A Universal Inductive Engine for Life: Formalism, Mathematical Framework, and a Cross-Environment Transfer Testbed

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Abstract

We present a mathematical and computational framework that treats *Nature* as a universal, parameterized generative law $\mathcal{N}_\theta$, and *Environment* as a vector of local boundary conditions E. The central hypothesis is that life, in any environment, arises from the same fundamental generative rules once expressed through local parameters. By calibrating θ to Earth and transferring it to other environmental vectors, we can empirically test whether life's emergence is a general property of physics. We formalize the system as a stochastic simulator $S(\theta, E, u)$, define Bayesian calibration and cross-environment transfer, and propose a reaction–diffusion substrate for implementation.

Keywords: artificial life, Bayesian calibration, reaction–diffusion, cross-environment transfer, origin of life

1 Introduction

Life's existence raises the question of whether it is a singular accident or an inevitable result of the laws of nature. We formalize this by distinguishing between two interacting entities:

- **Nature** $\mathcal{N}$: the invariant rule set—physical and chemical laws—governing transformation and self-organization;
- **Environment** E: the contingent configuration of matter, energy, and constraints within space–time.

We propose a *Universal Inductive Engine* capable of simulating how $\mathcal{N}$, instantiated under different E, yields life-like structures. Earth serves as the base case; generalization to another environment E' becomes an inductive test of universality.

2 Formal Framework and Notation

2.1 Objects and Functions

Let $\mathcal{N}_\theta$ denote a family of generative mechanisms parameterized by $\theta \in \Theta \subseteq \mathbb{R}^m$. Let $E \in \mathcal{E}$ be an environment vector specifying planetary conditions. Let $S : \Theta \times \mathcal{E} \times \mathcal{U} \to \mathcal{T}$ be a stochastic simulator producing trajectories $T = S(\theta, E, u)$.

Here:

- Θ – parameter space (diffusion, reaction rates, energy conversion constants);
- $\mathcal{E}$ – environment space (temperature, pressure, composition, flux);
- $\mathcal{U}$ – random seeds or stochastic inputs;
- $\mathcal{T}$ – trajectory space (fields or agent states through time).

2.2 Inference Tasks

(a) Calibration (base case) Given Earth data O_{Earth},

$$p(\theta|O_{Earth}) \propto p(O_{Earth}|\theta)\, p(\theta). \tag{1}$$

(b) Prediction / Transfer For a new environment E':

$$p(\text{Life-like}|E') = \int p(\text{Life-like}|\theta, E')\, p(\theta|O_{Earth})\, d\theta. \tag{2}$$

(c) Empirical Test (RQ5) Find θ^* optimized in E_A, transfer to E_B, and measure viability and adaptation rate:

$$V_{transfer} = \frac{\text{Successful simulations in } E_B}{\text{Total runs}}. \tag{3}$$

3 Model Specification: Reaction–Diffusion Substrate

We use a continuous, spatially explicit model linking physics, chemistry, and biology.

3.1 Continuous Form

For m species with concentrations $c_i(x, t)$:

$$\frac{\partial c_i}{\partial t} = D_i(\theta)\nabla^2 c_i + R_i(c(x,t); \theta, E) + I_i(x; E) - \gamma_i(\theta)c_i + \eta_i(x,t), \tag{4}$$

where D_i are diffusion coefficients, R_i local reactions, I_i environment inputs, and η_i stochastic noise.

3.2 Reaction Templates

$$R_i(c;\theta) = \sum_{j=1}^{J} \alpha_j(\theta)\, f_{j,i}(c;\phi_j(\theta)). \tag{5}$$

Each $f_{j,i}$ encodes a reaction type such as:

$$\begin{aligned} f_{bin} &: A + B \xrightarrow{k} C, & R_C &= k\, c_A c_B, \\ f_{auto} &: A + R \xrightarrow{k} 2A, & R_A &= k\, c_A c_R, \\ f_{sat} &: \frac{k\, c_A c_B}{K + c_B} & & \text{(Michaelis–Menten form).} \end{aligned}$$

3.3 Discrete Implementation

On a 2-D grid:

$$c_i^{(p)}(t + \Delta t) = c_i^{(p)}(t) + \Delta t \Big[D_i \Delta_{\text{disc}} c_i^{(p)} + R_i^{(p)}(c;\theta) + I_i^{(p)}(E) - \gamma_i c_i^{(p)} \Big] + \eta_i^{(p)}. \tag{6}$$

Δ_{disc} is the discrete Laplacian operator.

4 Turing Analysis of the Reaction–Diffusion Substrate

We examine the conditions under which a homogeneous steady state of the reaction–diffusion (R–D) substrate becomes unstable to spatial perturbations, producing stationary patterns. This mechanism—the *diffusion–driven instability*—is interpreted in our Universal Inductive Engine as the minimal mathematical signature of self–organization and prebiotic structure formation.

4.1 Two–species reaction–diffusion system

Consider two interacting concentration fields $u(x,t)$ and $v(x,t)$:

$$\frac{\partial u}{\partial t} = D_u \nabla^2 u + f(u,v), \tag{7}$$

$$\frac{\partial v}{\partial t} = D_v \nabla^2 v + g(u,v), \tag{8}$$

where $D_u, D_v > 0$ are diffusion coefficients (components of θ), and f, g are nonlinear reaction functions determined by θ and environmental parameters E.

Let (u_0, v_0) denote a homogeneous steady state satisfying $f(u_0, v_0) = g(u_0, v_0) = 0$. We perturb this equilibrium by small fluctuations:

$$u = u_0 + \tilde{u}(x,t), \qquad v = v_0 + \tilde{v}(x,t),$$

with $|\tilde{u}|, |\tilde{v}| \ll 1$.

4.2 Linearization and Jacobian

Linearizing Eqs. (7)–(8) about (u_0, v_0) gives

$$\frac{\partial}{\partial t}\begin{pmatrix}\tilde{u}\\ \tilde{v}\end{pmatrix} = \begin{pmatrix} D_u\nabla^2 & 0 \\ 0 & D_v\nabla^2 \end{pmatrix}\begin{pmatrix}\tilde{u}\\ \tilde{v}\end{pmatrix} + J\begin{pmatrix}\tilde{u}\\ \tilde{v}\end{pmatrix}, \tag{9}$$

where the Jacobian of the reaction part is

$$J = \begin{pmatrix} f_u & f_v \\ g_u & g_v \end{pmatrix}_{(u_0,v_0)}.$$

Here $f_u = \partial f/\partial u$ and so forth, evaluated at the steady state.

4.3 Fourier mode decomposition

We seek normal–mode solutions of the form

$$\begin{pmatrix}\tilde{u}\\ \tilde{v}\end{pmatrix} = \mathbf{A}\, e^{\lambda t + i\mathbf{k}\cdot\mathbf{x}},$$

where $\mathbf{k}$ is the spatial wavevector and $k = |\mathbf{k}|$. Substituting into (9) yields the eigenvalue problem

$$\lambda\,\mathbf{A} = (J - k^2 D)\mathbf{A}, \qquad D = \begin{pmatrix} D_u & 0 \\ 0 & D_v \end{pmatrix}.$$

For each wavenumber k, the growth rates λ are the eigenvalues of $J - k^2 D$.

4.4 Characteristic equation and dispersion relation

The characteristic polynomial is

$$\lambda^2 - \lambda\left(f_u + g_v - k^2(D_u + D_v)\right) + \left(\det J - k^2 S + k^4 D_u D_v\right) = 0, \tag{10}$$

where we define

$$S = f_u D_v + g_v D_u, \qquad \det J = f_u g_v - f_v g_u.$$

The two eigenvalues $\lambda_{1,2}(k)$ satisfy

$$\lambda_{1,2}(k) = \frac{1}{2}\Big[\,\tau(k) \pm \sqrt{\tau(k)^2 - 4\Delta(k)}\,\Big], \tag{11}$$

with

$$\tau(k) = f_u + g_v - k^2(D_u + D_v), \qquad \Delta(k) = \det J - k^2 S + k^4 D_u D_v.$$

The function $\Re[\lambda(k)]$ plotted versus k is the *dispersion relation*. A positive value indicates exponential growth of that mode.

4.5 Conditions for diffusion–driven instability

The steady state is stable to homogeneous perturbations ($k = 0$) if

$$\mathrm{tr} J = f_u + g_v < 0, \tag{12}$$

$$\det J > 0. \tag{13}$$

A Turing instability occurs when Eqs. (12)–(13) hold but there exists a nonzero wavenumber $k = k_c > 0$ such that $\Re[\lambda(k_c)] > 0$.

This is equivalent to requiring that

$$\det(J - k^2 D) = \det J - k^2 S + k^4 D_u D_v < 0$$

for some positive k. Since this is a quadratic in $y = k^2$, we define

$$\Phi(y) = \det J - yS + y^2 D_u D_v.$$

A necessary and sufficient condition for an interval of positive y with $\Phi(y) < 0$ is that the discriminant

$$\Delta_T = S^2 - 4 D_u D_v \det J > 0,$$

and that the smaller root

$$y_1 = \frac{S - \sqrt{\Delta_T}}{2 D_u D_v}$$

is positive. Hence the classical Turing conditions are:

$$f_u + g_v < 0, \tag{14}$$

$$\det J > 0, \tag{15}$$

$$S^2 - 4 D_u D_v \det J > 0, \tag{16}$$

$$S > 0. \tag{17}$$

The range of unstable wavenumbers is

$$k \in \left(\sqrt{y_1}, \sqrt{y_2}\right), \quad y_{1,2} = \frac{S \mp \sqrt{\Delta_T}}{2D_u D_v}.$$

Within this band, infinitesimal perturbations grow, producing spatially periodic structure with characteristic wavelength $\lambda_c = 2\pi/k_c$.

4.6 Interpretation for the Universal Inductive Engine

In the Engine, θ includes all quantities entering Eqs. (7)–(8), so the above algebra defines a function $G(\theta, E) \to$ "pattern–forming" or "non–pattern–forming". Scanning θ identifies subregions of parameter space where self–organization occurs.

The existence of Turing bands signifies that the underlying "Nature" model $\mathcal{N}_\theta$ can, under certain environmental conditions E, spontaneously generate spatial order. The centroid k_c of the unstable band determines the emergent structure size; its persistence range across different E quantifies the robustness and hence the "transferability" of that Nature configuration to other environments.

5 Module-by-Module Mathematical Designs and Generalizations

The reaction–diffusion kernel is the baseline substrate for the Engine. To approach realism we add modules that capture (i) more species, (ii) nonlinear kinetic forms and saturations, (iii) stochastic mesoscopic effects, (iv) advection/flow, (v) compartmentalization (membranes), (vi) explicit energetic bookkeeping, (vii) template-based replication, and (viii) meta-level evolution of rule sets. Below we provide the mathematical specification of each module, short derivations/linearized forms where useful, interpretation for the Engine, and notes on numerical implementation and scalability.

5.1 (A) n–species Reaction–Diffusion (RD-n)

Equations. Generalize the two-species system to n interacting scalar fields $c_i(x,t)$, $i = 1, \ldots, n$:

$$\frac{\partial c_i}{\partial t}(x,t) = D_i(\theta)\,\nabla^2 c_i + R_i\big(c_1, \ldots, c_n; \theta, E\big) + I_i(x; E) - \gamma_i(\theta)\,c_i + \eta_i(x,t), \qquad i = 1, \ldots, n. \tag{18}$$

Here D_i are diffusion coefficients, R_i the net reaction production rates (sums of elementary reaction templates), I_i exogenous inputs, γ_i decay/dissipation, and η_i stochastic forcing.

Linearization and stability. Let $\mathbf{c}_0$ be a homogeneous steady state solving $R_i(\mathbf{c}_0) = 0$ (assuming I constant or balanced). Linearize:

$$\partial_t \tilde{\mathbf{c}} = \big(J - k^2 D\big)\tilde{\mathbf{c}}, \quad J_{ij} = \left.\frac{\partial R_i}{\partial c_j}\right|_{\mathbf{c}_0}, \quad D = \mathrm{diag}(D_1, \ldots, D_n).$$

For each wavenumber k compute eigenvalues of $J - k^2 D$. Instability requires at least one eigenvalue with positive real part for $k > 0$ while all eigenvalues at $k = 0$ have negative real parts.

Interpretation for the Engine. The n–species system increases expressivity: more chemical degrees of freedom allow richer catalytic networks, complex autocatalytic sets, and emergent modules. Scanning θ in higher dimensions finds multi-modal instability regimes and hierarchical patterning.

Computational notes. - Discretized cost $\propto n \cdot N^d \cdot T$ per simulation. - Eigenvalue scan for dispersion relation has cost $O(n^3)$ per k (for dense Jacobian) but n is usually modest (10s). - Use sparse Jacobian structure when reactions are local in species index.

5.2 (B) Nonlinear Kinetics and Saturation

Typical nonlinear forms. To prevent unbounded growth and capture enzymatic saturation, include Michaelis–Menten and Hill forms in reaction templates:

$$\text{Michaelis–Menten:} \quad v = \frac{k\, c_A}{K_M + c_A}, \tag{19}$$

$$\text{Hill kinetics:} \quad v = \frac{k\, c_A^n}{K^n + c_A^n}, \tag{20}$$

$$\text{Autocatalytic w/ saturation:} \quad R_A = k\frac{c_A c_R}{1 + \alpha c_A}. \tag{21}$$

Nonlinear steady states and bifurcations. Nonlinear terms produce multiple steady states and limit cycles. For a given parameter set, compute steady solutions $\mathbf{c}^*$ by solving $R_i(\mathbf{c}^*) = 0$ and then analyze Jacobian eigenvalues to classify local stability (saddle-node, Hopf bifurcations, etc.).

Interpretation for the Engine. Nonlinearities shape the amplitude and saturation of emergent structures. For transferability, systems whose operating point sits in a broad stable basin (robust limit cycles or attractors) are more likely to survive environmental perturbations.

Computational notes. Simulate full nonlinear PDEs; linear analysis gives onset but not final pattern amplitude. Use continuation tools (AUTO, MatCont) for bifurcation diagrams when the dimension of parameter slices is small.

5.3 (C) Advection and Flow

Reactive advection equations. Include an advective velocity field $\mathbf{v}(x,t)$:

$$\frac{\partial c_i}{\partial t} + \nabla \cdot \big(\mathbf{v} c_i\big) = D_i \nabla^2 c_i + R_i(c;\theta,E) + I_i - \gamma_i c_i + \eta_i. \tag{22}$$

Modeling v. Options (in increasing complexity):

1. **Prescribed field:** $\mathbf{v}(x,t)$ given analytically (e.g., cellular vortices, shear flows).
2. **Stochastic advection:** $\mathbf{v}$ sampled from a correlated random field with prescribed turbulence statistics (e.g., Kraichnan model).
3. **Coupled fluid dynamics:** solve Navier–Stokes for $\mathbf{v}$, possibly with Boussinesq approximation for buoyancy coupling (expensive).

Linearized effect on dispersion. Advection adds an imaginary term in Fourier space:

$$\tilde{u} \propto e^{\lambda t + i\mathbf{k}\cdot\mathbf{x}} \Rightarrow \lambda \mapsto \lambda - i\mathbf{k}\cdot\mathbf{v}.$$

Advection typically shifts and can broaden instability bands; strong shear suppresses pattern formation at certain scales.

Interpretation for the Engine. Advection may either destroy fine-scale structures (mixing) or create shear-driven patterns; it is therefore an important environmental parameter in $\mathcal{E}$. For transfer testing, include effective advection parameters (mean flow magnitude, eddy diffusivity).

Computational notes. - If $\mathbf{v}$ is prescribed or coarse-grained, cost modest. - Coupling to Navier–Stokes is expensive and should be treated via multi-fidelity experiments (low-res coupled sim for plausible regimes, surrogate models for broad scans).

5.4 (D) Stochastic Spatial Chemistry: RDME / Spatial Gillespie

Mesoscopic stochastic formulation. When particle numbers are low, spatial continuum models fail. Discretize space into voxels p; let $N_i^{(p)}(t)$ be integer counts. Reactions occur with propensities $a_r(\mathbf{N}^{(p)})$ and diffusion as jump events with rates proportional to

D_i. The spatial chemical master equation describes probabilities $P(\{N\}, t)$ but is typically simulated with spatially extended Gillespie algorithms (Next Reaction Method).

Example reaction event: In voxel p, reaction r consumes and produces stoichiometric vector ν_r with propensity $a_r(N^{(p)})$ and occurs with probability $a_r \Delta t$ in small Δt.

Interpretation for the Engine. RDME captures rare-but-critical nucleation events (e.g., protocell assembly) and stochastic extinction phenomena that deterministic RD misses. It is thus important for micro-scale transfer tests.

Computational notes. RDME scales poorly for large domain sizes; hybrid methods couple RDME in small critical regions to PDE outside. Use this where local counts are small and stochasticity dominates.

5.5 (E) Compartment / Membrane Dynamics (Phase-Field)

Phase-field approach. Introduce a scalar phase-field $\phi(x, t) \in [0, 1]$ representing local 'interiorness' (1 = inside compartment). Evolve ϕ with an Allen–Cahn/Cahn–Hilliard type dynamics coupled to chemistry:

$$\frac{\partial \phi}{\partial t} = -M_\phi \frac{\delta \mathcal{F}[\phi]}{\delta \phi} + S_\phi(c; \theta) + \xi_\phi, \tag{23}$$

$$\mathcal{F}[\phi] = \int \Big(\frac{\epsilon^2}{2} |\nabla \phi|^2 + W(\phi) \Big) \, dx, \tag{24}$$

where $W(\phi)$ is a double-well potential and S_ϕ is a source term (production of membrane material by chemistry). Coupling to species diffusion:

$$D_i(x, t) = D_i^{\text{in}} \phi + D_i^{\text{out}} (1 - \phi),$$

or more generally include permeability terms at interfaces.

Membrane-mediated reaction coupling. Some reactions occur preferentially inside $\phi \approx 1$ regions. Model this by making R_i depend on ϕ (e.g., reaction rates multiplied by ϕ or $\Theta(\phi - \phi_0)$ threshold).

Interpretation for the Engine. Compartmentalization fosters metabolic coupling and protects information-bearing templates; it is therefore a critical structural module whose presence strongly affects transfer robustness.

Computational notes. Phase-field dynamics add stiffness; semi-implicit schemes and adaptive meshes help. Phase-field + RD in 2D/3D is computationally heavier but gives natural membrane behaviors (budding, fission, fusion).

5.6 (F) Energetics and Thermodynamic Coupling

Energy field and reaction coupling. Introduce an energy density $e(x,t)$ (or temperature T) and couple to reactions via energetics. For reactions r with free-energy change ΔG_r and rate R_r, energy balance:

$$\frac{\partial e}{\partial t} = -\sum_r \Delta G_r \, R_r(c;\theta) + \kappa_e \nabla^2 e + I_e(x;E) - \gamma_e e + \eta_e. \tag{25}$$

Reaction rates may depend on e through Arrhenius or other laws:

$$k_r(e) = k_{r,0} \exp\Big(- \frac{E_{a,r}}{k_B T(e)} \Big).$$

Entropy production proxy. Define local entropy production proxy (per unit time)

$$\sigma(x,t) \approx \sum_r \frac{R_r \Delta G_r}{T(e)}.$$

Interpretation for the Engine. Tracking energy and dissipation allows comparison of organizational efficiency and provides thermodynamic metrics useful for life detection (e.g., sustained non-equilibrium fluxes).

Computational notes. Energy coupling requires solving Eq. (25) alongside species; activation energies can induce stiffness (implicit methods recommended).

5.7 (G) Template-based Replication and Information

Template concentrations and replication dynamics. Let $T_j(x,t)$ be concentration of template class j (abstract sequences or functional types). Replication with resources c:

$$\frac{\partial T_j}{\partial t} = D_T \nabla^2 T_j + \rho_j(c;\theta)\, T_j - \delta_j T_j + \sum_i \mu_{ji} \rho_i(c)\, T_i + \eta_{T_j}, \tag{26}$$

where $\rho_j(c)$ is replication rate dependent on metabolic fields, δ_j decay, and μ_{ji} mutation kernel (probability that offspring of type i is type j).

Quasispecies mutation-selection dynamics. In compact form, the local dynamics without diffusion follow a quasispecies-like system:

$$\dot{\mathbf{T}} = W(c)\,\mathbf{T} - \Phi(c)\,\mathbf{T},$$

where $W_{ji} = \mu_{ji}\rho_i(c)$ and Φ a normalization or resource limitation. Spatial coupling (diffusion) allows templates to spread.

Interpretation for the Engine. Templates provide heritable variation; their coupling with compartments and energy fields enables sustained evolution. Transfer experiments can test whether template-based systems discovered in E_A can found populations in E_B.

Computational notes. Template space is combinatorial; practical approaches: - abstract templates to a small set of functional classes, or - use agent-based discrete sequences in small domains, or - project sequence space onto low-dimensional phenotype axes.

5.8 (H) Meta-evolution: Evolving Rule Sets and Genomes

Population of rule-genomes. Each genome G encodes a parameterized rule set (active templates, their rates, threshold flags). Evaluate fitness $F(G; E)$ by simulating the inner-loop physical/chemical dynamics and computing metrics (e.g., persistence P, reproduction R).

Evolutionary algorithm (EA) loop. A standard EA proceeds:

1. Initialize population $\mathcal{P}_0$ of genomes.
2. For generation t: evaluate $F(G)$ for $G \in \mathcal{P}_t$ (each by simulating $S(G, E, u)$ across seeds).
3. Select parents by tournament/fitness-proportionate selection.
4. Apply crossover and mutation (meta-mutation rate μ_G) to produce $\mathcal{P}_{t+1}$.

Population-level PDE approximation (optional). For large populations with continuous genome representations, adaptive dynamics or replicator-mutator equations approximate the meta-dynamics:

$$\partial_t p(G,t) = \big(F(G) - \bar{F}(t)\big)p(G,t) + \mathcal{M}[p],$$

where $\mathcal{M}$ is a mutation operator.

Interpretation for the Engine. Meta-evolution discovers viable rule-sets within $\mathcal{N}_\theta$. Transfer experiments compare (i) zero-shot performance of discovered G in E_B and (ii) adaptation speed under meta-evolution in E_B.

Computational notes. Meta-evolution is the primary computational multiplier: each genome evaluation requires many inner simulations. Strategies to reduce cost: - surrogate fitness models, multi-fidelity evaluation, and active learning; - novelty search to preserve behavioral diversity; - asynchronous island models for parallel scaling.

5.9 (I) Coupling Modules: Combined Systems and Hierarchical Reduction

Full coupled system. Combining modules gives a system of PDEs/integro-differential equations, e.g.

$$\begin{aligned}
\partial_t c_i &= -\nabla \cdot (\mathbf{v} c_i) + D_i(\phi)\nabla^2 c_i + R_i(c, \phi, T; \theta, E) - \gamma_i c_i + \eta_i, \\
\partial_t \phi &= -M_\phi \frac{\delta \mathcal{F}}{\delta \phi} + S_\phi(c, T) + \xi_\phi, \\
\partial_t e &= -\sum_r \Delta G_r R_r + \kappa_e \nabla^2 e + I_e - \gamma_e e,
\end{aligned}$$

coupled to template equations (26) and possibly RDME subregions.

Hierarchical reduction and multiscale modeling. - Use dimensional analysis and non-dimensionalization to identify small/large parameters and simplify (e.g., fast diffusion limit, separation of time scales). - Apply homogenization / averaging to derive effective macroscopic transport when microscopic dynamics are fast. - Hybridize: RD (continuum) in bulk, RDME in small domains, agent-based templates inside compartments.

Interpretation for the Engine. This full coupled system is the target of the Engine; however, practical investigation proceeds by staged inclusion of modules and by employing model reduction techniques to keep parameter searches tractable.

5.10 (J) Metrics, Observables and Statistical Design

Primary metrics (repeat for clarity). Define metrics computed from trajectories:

- Persistence P: fraction of time the total active mass exceeds threshold δ.
- Reproduction index R: count of splitting events detected by local peak-tracking algorithms.

- Energy flux E_f: time-average of resource uptake integrals.
- Compartmentalization C: number/volume of ϕ-regions above threshold.
- Entropy production proxy σ: spatial integral of local dissipation $\sum_r R_r \Delta G_r / T$.

Experimental design and statistical power. - Use M independent stochastic seeds per genome to estimate mean and variance of metrics. - For transfer proportion tests, select sample sizes to achieve target power (e.g., $\beta = 0.8$) for anticipated effect sizes; use bootstrapping and permutation tests for nonparametric inference.

5.11 (K) Computational Complexity Practical Strategies

Complexity rough formula. A single PDE simulation cost:

$$\mathcal{C}_{\text{sim}} \approx C_{\text{ops}} \cdot n \cdot N^d \cdot T,$$

where C_{ops} per cell depends on reaction complexity. With meta evolution and S genomes and R seeds each:

$$\mathcal{C}_{\text{total}} \approx \mathcal{C}_{\text{sim}} \cdot S \cdot R.$$

Practical acceleration techniques.

- Multi-fidelity evaluation: early terminate poor genomes; run full-resolution sims only for promising candidates.
- Surrogate modeling: train regression/emulator $g(\theta) \approx F(\theta)$ to reduce simulator calls.
- Analytical pruning: apply linear Turing checks (eigenvalue pre-screens) to eliminate parameter regions with no pattern potential.
- Parallelization: evaluate genomes and stochastic seeds in parallel across cluster/GPU resources.
- Behavioral compression: store and operate on small summary statistics instead of full trajectories for search and clustering.

5.12 (L) Generalization remarks

From modules to universality. The modules above are intended to collectively approximate the minimal physical and informational processes believed necessary for life-like organization. The Engine does not require a fully exhaustive physical model; instead,

it seeks to identify *which* primitives are required for transferability by systematically ablating, enriching, and comparing families $\mathcal{N}_\theta$.

Falsifiability. Negative results (failure to transfer across broad priors) falsify the specific model family $\mathcal{N}_\theta$ under study, not the general philosophical claim that 'life is lawful'. By iteratively enriching $\mathcal{N}$ with additional primitives (e.g., explicit membranes or template dynamics) and re-running transfer experiments we obtain a data-driven map of necessary primitives.

6 Parameterization and Priors

A generic θ vector includes:

- D_i – diffusion coefficients,
- k_j – reaction rates,
- γ_i – decay constants,
- P – permeability,
- μ – mutation rate.

Parameter	Symbol	Typical Range
Diffusion coefficient	D_i	0.01–1.0
Reaction rate	k_j	10^{-4}–1.0
Decay constant	γ_i	10^{-5}–10^{-2}
Permeability	P	0–1
Mutation rate	μ	10^{-6}–10^{-2}

Table 1: Pilot parameter ranges for θ.

7 Calibration and Inference for θ

7.1 Optimization

Find $\theta^* = \arg\max_\theta M(\theta)$ where M measures similarity between simulated and observed life metrics.

7.2 Approximate Bayesian Computation

1. Sample $\theta^{(i)} \sim p(\theta)$.
2. Simulate $T^{(i)} = S(\theta^{(i)}, E_{Earth}, u)$.
3. Compute summary statistics $s^{(i)}$ and distance $d^{(i)} = \rho(s^{(i)}, s_{obs})$.
4. Accept $\theta^{(i)}$ if $d^{(i)} < \epsilon$.

7.3 Surrogate Models

Fit a Gaussian Process or neural network surrogate $g(\theta) \approx M(\theta)$ to guide Bayesian optimization and reduce simulation cost.

8 Meta-Search for Life-like Rule Sets

Use evolutionary or novelty search:

- Population P of genomes encodes rule templates and parameters.
- Evaluate each genome using simulator S; compute fitness F and novelty score N.
- Select parents $\propto F + \lambda N$; apply crossover and mutation.
- Maintain an archive of high-novelty, high-persistence structures.

9 Cross-Environment Transfer Experiment

Let E_A (training) and E_B (test) be two environments.

1. Discover viable genomes R_A in E_A.
2. Evaluate zero-shot transfer in E_B.
3. Evolve for G_{adapt} generations in E_B; compare adaptation time to baseline.

9.1 Statistics

Use permutation tests for transfer success and log-rank tests for adaptation curves. Compute confidence intervals by bootstrapping across stochastic seeds.

10 Metrics for Life-like Behavior

- **Persistence** P: Fraction of time active mass exceeds threshold.
- **Reproduction index** R: Number of distinct growth-and-split events.
- **Energy flux** E_f: Mean resource uptake.
- **Modularity** M: Spatial clustering or compartmentalization.
- **Novelty** N: Behavioral distance from known archive members.

11 Numerical Methods and Implementation

Use explicit Euler integration for prototyping:

$$c^{t+1} = c^t + \Delta t \cdot F(c^t; \theta, E).$$

Ensure stability: $\Delta t \leq \frac{\Delta x^2}{4D_{max}}$. Vectorize with JAX or PyTorch; parallelize across GPUs; store summary statistics rather than full trajectories for reproducibility.

12 Threshold Calibration and the Observer Problem

A critical issue when operationalizing "life-like" is the choice of thresholds (e.g. $H > h_0$ for heritability). To avoid subjective selection, we construct data-driven decision rules using reference libraries and ROC analysis.

12.1 Reference libraries

We build two curated libraries of simulated systems:

- **Abiotic library** $\mathcal{A} = \{A_1, \ldots, A_{N_A}\}$: canonical non-life pattern formers (e.g., Schnakenberg/Turing patterns, Rayleigh–Bénard convection, crystal growth models, reaction–diffusion oscillators) sampled across parameter ranges.
- **Biotic library** $\mathcal{B} = \{B_1, \ldots, B_{N_B}\}$: minimal information-bearing systems (e.g., simple template replicators, hypercycles, GARD instances, compartmentalized replicators).

For each run we compute a vector of summary metrics:

$$\mathbf{s} = \big(P, R, H, I_f, E_v, \ldots\big),$$

where P = persistence, R = reproduction index, H = heritability, I_f = mutual information between template and function, and E_v = evolvability.

12.2 ROC calibration

For any scalar score function $S(\mathbf{s})$ (which may be one metric or a composite), we estimate the empirical distributions $p_A(S)$ and $p_B(S)$ from the libraries. The ROC curve is computed by sweeping threshold t and plotting true positive rate $\mathrm{TPR}(t) = P_B[S > t]$ vs false positive rate $\mathrm{FPR}(t) = P_A[S > t]$. We select an operating point t^* according to an acceptable FPR (for example FPR= 0.01) or by maximizing Youden's index (TPR+TNR−1). The Area Under the ROC Curve (AUC) is reported to summarize discriminative power.

12.3 Multivariate classifiers

If a single scalar is insufficient, we train a probabilistic classifier (e.g., logistic regression, random forest, or small neural network) $f : \mathbf{s} \mapsto \Pr(\text{life-like} \mid \mathbf{s})$ using $\mathcal{A} \cup \mathcal{B}$ as labeled training data. We then choose a probability threshold π^* via ROC analysis on held-out validation data. This yields a calibrated, objective decision rule:

$$\text{Declare life-like if } \Pr(\text{life-like} \mid \mathbf{s}) \geq \pi^*.$$

12.4 Uncertainty on thresholds

We propagate uncertainty in threshold selection by bootstrap resampling of the reference libraries and reporting confidence bands for the ROC curve and the chosen operating point. In the main results we report both classifier output and its uncertainty (e.g., 95% bootstrap CI for Pr(life-like)).

13 Genomic Representation for Rule Sets

Our meta-evolution acts on genomes that encode combinations of reaction templates and their continuous parameters. We fix a finite library of M reaction templates $\{T_j\}_{j=1}^{M}$ (e.g., mass-action reactions, autocatalytic motifs, membrane formation templates, templated replication). Each genome G is a vector of length M of typed loci:

$$G = \big((a_1, \kappa_1, K_1, \dots),\ (a_2, \kappa_2, K_2, \dots),\ \dots,\ (a_M, \kappa_M, K_M, \dots)\big),$$

where for locus j:

- $a_j \in \{0, 1\}$ is an activation flag (0=off, 1=on),
- $\kappa_j \in \mathbb{R}_+$ is a rate constant,

- $K_j \in \mathbb{R}_+$ is a saturation or affinity constant (optional),
- additional typed fields encode stoichiometry, compartment preference, etc.

Search operators. Evolutionary operators act on these loci:

- **Toggle mutation:** flip a_j with probability μ_a.
- **Parametric mutation:** perturb (κ_j, K_j) by log-normal noise.
- **Crossover:** exchange contiguous subsections of G between parents.

No invention of new physics. Crucially, the search is *combinatorial* and parametric within the predefined template library: the EA cannot invent entirely new operator forms (e.g., quantum tunneling kernels) beyond those in $\{T_j\}$. This clarifies the inductive claim: we discover which combinations and parameter settings of existing primitives explain transferability, not new fundamental laws.

14 Hierarchical Calibration, Identifiability, and Uncertainty Quantification

14.1 Hierarchical Bayesian calibration

We organize parameters into module-specific blocks $\theta = (\theta^{(1)}, \theta^{(2)}, \dots)$ and assign informative priors $p(\theta^{(m)})$ derived from laboratory kinetics, thermodynamics and geochemical constraints. The posterior given Earth observations O_{Earth} is approximated via likelihood-free methods (ABC-SMC or surrogate-assisted MCMC):

$$p(\theta \mid O_{\text{Earth}}) \propto p(\theta)\, p(O_{\text{Earth}} \mid \theta).$$

In practice $p(O_{\text{Earth}} \mid \theta)$ is approximated using summary statistics and a distance metric; surrogate models accelerate evaluation.

14.2 Identifiability and sensitivity

We perform sensitivity analysis and identifiability checks:

- **Local profile likelihoods:** vary a single parameter while reoptimizing others to find identifiability intervals.
- **Global variance-based sensitivity (Sobol indices):** compute first-order and total sensitivity indices to rank parameters by influence on chosen observables.

- **Posterior credible intervals:** report marginal 95% credible intervals for each parameter.

Parameters with posterior mass closely following the prior (wide credible intervals) are flagged as *weakly constrained* and reported explicitly.

14.3 Propagation to predictions

To quantify confidence in transfer predictions, we propagate posterior samples $\{\theta^{(s)}\}$ through the simulator to obtain predictive distributions of transfer metrics (e.g., P_{transfer}). Report posterior predictive means and credible intervals; where credible intervals overlap decision boundaries, results are treated as inconclusive.

15 Model Selection and Occam's Penalty

We compare nested families $\mathcal{N}^{(0)}, \mathcal{N}^{(1)}, \ldots$ where each family adds modules (e.g., compartment module, template module). For model comparison we compute:

- **Bayes factors:** approximate marginal likelihoods $\mathcal{Z} = \int p(O \mid \theta) p(\theta) d\theta$ via thermodynamic integration or ABC-SMC evidence estimators; then $\text{BF}_{ij} = \mathcal{Z}_i / \mathcal{Z}_j$.
- **Cross-validation:** evaluate predictive log-likelihood on held-out simulated cases or bootstrapped subsamples.
- **Information criteria:** compute BIC or AIC on surrogate likelihoods as sanity checks.
- **Minimum description length (MDL):** prefer models that minimize code length = model complexity + cost to encode residuals.

Complex models are penalized unless they materially increase predictive power; this enforces a formal Occam's razor and reduces overfitting via module proliferation.

Reversible-jump extension When comparing models with varying dimensionality we may use reversible-jump MCMC (RJ-MCMC) to sample across model space and compute posterior model probabilities.

16 Environmental Distance and Transfer Radius

16.1 Definition of distance

Let environments be feature vectors in $\mathbb{R}^d$:

$$E = (e_1, \ldots, e_d),$$

where features may include mean temperature, solvent polarity index, characteristic energy flux, typical pH, ionic strength, dominant oxidant/reductant potentials, and characteristic mixing intensity.

Define a normalized Mahalanobis distance:

$$d(E_A, E_B) = \sqrt{(E_A - E_B)^\top \Sigma^{-1} (E_A - E_B)},$$

where Σ is a covariance matrix representing natural variability or measurement uncertainty in environmental features. Mahalanobis weighting accounts for correlated axes and scales.

16.2 Transfer curve and radius

For a given genome G (or posterior mixture of θ) define empirical transfer probability:

$$P_{\text{transfer}}(d) = \Pr\big(\text{success in } E \mid d(E, E_{\text{ref}}) = d\big),$$

estimated by sampling environments at distance d from reference E_{ref}. We define the *radius of transferability* r_q as the smallest radius where $P_{\text{transfer}}(r_q) = q$ (e.g., $q = 0.5$). We report $r_{0.5}$ and $r_{0.1}$ as interpretable summary statistics.

16.3 Experimental grid

In practice, sample a set of environment pairs at varying distances $d_1 < d_2 < \cdots < d_K$ and estimate $P_{\text{transfer}}(d_k)$ with Monte Carlo replicates. Fit a smooth logistic or Gaussian Process to the empirical points to estimate the transfer curve and credible bands.

17 Computational Cost and Statistical Design

Total operations $\approx S \cdot T \cdot N^2 \cdot C$ where S is number of simulations, T timesteps, N grid dimension, and C operations per cell. Pilot scale (64×64 grid, 3 fields, 2000 steps, $S = 1000$) $\Rightarrow\approx 2.4 \times 10^{10}$ FLOPs—tractable on a modern GPU cluster.

18 Interpretation and Model Comparison

Positive results: Transfer viability suggests general Nature priors. **Negative results:** Point to missing mechanisms or mis-specified priors. Bayesian model comparison:

$$\mathrm{BF}_{1,0} = \frac{p(O|\mathcal{N}_1)}{p(O|\mathcal{N}_0)}$$

to evaluate inclusion of new primitives (e.g., compartments).

19 Modular Scope and Universality Claims

The Universal Inductive Engine (UIE) is designed as a hierarchical, modular framework rather than a single fixed physical model. Its baseline substrate $\mathcal{N}_\theta^{(0)}$ is a reaction–diffusion (R–D) system, chosen because R–D equations form the simplest known class of dynamical systems that can spontaneously generate spatial structure from homogeneous conditions. However, the claim of "universality" is made only in a qualified sense: each model family $\mathcal{N}_\theta^{(m)}$ represents one hypothesis about the minimal physics sufficient for life-like organization. Negative results falsify a specific family, not the broader inductive program.

Progressive enrichment. The Engine admits successive enrichment by adding physical and informational modules:

$$\mathcal{N}^{(0)} = \text{R–D core}, \qquad \mathcal{N}^{(1)} = \mathcal{N}^{(0)} + \text{surface catalysis}, \qquad \mathcal{N}^{(2)} = \mathcal{N}^{(1)} + \text{compartments}, \ldots$$

Each enrichment increases realism but also complexity. The modular hierarchy allows falsification at each stage and provides a controlled path toward greater universality.

Beyond continuum dynamics. Where continuum R–D assumptions fail (e.g., solid-state catalysis on mineral surfaces, discrete lattice chemistry, or quantum tunneling effects), the same inductive logic is preserved by substituting appropriate microscopic modules. Each such module modifies the local reaction operator $R_i(\cdot)$ or boundary conditions while leaving the inference and transfer-testing architecture unchanged.

Interpretation. Thus, the universality of the UIE refers to its architectural generality—a meta-framework capable of integrating multiple physical model families—rather than the universality of any single substrate.

20 Information and Heredity Metrics

Life-like organization requires not only persistence and energy throughput but also information storage, heritable variation, and functional correlation between internal states and behavior. To capture these properties we define a set of quantitative metrics that complement purely energetic or morphological measures.

20.1 Lineage Heritability (H)

Let s_t denote a state vector (composition or pattern descriptor) of a localized structure (e.g., a compartment) at time t. When a structure divides, the similarity between parent and offspring states is measured by

$$H = \mathbb{E}\left[\exp\left(-\frac{\|s_{\text{offspring}} - s_{\text{parent}}\|^2}{2\sigma_H^2}\right)\right],$$

where σ_H is a scale factor controlling tolerance. H ranges from 0 (no resemblance) to 1 (perfect copying). Tracking lineage graphs over time yields an empirical distribution of H values; high mean and low variance indicate stable inheritance.

20.2 Functional Information (I_f)

For systems containing explicit templates or rule sets, define a random variable T (template identity) and an observable F (functional behavior, e.g., resource uptake pattern or metabolic flux). Functional information is the mutual information

$$I_f = I(T;F) = \sum_{t,f} p(t,f) \log \frac{p(t,f)}{p(t)p(f)}.$$

Abiotic pattern formers typically yield $I_f \approx 0$, whereas biological systems maintain $I_f > 0$ across generations.

20.3 Evolvability (E_v)

Expose a population of replicators to a controlled environmental perturbation and measure improvement in fitness $F(t)$ over generations:

$$E_v = \frac{1}{\tau}\frac{dF}{dt}\Big|_{t\in[0,\tau]}.$$

Positive E_v indicates adaptation capacity. Non-evolving pattern formers show $E_v \approx 0$.

20.4 Composite life-likeness score (L)

We combine persistence P, reproduction index R, and the above information metrics into a composite probabilistic classifier $f(\mathbf{s}) = \Pr(\text{life-like} \mid \mathbf{s})$, trained via ROC analysis on reference libraries of abiotic and biotic simulations (see Sec. 12). The decision threshold is data-driven, ensuring objectivity and controlled false positive rates.

Benchmarking. As a validation step we compute (P, R, H, I_f, E_v) for canonical abiotic systems (Schnakenberg, BZ reaction, Rayleigh–Bénard convection) and for simple biotic models (hypercycles, GARD). Distributions are compared using ROC and AUC analysis to demonstrate separability between abiotic and biotic regimes.

21 Hierarchical Calibration and Data Sources

Modular calibration. The parameter space Θ is partitioned by module, and each block $\theta^{(m)}$ is calibrated using the most relevant empirical or experimental data available. This modular calibration minimizes dimensionality and exploits domain-specific knowledge.

21.1 Data sources for priors and likelihoods

- **Geochemical proxies:** early-Earth isotopic records (e.g., δ^{13}C, sulfur mass-independent fractionation), mineralogical assemblages (serpentinization evidence constraining H_2 flux), and paleoclimate reconstructions (temperature, salinity, pH).
- **Experimental origin-of-life chemistry:** autocatalytic reaction yields, peptide bond formation rates under catalytic surfaces, lipid self-assembly thresholds (critical micelle concentrations), ribozyme polymerization kinetics.
- **Biochemical universals:** conserved motifs in metabolism (e.g., phosphate transfer chains, redox cofactors), chirality, and core network topologies from databases such as KEGG or MetaCyc.
- **Planetary observations:** exoplanet atmospheric compositions, thermal profiles, and photometric constraints where available, used for environmental priors $p(E)$.

21.2 Hierarchical Bayesian framework

Calibration proceeds hierarchically:

$$p(\theta \mid O_{\text{Earth}}) \propto p(\theta)\, p(O_{\text{Earth}} \mid \theta),$$

with module-level priors $p(\theta^{(m)})$ derived from the above sources. Likelihoods are computed on informative summary statistics rather than raw trajectories (Approximate Bayesian Computation or emulator-assisted MCMC). Posterior samples provide both parameter estimates and uncertainty bounds.

21.3 Uncertainty quantification

We propagate posterior samples through simulations to obtain predictive distributions for key observables (e.g., transfer success probabilities). Parameters exhibiting posterior distributions close to their priors are reported as weakly constrained. Global sensitivity analysis (Sobol indices) quantifies which parameters most influence observables. Uncertainty bands on predictions are shown in all figures where applicable.

22 Computational Strategy and Cost Analysis

Scalability and complexity. Each simulation involves solving coupled PDEs or stochastic differential equations over a discretized spatial domain. The computational cost scales as

$$\mathcal{C}_{\text{sim}} \approx C_{\text{ops}}\, n\, N^d\, T,$$

where n is the number of fields, N^d the number of spatial grid points, T the number of time steps, and C_{ops} the per-cell operation count. With $n = 6$, $N = 128$, and $T = 5 \times 10^3$, we estimate $\mathcal{C}_{\text{sim}} \approx 2.5 \times 10^{11}$ FLOPs. Meta-evolution with $S = 200$ genomes and $R = 5$ stochastic seeds thus requires $\sim 2.5 \times 10^{14}$ FLOPs, or roughly two minutes on a modern GPU sustaining 2 TFLOP/s. Heavier configurations (256^2 grid, $n = 12$, $T = 2 \times 10^4$) require days of runtime on a small cluster but remain tractable.

Acceleration strategies. To manage cost the Engine employs:

- **Analytic pre-screening:** discard parameter sets failing basic Turing instability or energy-balance checks before simulation.
- **Multi-fidelity hierarchy:** progressively refine promising candidates from coarse (32^2) to full (256^2) resolution.
- **Surrogate modeling:** train emulators $g(\theta) \approx F(\theta)$ to replace expensive simulations in the inner optimization loop.
- **Parallel evaluation:** run genome populations and stochastic replicates independently across GPU nodes; scaling is nearly linear.
- **Adaptive seeding:** allocate more replicates to high-performing genomes to refine uncertainty while early-terminating poor candidates.

Feasibility. Under these strategies moderate experiments complete in hours, and full meta-evolutionary sweeps in days using tens of GPUs—comparable to other large-scale agent-based or evolutionary simulations. Computations are thus ambitious but feasible with current resources.

23 Remaining Practical Challenges and Validation Strategies

Although the Universal Inductive Engine (UIE) is conceptually complete and mathematically well posed, its ultimate success depends on the practical quality of data, parametrization, and computational surrogates. The following challenges are therefore implementation—not theoretical—limitations. Each represents an avenue for empirical validation rather than a flaw in the framework.

23.1 Library Exhaustiveness: The Genomic Grammar

The discovery capacity of the Engine is bounded by the expressivity of its reaction-template library $\mathcal{T} = \{T_j\}_{j=1}^{M}$. If crucial prebiotic reaction motifs are absent, the system may fail to generate life-like dynamics even though such processes exist in nature. This limitation reflects the current incompleteness of chemical knowledge rather than a defect of the inductive framework.

Mitigation and validation. To address this, $\mathcal{T}$ will be constructed as an evolving, open-ended database. Templates are sourced from (i) empirical prebiotic chemistry literature, (ii) known metabolic motifs from modern biochemistry, and (iii) ab initio reaction network generators constrained by stoichiometry, elemental conservation, and thermodynamic feasibility. The discovery of new experimental pathways (e.g., UV-driven syntheses, mineral-catalyzed cycles) will expand $\mathcal{T}$ dynamically. To quantify coverage, a chemical similarity metric $\rho(T_i, T_j)$ based on reactant–product graphs is used to compute library diversity. The mean pairwise distance $\bar{\rho}$ serves as an empirical proxy for library completeness. The Engine thus functions as a testable hypothesis generator: failure to find life-like solutions under a given $\mathcal{T}$ implies incompleteness of $\mathcal{T}$, not falsification of life's universality.

23.2 Surrogate Model Fidelity

Computational feasibility depends on surrogate models $g(\theta) \approx F(\theta)$ that emulate the full simulator $S(\theta)$. However, the non-linear and often chaotic nature of the underlying dynamics imposes a risk of model error, particularly near bifurcations and phase-transition

boundaries.

Validation and uncertainty estimation. Each surrogate is trained on a Latin-hypercube sample of Θ and validated by k-fold cross-validation using the full simulator. We quantify generalization error $\epsilon_g(\theta) = |F(\theta) - g(\theta)|$ on a withheld validation set and propagate this error as an additional uncertainty term in all Bayesian updates:

$$p(O \mid \theta, g) \propto \exp\left[-\frac{(O - g(\theta))^2}{2(\sigma_O^2 + \sigma_g^2)}\right],$$

where σ_g is the surrogate error estimate. Periodic active learning cycles sample new points in regions of high ϵ_g, thereby maintaining fidelity across the domain. Surrogate validity is continuously monitored; if ϵ_g exceeds tolerance in a subregion, that subspace is resimulated directly with $S(\theta)$.

Empirical benchmarking. Surrogate accuracy will be reported using standard regression diagnostics (R^2, RMSE) and coverage probability of predictive intervals. Benchmarks on known chaotic and pattern-forming systems (e.g., Gray–Scott model) serve as external validation cases.

23.3 Geochemical Prior Bias and Sensitivity

Informative priors $p(\theta)$ derived from geochemical data anchor the Bayesian calibration (Sec. 21), but the geological record of early Earth is sparse and uncertain. Bias in these priors may propagate to posterior inferences $p(\theta \mid O_{\text{Earth}})$, distorting the inferred parameter ranges.

Quantifying prior sensitivity. We explicitly quantify the impact of prior uncertainty by defining a *prior influence index*:

$$\Delta_{\text{prior}} = \frac{1}{2} \int |p(\theta \mid O_{\text{Earth}}) - p(\theta)| \, d\theta.$$

Large Δ_{prior} indicates strong posterior divergence driven by data, while small Δ_{prior} implies that results remain prior-dominated. Sensitivity analysis is performed by perturbing priors within plausible geochemical ranges (e.g., $\pm 1\sigma$ in pH, redox potential, flux rates) and recomputing posterior summaries. Posterior predictive checks then show how uncertainties in early-Earth parameters affect inferred transferability metrics.

Robustness reporting. All posterior predictions are accompanied by uncertainty bands derived from prior ensembles. Parameters with posterior distributions invariant under

wide prior perturbations are deemed robust; those with strong dependence are flagged for future refinement as better geochemical data become available.

23.4 Summary of Implementation Risk

The three issues above—template coverage, surrogate fidelity, and prior bias—define the primary empirical frontiers for the Engine. Each can be iteratively improved: chemistry via new experiments, surrogates via active learning, and priors via refined geochemical evidence. These challenges are thus not theoretical weaknesses but practical frontiers that will determine the speed and precision with which the Engine approaches universality.

24 Discussion

The Universal Inductive Engine (UIE) represents a synthesis between philosophical generalization and empirical modeling. It operationalizes the hypothesis that life is not a singular accident of terrestrial chemistry but an emergent class of lawful, self-organizing processes driven by universal principles of nonequilibrium dynamics and information propagation. By framing these principles as a parameterized family of generative priors $\mathcal{N}_\theta$ acting on environment vectors E, the Engine offers a way to test whether the same underlying "Nature" can reproduce life's signatures across disparate physical substrates.

From philosophy to falsifiability. Historically, origin-of-life research has oscillated between narrative and experiment. The UIE closes this gap by providing a falsifiable computational architecture: each module—chemical, physical, or informational—constitutes a hypothesis that can be individually confirmed or ruled out. A negative result does not refute the broader principle that life is lawful; rather, it falsifies a particular instantiation of $\mathcal{N}_\theta$. This modular philosophy converts metaphysical questions into algorithmic ones.

Empirical testability. The framework enables testable predictions along several axes: (i) the environmental radius of transferability $r_{0.5}$ quantifies the robustness of a given "Nature" to environmental perturbation; (ii) the hierarchy of modules reveals which physical primitives (diffusion, energy flux, compartmentalization, heredity) are minimally sufficient for life-like persistence; and (iii) the information metrics (H, I_f, E_v) separate genuine evolutionary systems from abiotic pattern formers. Each of these quantities can be measured, simulated, and compared across models, allowing systematic progress rather than speculation.

Relationship to existing work. Conceptually, the Engine extends the lineage of Schrödinger's *What is Life?* and Prigogine's work on dissipative structures, while inte-

grating formalisms from reaction–diffusion theory, artificial life, Bayesian inference, and evolutionary computation. It bridges astrobiology and complex systems science by offering a shared language for life detection, independent of terrestrial biochemistry.

Limitations and frontiers. The main uncertainties are pragmatic rather than theoretical: the completeness of the reaction-template library, the fidelity of surrogate models, and the bias of geochemical priors. Each can be empirically improved without altering the core logic of the framework. In practice, the first generations of the Engine will explore reduced models—two-dimensional chemistry, simplified energetics, or coarse-grained heredity—to calibrate the pipeline and benchmark performance. As experimental chemistry and planetary data advance, modules can be expanded to higher fidelity.

Broader implications. If successful, the UIE would not only model potential extraterrestrial life but also function as a diagnostic instrument for our own scientific assumptions. A failure of the Engine under well-constrained conditions would imply that one or more foundational theories—in prebiotic chemistry, thermodynamics, or even cosmology—require revision. In this sense the Engine acts as a "wind tunnel for life," enabling controlled experiments on the generative laws of nature itself.

Outlook. The UIE is therefore not a final theory but a platform: an extensible computational laboratory where hypotheses about life's universality can be formulated, tested, and iteratively refined. Its value lies not in predicting a single outcome but in delineating the lawful space of possibilities. As new data, new chemistry, and new computing paradigms emerge, the Engine can evolve accordingly—continuing the inductive ascent from Earth's singular experiment toward a general theory of living matter.

25 Conclusion

The Universal Inductive Engine operationalizes the intuition that life is a lawful outcome of physical dynamics. By formalizing *Nature* as a parameterized law family and coupling it with empirical Bayesian inference, this framework connects philosophy, mathematics, and simulation into a unified, testable model for life across environments.

References