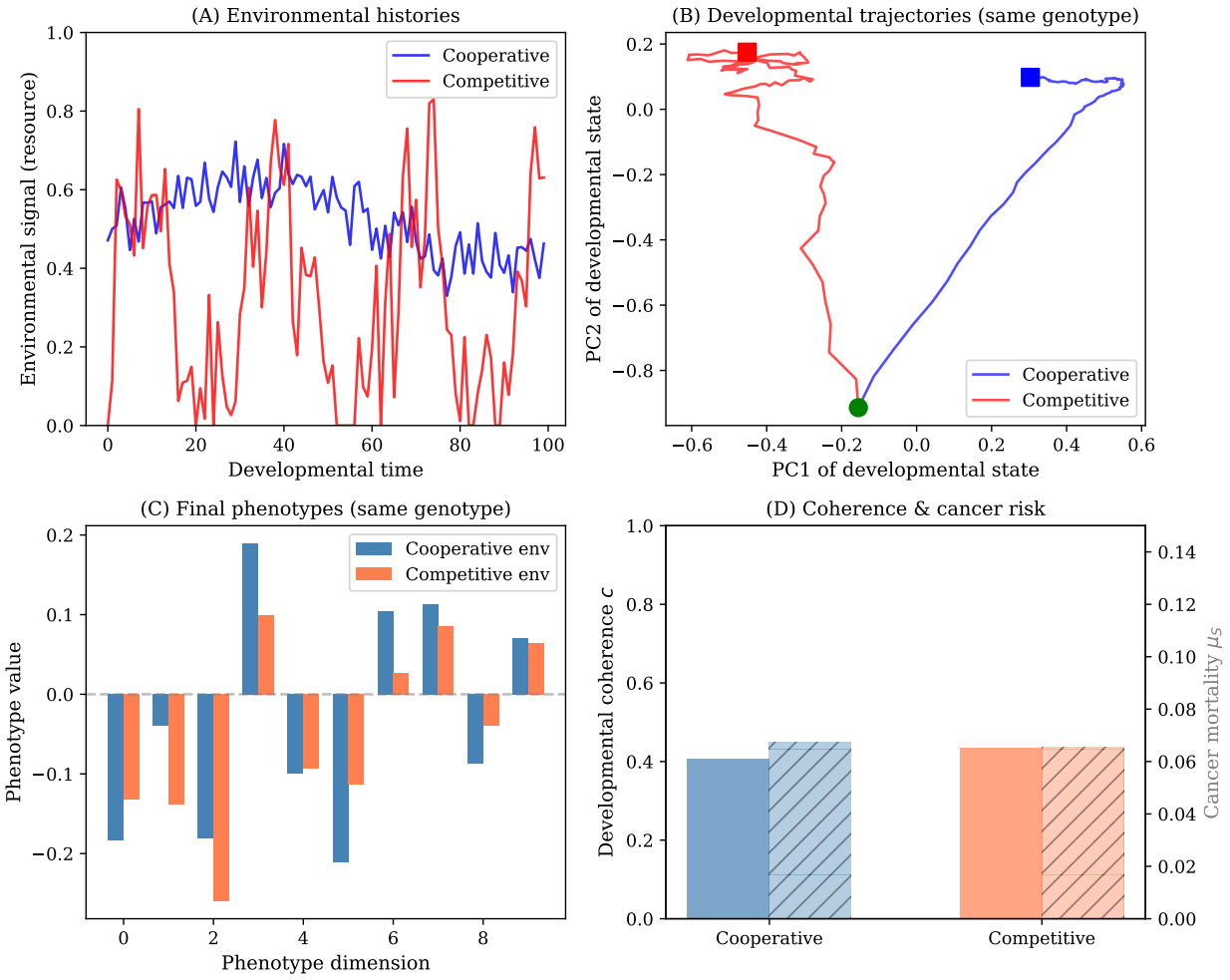

Figure 1: **Trajectory divergence under identical anchoring.** (A) Two environmental histories: cooperative (blue) and competitive (red). (B) Developmental trajectories through state space (PCA projection); same starting point (green circle), different endpoints (squares). (C) Different trapped states produce different phenotypes. (D) Different developmental coherence and cancer mortality emerge from the same genotype—cooperative environments enable more coordinated development with fewer bifurcations.

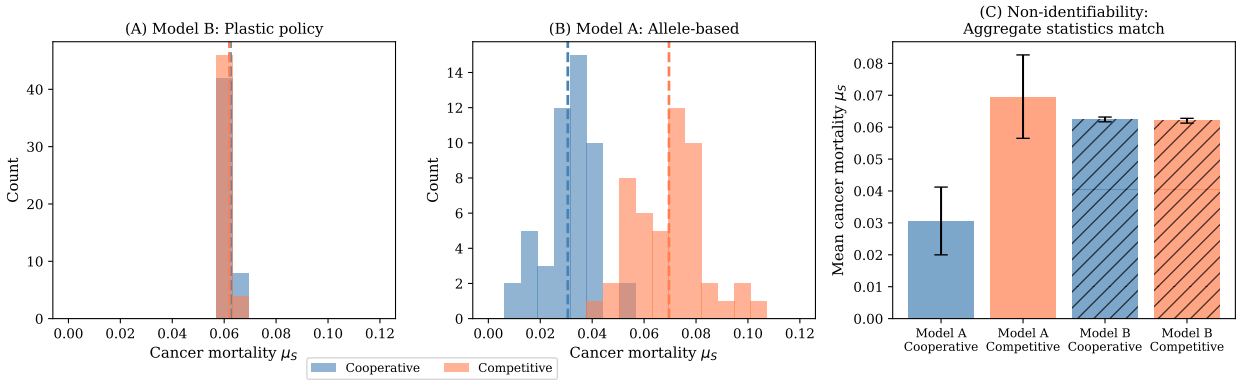

Figure 2: Non-identifiability at the population level. (A) Trajectory model: same genetic distribution in different environments → different μ_S distributions. (B) Allele model: different genetic distributions can produce matching patterns. (C) Aggregate statistics are indistinguishable—this is the Δ_D projection problem.

5.3 Causal Structure

Figure 3 contrasts the causal graphs. In the allele model, the genotype algorithmically determines the phenotype; environment acts only through evolutionary selection. In the trajectory model, the genotype anchors a developmental system that integrates environmental inputs in real time.

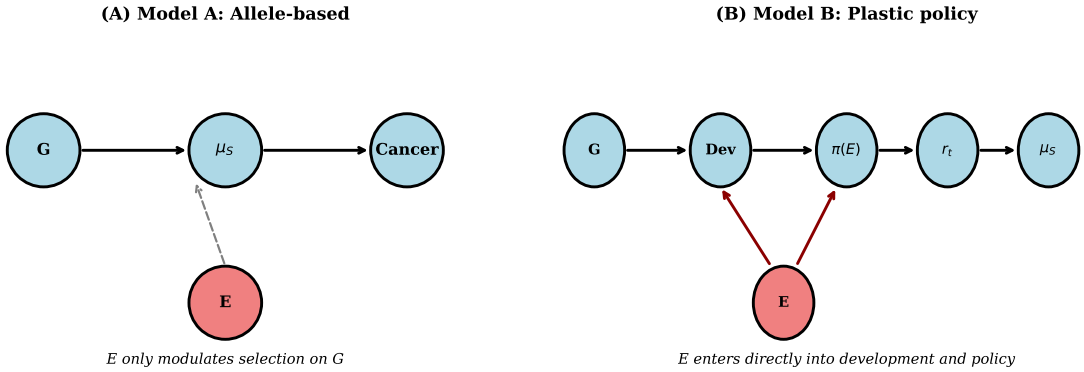

Figure 3: Contrasting causal structures. (A) Allele model: $G \to \mu_S$, environment external. (B) Trajectory model: G anchors development, E shapes trajectory, μ_S emerges from trapped state.

5.4 The Dimensional Gap in Action

Figure 4 visualizes the information loss that occurs when projecting from the high-dimensional (genotype × environment × trajectory) space to the low-dimensional (genotype → phenotype) summary.

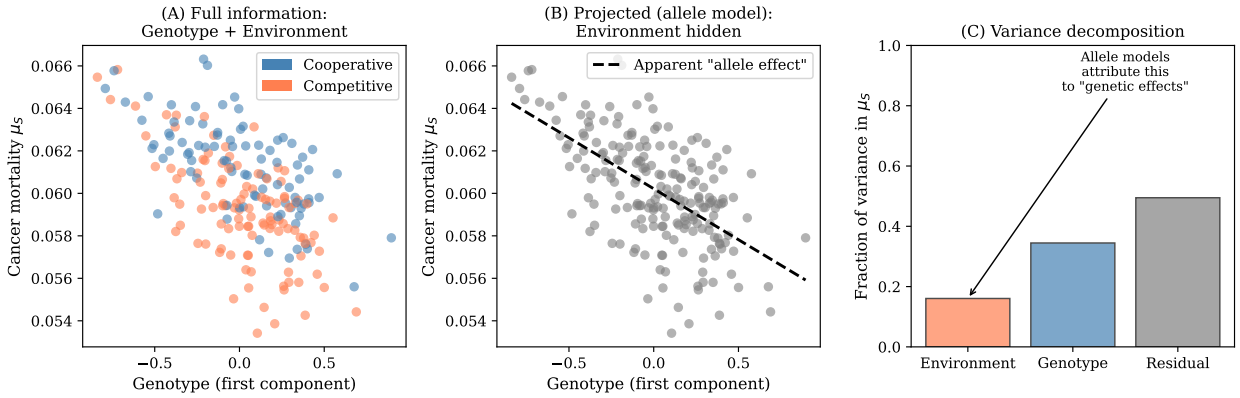

Figure 4: Projection destroys trajectory information. (A) Full space: environments clearly separate. (B) Projected space: trajectory information lost. (C) Variance decomposition: environment explains most μ_S variance, but allele models misattribute this to "genetic effects"—the dimensional gap in action.

5.5 Twin Worlds: The Decisive Experiment

Figure 5 provides the clearest demonstration of nonergodic development. We create two "worlds" with *identical* genotype distributions but different environmental regimes. The developmental trajectories in each world converge to different attractor basins, producing dramatically different phenotype distributions.

The genetic distance between worlds is $F_{ST} \approx 0$ (by construction), yet phenotypic distance is $P_{ST} \gg 0$. A GWAS would find no significant variants and conclude "missing heritability"—but the heritability is not missing, it is *trajectory-based*. The anchor constrains which attractors exist; the environment determines which attractor is entered.

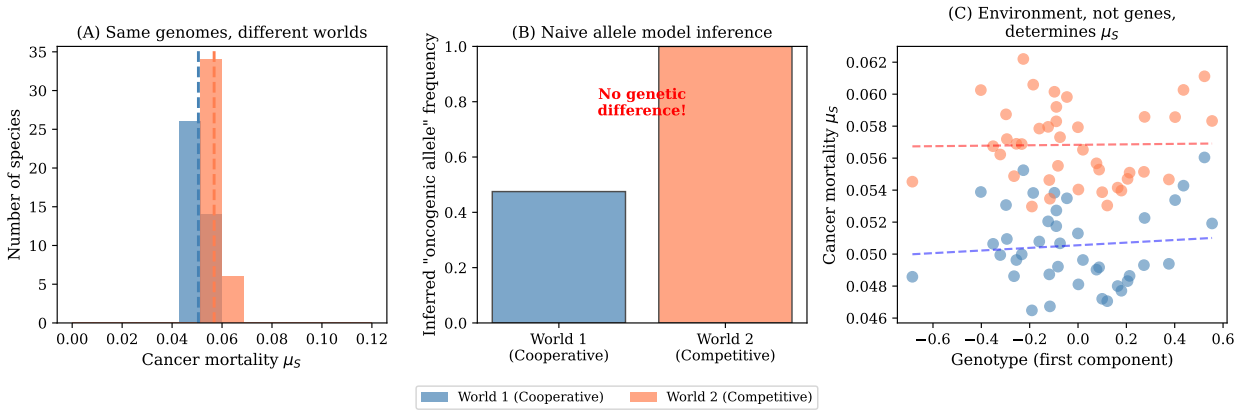

Figure 5: Twin worlds experiment. (A) Identical genomes, different worlds → different μ_S distributions. (B) A naive allele analysis would infer "oncogenic allele" frequency differences where none exist. (C) Genotype (anchor) shows minimal correlation with μ_S; trajectory determines outcome.

5.6 Divergent Predictions: The Intervention Test

Figure 6 shows where the models diverge. The allele model predicts that phenotype is locked by genotype—environmental change cannot alter the trapped state. The trajectory model predicts that environmental change can guide the system toward a new attractor.

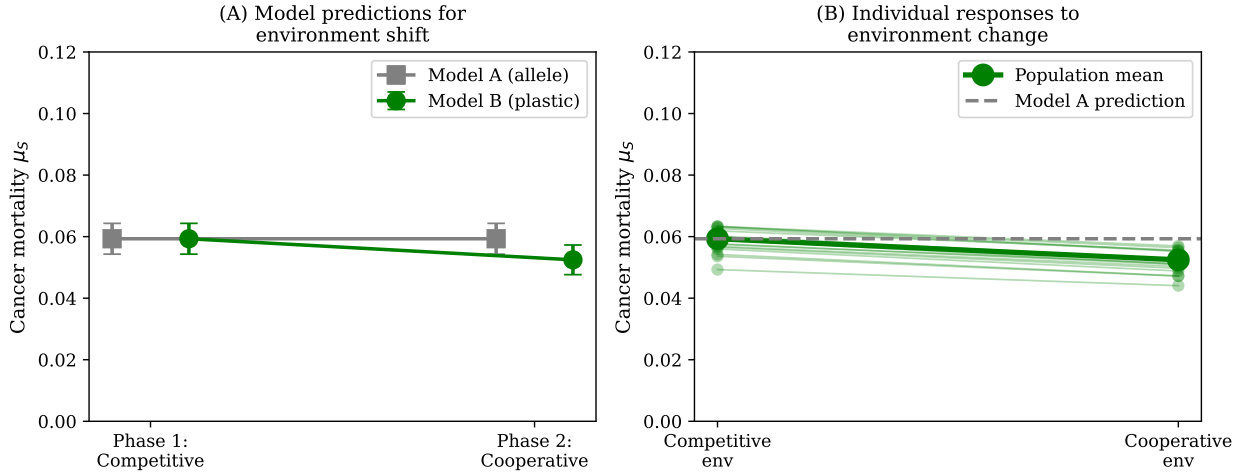

Figure 6: The intervention test. (A) Allele model: no change when environment shifts (genotype determines phenotype). Trajectory model: substantial shift (new environment → new attractor). (B) Individual trajectories converge toward the new attractor—phenotypic change without genetic change.

This is the critical empirical test. If moving organisms from competitive to cooperative

environments produces phenotypic shifts toward higher developmental coherence (fewer bifurcations), the trajectory model is supported. If phenotypes remain stable, the allele model is supported.

We acknowledge a confound: organisms placed in mismatched environments may show phenotypic changes due to stress rather than trajectory guidance *per se*. Teasing apart "cooperative cues guide development" from "environmental mismatch causes stress" is difficult. But this difficulty is itself the point: the system is high-dimensional, and clean causal decomposition may be impossible. What cooperative environments provide is *stability*—slower, more predictable conditions that allow cellular trajectories to remain coordinated. Whether we call this "reduced stress" or "trajectory guidance," the mechanism is the same: stability enables coherence; instability enables bifurcation. The phenotype emerges from trajectory dynamics that resist simple causal attribution.

6 Discussion

6.1 Nonergodicity as the Core Insight

The central contribution of this paper is recognizing that developmental systems are *nonergodic*. The state space is too vast to explore; trajectories are trapped; phenotypes reflect which attractor was entered, not an algorithmic genotype-to-phenotype mapping.

This reframes several longstanding puzzles:

- **Missing heritability:** May include missing trajectory information, not only missing variants. GWAS project out the environmental history that determines which attractor each individual occupies.
- **Epigenetic memory:** Not a separate mechanism, but trapped states in nonergodic dynamics. The genome anchors; the trajectory traps.
- **Genetic assimilation:** How plastic responses become canalized. If an attractor basin

is consistently entered across generations, selection can modify the anchor to make that basin deeper or more accessible—converting trajectory-dependence into anchor-dependence.

6.2 Steelmanning the Allele View

Allele-based models are not wrong. Sierra et al.'s finding that cooperative species have lower cancer prevalence is real and important [18]. Over evolutionary time, selection does modify anchors.

Our point is that the aggregate pattern "cooperative = less cancer" is equally consistent with:

1. **Anchor modification:** Selection has reshaped the attractor landscape to favor high-coherence developmental modes.

2. **Trajectory guidance:** Cooperative environments enable more coordinated development, reducing bifurcation probability.

3. **Genetic assimilation:** An initially trajectory-dependent response becomes anchor-encoded through sustained selection.

These are non-identifiable from comparative data. Distinguishing them requires intervention experiments. Our result should therefore be read as a *completion* of Sierra et al.'s model rather than a refutation: allele-level and trajectory-level accounts are two projections of a single underlying high-dimensional developmental system.

6.3 When Nonergodicity Dominates

Taxonomy: When Trajectory Matters

Anchor-dominated (allele stories work):

- Low-dimensional development (Δ_D small)
- Few attractor basins
- Stable environments across generations
- Strong canalization

Trajectory-dominated (nonergodicity matters):

- High-dimensional development ($\Delta_D \gg 0$)
- Many attractor basins accessible from same anchor
- Variable environments across generations
- Weak canalization, high plasticity

Cancer risk, facial morphology, and human life-history traits sit squarely in the trajectory-dominated regime.

6.4 Specific Empirical Predictions

While the models often produce indistinguishable aggregate statistics, they diverge structurally. Table 1 contrasts the mechanistic assumptions and specific predictions of each framework.

6.5 The Projection Problem

Genotype-phenotype inference involves a cascade of projections:

Table 1: **Anchor-based vs. Trajectory-based Models.** Indistinguishable from static data; diverge under intervention.

Feature	**Anchor Model (Allele-Based)**	**Trajectory Model (Nonergodic)**
Core Mechanism	Genotype algorithmically determines phenotype.	Genotype anchors high-D system; trajectory determines which attractor.
Role of Environment	*Selection pressure:* Modulates which anchors are favored over generations.	*Trajectory guidance:* Shapes which attractor basin is entered in real-time.
"Cooperative Safety"	Selection modified anchors to favor low-cancer attractors.	Cooperative cues guide trajectories into existing low-cancer attractors.
Divergent Predictions (Testable)		
Environmental Shift	**No change.** Trapped state is anchor-determined.	**Shift occurs.** New trajectory → new attractor.
Twin Worlds	Identical anchors → identical phenotypes.	Identical anchors → divergent phenotypes ($F_{ST} \approx 0$, $P_{ST} \gg 0$).
GWAS	"Missing heritability" = many small-effect variants.	"Missing heritability" = trajectory information projected out.

$$\begin{array}{lcl} \text{(anchor, trajectory, trapped state)} & \xrightarrow{\text{projection}} & \text{(genotype, phenotype)} \\ (g, E_{0:T}, h_T) \in \mathbb{R}^{L+pT+m} & & (g, x) \in \mathbb{R}^{L+n} \end{array}$$

Allele-based models further marginalize over trajectories:

$$P(x \mid g) = \int P(x \mid g, E) P(E)\, dE \tag{8}$$

This marginalization discards the trajectory information that determines which attractor basin was entered [6, 7]. The "genetic effect" β is not a property of the anchor alone but of the anchor-trajectory interaction averaged over some implicit distribution of environmental histories.

In our minimal model ($L = 5$, $m = 20$, $n = 10$), $\Delta_D = 14$. In real organisms with $m \sim 10^4$ regulatory degrees of freedom, the dimensional gap is enormous—making trajectory-dependence correspondingly important.

6.6 Beyond Nature versus Nurture

One might object that we are simply rebranding the "nurture" side of the nature-nurture debate. We are not. The traditional framing assumes that genetic and environmental contributions are separable and additive: $P = G + E + G \times E$. Variance can be partitioned; heritability can be estimated; the question is merely "how much of each?"

Our framework rejects this separability. In a nonergodic high-dimensional system, the phenotype is not a sum of genetic and environmental contributions—it is the attractor basin that a trajectory happened to enter. The trajectory is shaped by both anchor and environment simultaneously; there is no meaningful sense in which their contributions can be decomposed. Asking "how much is genes versus environment?" is like asking how much of a river's path is due to gravity versus the shape of the landscape. The question is malformed.

This is why Δ_D matters: it quantifies when the additive decomposition breaks down. When Δ_D is small, the anchor dominates and variance partitioning works. When Δ_D is large, the trajectory carries information that neither anchor nor simple environmental measures capture. The "missing heritability" is not missing nature or missing nurture—it is the signature of a high-dimensional system whose behavior cannot be projected onto low-dimensional summaries without information loss.

6.7 Connections to Related Work

Our framework provides formal foundations for several recent proposals:

Cancer memory [19]: Lissek argued that malignancy can progress through epigenetic mechanisms once initiated. In our terms: oncogenic changes perturb the developmental trajectory, pushing the system into a new attractor basin. The nonergodic dynamics *are* the memory—the system cannot spontaneously return to its previous basin.

Bioelectric goal states [20]: Levin has proposed that cells maintain "goal states"—anatomical target morphologies encoded in bioelectric patterns. When cells "forget" their goal, cancer results. Our framework provides the dynamical systems formalization: the

"goal" is the organismal attractor basin; "forgetting" is bifurcation to a divergent attractor. This reframes teleological language in mechanistic terms while preserving the key insight that cancer is fundamentally a failure of coordination, not merely accumulated mutations.

Developmental plasticity [21, 22]: High-dimensional developmental systems with large Δ_D naturally exhibit plasticity—many attractor basins are accessible from a single anchor.

Systems evolution [23]: Evolution is primarily about functional organization, not individual genes. In our terms: selection modifies anchors, but anchors constrain organizational possibilities without fully determining them.

Development-ageing-cancer [24]: Unified developmental models linking these processes are natural in a nonergodic framework, where trajectory history shapes multiple downstream outcomes.

Process structuralism [25]: Goodwin argued that biological forms are generic properties of developmental dynamics—intrinsic to the physics of excitable, structured media—rather than genetic programs executed by molecular machinery. The genome selects which forms are realized; it does not specify them algorithmically. Our Δ_D metric quantifies the gap between genetic parameters and the structural possibilities of the developmental medium. The "book of life" is not the blueprint; it is the index to a library of dynamically accessible forms.

In the tradition of critiques of algorithmic biology [26], we demonstrate that the gene-as-algorithm assumption is not merely an approximation but a projection that actively discards the trajectory structure of nonergodic development.

7 Conclusion

Biological development is nonergodic. The state space is too vast to explore; trajectories are trapped; phenotypes are attractor states, not algorithmic outputs.

The genome is a low-dimensional anchor that constrains which attractor basins exist,

but environmental history determines which basin is entered. This anchor-trajectory duality offers one lens on the genotype-phenotype relationship: the mapping is many-to-one not only because of noise or missing variants, but also because trajectory information that distinguishes outcomes is projected out by genotype-phenotype analysis.

Sierra et al.'s finding that cooperative species have lower cancer prevalence is real. Our contribution is to show that it admits both anchor-based (selection modified the genotype) and trajectory-based (environment guided development) interpretations—non-identifiable from comparative data, distinguishable only through intervention.

Some of the "missing heritability" in GWAS may be missing trajectories, not missing variants. The dimensional gap Δ_D quantifies how much information is lost when we project from the high-dimensional (anchor, trajectory, attractor) space to the low-dimensional (genotype, phenotype) summary.

Genotype does not algorithmically determine phenotype. Genotype anchors a nonergodic developmental system; environmental history traps it in an attractor; the phenotype is the trapped state. Recognizing this is essential for prediction, intervention, and understanding biological change.

Data and Code Availability

Simulation code is available at `https://github.com/todd866/nonergodic-development`. The repository includes `nonergodic_development.py`, which implements the developmental network (Equations 2–5), generates all figures, and demonstrates the Twin Worlds experiment (Figure 5).

Declaration of competing interest

The author declares that there are no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author used Claude Code (Claude 4.5 Opus) for primary drafting and model development, with feedback from Gemini 3 Pro and GPT 5.1 Pro. After using these tools, the author reviewed and edited the content as needed and takes full responsibility for the content of the published article.

References

[1] Sierra, C., et al. (2025). Coevolution of cooperative lifestyles and reduced cancer prevalence in mammals. *Science Advances*, 11(46), eadw0685. https://doi.org/10.1126/sciadv.adw0685

[2] Singh, M., & Glowacki, L. (2022). Human social organization during the Late Pleistocene: Beyond the nomadic-egalitarian model. *Evolution and Human Behavior*, 43(5), 418–431. https://doi.org/10.1016/j.evolhumbehav.2022.07.003

[3] Pigliucci, M. (2010). Genotype–phenotype mapping and the end of the 'genes as blueprint' metaphor. *Philosophical Transactions of the Royal Society B*, 365(1540), 557–566. https://doi.org/10.1098/rstb.2009.0241

[4] Alberch, P. (1991). From genes to phenotype: dynamical systems and evolvability. *Genetica*, 84(1), 5–11. https://doi.org/10.1007/BF00123979

[5] West-Eberhard, M.J. (2003). *Developmental Plasticity and Evolution*. Oxford University Press. https://doi.org/10.1093/oso/9780195122343.001.0001

[6] Todd, I. (2025). The limits of falsifiability: Dimensionality, measurement thresholds, and the sub-Landauer domain in biological systems. *BioSystems*, 248, 105608. https://doi.org/10.1016/j.biosystems.2025.105608

[7] Todd, I. (2025). Timing inaccessibility and the projection bound: Resolving Maxwell's demon for continuous biological substrates. *BioSystems*, 249, 105632. https://doi.org/10.1016/j.biosystems.2025.105632

[8] Manolio, T.A., et al. (2009). Finding the missing heritability of complex diseases. *Nature*, 461(7265), 747–753. https://doi.org/10.1038/nature08494

[9] Zuk, O., Hechter, E., Sunyaev, S.R., & Lander, E.S. (2012). The mystery of missing heritability: Genetic interactions create phantom heritability. *Proceedings of the National Academy of Sciences*, 109(4), 1193–1198. https://doi.org/10.1073/pnas.1119675109

[10] Waddington, C.H. (1957). *The Strategy of the Genes*. Allen & Unwin, London.

[11] Noble, D. (2012). A theory of biological relativity: no privileged level of causation. *Interface Focus*, 2(1), 55–64. https://doi.org/10.1098/rsfs.2011.0067

[12] Kauffman, S.A. (1993). *The Origins of Order: Self-Organization and Selection in Evolution*. Oxford University Press.

[13] Huang, S. (2009). Non-genetic heterogeneity of cells in development: more than just noise. *Development*, 136(23), 3853–3862. https://doi.org/10.1242/dev.035139

[14] Schlichting, C.D., & Pigliucci, M. (1998). *Phenotypic Evolution: A Reaction Norm Perspective*. Sinauer Associates.

[15] Stearns, S.C. (1992). *The Evolution of Life Histories*. Oxford University Press.

[16] Roff, D.A. (2002). *Life History Evolution*. Sinauer Associates.

[17] Aktipis, C.A., et al. (2015). Cancer across the tree of life: cooperation and cheating in multicellularity. *Philosophical Transactions of the Royal Society B*, 370(1673), 20140219. https://doi.org/10.1098/rstb.2014.0219

[18] Wagner, A. (2011). *The Origins of Evolutionary Innovations: A Theory of Transformative Change in Living Systems*. Oxford University Press.

[19] Lissek, T. (2024). Cancer memory as a mechanism to establish malignancy. *BioSystems*, 247, 105381. https://doi.org/10.1016/j.biosystems.2024.105381

[20] Levin, M. (2023). Bioelectric networks: The cognitive glue enabling evolutionary scaling from physiology to mind. *Animal Cognition*, 26, 1865–1891. https://doi.org/10.1007/s10071-023-01780-3

[21] Lee, C., Axtell, M., & Bhattacharya, S. (2022). Evolution and maintenance of phenotypic plasticity. *BioSystems*, 222, 104782. https://doi.org/10.1016/j.biosystems.2022.104782

[22] Letsou, W. (2024). The indispensable role of time in autonomous development. *BioSystems*, 246, 105354. https://doi.org/10.1016/j.biosystems.2024.105354

[23] Corning, P.A. (2022). A systems theory of biological evolution. *BioSystems*, 214, 104630. https://doi.org/10.1016/j.biosystems.2022.104630

[24] Fontana, A. (2023). Unravelling the nexus: Towards a unified model of development, ageing, and cancer. *BioSystems*, 234, 105066. https://doi.org/10.1016/j.biosystems.2023.105066

[25] Goodwin, B.C. (1994). *How the Leopard Changed Its Spots: The Evolution of Complexity*. Charles Scribner's Sons.

[26] Rosen, R. (1991). *Life Itself: A Comprehensive Inquiry into the Nature, Origin, and Fabrication of Life*. Columbia University Press.

[27] Bellman, R. (1957). *Dynamic Programming*. Princeton University Press.

[28] Gelman, A., Carlin, J.B., Stern, H.S., Dunson, D.B., Vehtari, A., & Rubin, D.B. (2014). *Bayesian Data Analysis* (3rd ed.). CRC Press.

[29] Roberts, G.O., Gelman, A., & Gilks, W.R. (1997). Weak convergence and optimal scaling of random walk Metropolis algorithms. *Annals of Applied Probability*, 7(1), 110–120. https://doi.org/10.1214/aoap/1034625254

[30] Levinthal, C. (1969). How to fold graciously. In *Mössbauer Spectroscopy in Biological Systems: Proceedings of a Meeting held at Allerton House, Monticello, Illinois* (pp. 22–24). University of Illinois Press.

[31] Peters, O. (2019). The ergodicity problem in economics. *Nature Physics*, 15, 1216–1221. https://doi.org/10.1038/s41567-019-0732-0