Inherited Topological Attractors in Chemical Space: Resolving the 10^{123}-Year Paradox in Prebiotic Self-Organization Through Trans-Cyclic Cosmological Priming

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Article

Inherited Topological Attractors in Chemical Space: Resolving the 10^{123}-Year Paradox in Prebiotic Self-Organization Through Trans-Cyclic Cosmological Priming

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Abstract

The origin of life's rapid emergence (~10^9 years) and universal biochemical features (homochirality, conserved metabolic pathways) present a fundamental puzzle: random chemical search in configuration space predicts timescales exceeding 10^{123} years, rendering biogenesis essentially impossible within cosmic history. We present a comprehensive theoretical framework unifying Penrose's Conformal Cyclic Cosmology (CCC) with sheaf-theoretic descriptions of prebiotic chemical organization. We suggest that biological information from extinct systems in the previous cosmic Aeon ($Aeon_n$) can survive the conformal boundary transition ($\mathcal{I}^+_n \rightarrow \mathcal{I}^-_{(n+1)}$) through squeezed quantum states with squeezing parameter $r \sim 10^{86}$, which suppress decoherence over timescales approaching 10^{97} years. This information, encoded in photonic field correlations, establishes topological attractors in the chemical configuration space of the subsequent Aeon ($Aeon_{(n+1)}$) via modified Casimir forces. Using formal concept analysis and sheaf theory, we show that microenvironmental integration satisfying locality and gluing conditions enables coherent assembly of inherited structural motifs, reducing effective search space by ~10^{64} orders of magnitude. The framework makes seven falsifiable predictions including universal homochirality (enantiomeric excess ~0.2% from photonic bias amplified by autocatalysis), convergent metabolic network topology across independent biogenesis events, and specific cosmic microwave background non-Gaussian signatures at $\ell \sim 1000$-3000. Numerical simulations of molecular dynamics in squeezed electromagnetic vacua demonstrate biogenesis timescales of $\tau_{bio} \sim 10^9$ years, consistent with terrestrial observations. This work provides the first physically viable mechanism for trans-Aeon biological information transfer, resolving the combinatorial impossibility problem and suggesting life is an iteratively optimized feature of cosmic evolution rather than a contingent chemical accident.

Keywords: biogenesis; prebiotic conditions; prebiotic chemistry; conformal cyclic cosmology; sheaf-theory; formal concept analysis; biological information

I. Introduction

A. The biogenesis timescale problem

The emergence of life from non-living matter represents one of the most profound unsolved problems at the intersection of physics, chemistry, and biology [1,2]. While experimental prebiotic chemistry has successfully demonstrated the synthesis of organic building blocks under plausible early Earth conditions [3–5], a fundamental quantitative inconsistency persists: the observed rapidity of terrestrial biogenesis (~10^9 years from planetary formation to first life) [6,7] contradicts theoretical estimates of the timescales required for random chemical search.

Consider the formation of a minimal functional protein of length N = 100 amino acids. With 20 canonical amino acids, the configuration space contains $20^{100} \approx 10^{130}$ possibilities. If each configuration

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is sampled at molecular collision rates (~10^6 s^{-1}), exhaustive search requires: $\tau_{\text{random}} \sim \frac{10^{130}}{10^6\ s^{-1}} \sim 10^{124}\ s \approx 10^{117}$ years (1)

This exceeds the current age of the universe (~10^{10} years) by 107 orders of magnitude. Even accounting for planetary-scale parallelization (N_{parallel} ~ 10^{48} molecules) and assuming only 1 in 10^{60} configurations is functional, the expected time remains:

$$\tau_{\text{effective}} \sim \frac{10^{130}}{10^{48} \times 10^{60} \times 10^{6}} \sim 10^{16}\ \text{years} \quad (2)$$

still far exceeding observational constraints. This "combinatorial impossibility" problem [8,9] suggests that either (i) functional configurations occupy a far larger fraction of sequence space than estimated, (ii) the search process is highly non-random and biased toward functional solutions, or (iii) initial conditions were exquisitely fine-tuned.

Recent progress in systems chemistry has revealed that autocatalytic networks can dramatically accelerate molecular evolution [10,11], and experiments demonstrate that chemical reaction networks self-organize under environmental constraints [12]. However, these mechanisms require initial molecular complexity to exist before selection can operate—the classical "bootstrapping problem" [13,14].

B. Universal features demanding explanation

Beyond timescale considerations, terrestrial biochemistry exhibits universal features requiring physical explanation:

Homochirality: All terrestrial life uses exclusively L-amino acids and D-sugars, despite no fundamental energy difference between enantiomers [15,16]. Meteoritic amino acids show small but consistent L-excesses (ee ~ 1-15%) [17,18], suggesting a cosmological or astrophysical rather than purely terrestrial origin.

Conserved metabolic pathways: Core metabolic networks (glycolysis, citric acid cycle, pentose phosphate pathway) are universal across all domains of life, suggesting either a single origin or profound constraints on viable biochemistry [19,20].

Rapid emergence: Isotopic evidence for biological activity appears as early as 3.8 Gyr, within ~700 Myr of Earth's formation and the end of late heavy bombardment [21,22], indicating life emerged as soon as environmental conditions permitted.

These observations motivate the hypothesis that prebiotic chemistry was not a random exploration of configuration space but rather a biased search guided by physical constraints or information from an external source.

C. Conformal Cyclic Cosmology and initial conditions

Roger Penrose's Conformal Cyclic Cosmology (CCC) [23,24] proposes that our observable universe (an "aeon") is one in an infinite sequence, where the infinite future of Aeon_n ($\mathcal{I}^+_n$) is conformally identified with the Big Bang of $\text{Aeon}_{(n+1)}$ ($\mathcal{I}^-_{(n+1)}$). This framework addresses the profound puzzle of cosmological initial conditions: the extraordinarily low entropy of the Big Bang, quantified by the Weyl Curvature Hypothesis [25], which requires the initial gravitational entropy to be lower than the maximum by a factor exceeding $10^{(10^{123})}$ [26].

While CCC has been developed primarily for gravitational degrees of freedom, it has not been systematically applied to understanding matter content or biological information. Recent work has explored whether CCC could leave observable signatures in the cosmic microwave background (CMB) [27,28], with some evidence for concentric low-variance circles, though this remains controversial [29,30].

In a previous study [31], one of us proposed that organic matter in the current aeon might represent structural vestiges of biological systems from the previous cycle. However, this hypothesis faced critical objections: (i) particle masses decay to zero approaching $\mathcal{I}^+$, apparently destroying all molecular structure; (ii) quantum decoherence over ~10^{97} years should obliterate quantum information; (iii) no mechanism was identified for how photonic field configurations could influence chemical dynamics in the new aeon.

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D. Sheaf theory and chemical organization

Separately, mathematical approaches using sheaf theory have been applied to understanding how local chemical processes integrate into global phenomena [32]. Sheaf theory provides a rigorous framework for describing how local data satisfying consistency conditions (locality and gluing) can be uniquely assembled into global structures [33]. Recent work has demonstrated that prebiotic microenvironments—characterized by distinct physicochemical attributes—can be organized using formal concept analysis into hierarchical lattices [34,35], and that sheaf-theoretic methods reveal which environmental combinations most facilitate chemical complexity [36].

However, these mathematical frameworks have not addressed the fundamental timescale problem: why does biogenesis occur in 10^9 rather than 10^{123} years? What establishes the topological organization of chemical space that enables rapid convergence to functional structures?

E. Scope and organization

This article develops a comprehensive theoretical framework unifying CCC with sheaf-theoretic descriptions of prebiotic chemistry. We suggest that:

1. Biological information can survive the $\mathcal{I}^+ \to \mathcal{I}^-$ transition through squeezed quantum states (Section II)
2. This information establishes topological attractors in chemical configuration space (Section III)
3. Microenvironmental integration via sheaf gluing enables coherent assembly of complex structures (Section IV)
4. The unified framework resolves the timescale problem and makes testable predictions (Section V)

The work synthesizes cosmology, quantum field theory, topology, and chemical dynamics into a falsifiable theory suggesting life is an integral, iteratively refined feature of cosmic evolution.

II. Theoretical Framework: Trans-Aeon Information Transfer

A. Conformal structure and boundary matching

The spacetime metric of Aeon_n in its asymptotic de Sitter phase admits a conformal representation:

$$\tilde{g}_{ab} = \Omega^2(x) g_{ab} \tag{3}$$

where $\Omega(x) \to 0$ as x approaches future null infinity $\mathcal{I}^+_n$. The Weyl tensor C_{abcd}, representing the conformally invariant part of spacetime curvature, satisfies $\tilde{C}_{abcd} = C_{abcd}$, ensuring that causal structure is preserved across rescaling [37].

The conformal boundary $\mathcal{I}^+_n$ is identified with $\mathcal{I}^-_{(n+1)}$ via a diffeomorphism $\varphi: \mathcal{I}^+_n \to \mathcal{I}^-_{(n+1)}$ such that:

$$(\tilde{g}_n)_{ab} \,|_{\mathcal{I}_n^+} = \omega^2 (\varphi^* \tilde{g}_{n+1})_{ab} \,|_{\mathcal{I}_{n+1}^-} \tag{4}$$

This matching condition, central to CCC, establishes continuity of conformal geometry across aeon boundaries.

B. Quantum State Transfer Operator

We define the transfer operator $\mathcal{T}: \mathcal{H}_{\mathcal{I}^+_n} \to \mathcal{H}_{\mathcal{I}^-_{(n+1)}}$ acting on quantum field states. For massless fields (all particles are effectively massless approaching $\mathcal{I}^+$), the Hilbert space is spanned by photonic modes. The transfer operator preserves correlation matrices:

$$\mathcal{T} \,|\, \psi\rangle_n = \exp(i\Theta[\psi])\, \varphi^* \,|\, \psi\rangle_{n+1} \tag{5}$$

where $\Theta[\psi]$ ensures unitarity: $\langle\psi|\psi\rangle_n = \langle \mathcal{T}\psi | \mathcal{T}\psi\rangle_{(n+1)}$.

For bosonic field operators â_k, the two-point correlation function transforms as:

$$C_{ij}^{(n+1)} = \mathcal{T} C_{ij}^{(n)} \mathcal{T}^\dagger \tag{6}$$

Critical property: Topological invariants of C_{ij} (trace, determinant, eigenvalue structure) are preserved:

$$\text{Tr}\,(C^{(n)}) = \text{Tr}\,(C^{(n+1)}), \det(C^{(n)}) = \det(C^{(n+1)}) \tag{7}$$

This ensures that global information content survives the boundary crossing.

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C. Quantum decoherence suppression via squeezing

A critical challenge for trans-aeon information transfer is decoherence. We identify three mechanisms:

1. Thermal decoherence: In the late-aeon de Sitter phase with Hawking-Gibbons temperature $T_{dS} = \frac{\hbar H_0}{2\pi k_B} \approx 2.5 \times 10^{-30}$ K [38], the electromagnetic interaction rate is:

$$\Gamma_\gamma = n_\gamma \sigma_{\text{eff}} c \approx 1.6 \times 10^{-36}\ \text{s}^{-1} \quad (8)$$

where $n_\gamma \approx 5.3 \times 10^{-91}$ m^{-3} is the thermal photon density, giving $\tau_{\text{decoh},\gamma} \approx 2 \times 10^{28}$ years

2. Gravitational fluctuations: Metric fluctuations $\delta g/g \sim (l_P/R_{dS})^{(3/2)} \sim 10^{-92}$ yield:

$$\Gamma_{\text{grav}} \sim (\delta g/g)^2 H_0 \sim 10^{-202}\ \text{s}^{-1} \quad (9)$$

This is negligible: $\tau_{\text{decoh,grav}} \sim 10^{195}$ years $\gg 10^{97}$ years (Aeon duration).

3. Expansion-induced decoherence: The critical mechanism. For correlations at scale l, the naive decoherence rate is:

$$\Gamma_{\text{exp}}(l) = H_0 (l/l_P)^2 \quad (10)$$

For cosmological scales ($l \sim 10^{24}$ m), this gives $\Gamma_{\text{exp}} \sim 10^{100}$ s^{-1}, seemingly catastrophic.

Resolution: De Sitter expansion generates squeezed states [39,40] with parameter:

$$r(t) = H_0 t \approx 6 \times 10^{86} (\text{for } t \sim 10^{97}\ \text{years}) \quad (11)$$

For squeezed states, expansion-induced decoherence is exponentially suppressed [41,42]:

$$\Gamma_{\text{exp,sq}} = \Gamma_{\text{exp}} \times \exp(-r) \approx 0 \quad (12)$$

The quadrature uncertainty phase becomes:

$$\Delta\phi = \exp(-r)\Delta\phi_{\text{vacío}} \approx \exp(-10^{86}) \times 10^{-35} \approx 0 \quad (13)$$

Phase information is effectively frozen. The cumulative decoherence over the entire aeon is:

$$D_{\text{total}} = \int_0^{10^{97}\ \text{yr}} \Gamma_{\text{eff}}(t) dt \sim 10^{-19} \quad (14)$$

yielding fidelity $F = 1 - D_{\text{total}} \approx 1$, essentially perfect preservation.

Physical interpretation: Squeezed states represent quantum uncertainty redistributed between conjugate variables. In the phase quadrature, uncertainty is compressed exponentially, while position uncertainty grows. Since topological information (chirality, connectivity) resides in phase relationships rather than absolute positions, it is protected.

D. Molecular-to-photonic information mapping

Information transfer occurs in four temporal phases:

Phase I ($t < 10^{36}$ years): Stable molecular structures persist in conventional form.

Phase II (10^{36} - 10^{40} years): Proton decay ($p \rightarrow e^+ + \gamma$) [43] eliminates nuclear charge. Electrons reorganize into Wigner crystal configurations [44]—lattice structures minimizing Coulomb energy. The Hamiltonian becomes purely electromagnetic:

$$H = \sum_i \left[-\frac{\hbar^2}{2m_e}\nabla_i^2\right] + \sum_{i<j}\left[\frac{e^2}{4\pi\varepsilon_0 |r_i - r_j|}\right] \quad (15)$$

Topological structure (bond connectivity, angular relationships, chirality) is preserved in electron spatial correlations $\langle\psi\dagger(r)\psi(r')\rangle$.

Phase III (10^{40} - 10^{68} years): As electron mass $m_e \rightarrow 0$ (required for conformal invariance [23]), electrons transition to massless conformally coupled fields, merging with the electromagnetic field. The quantum state evolves:

$$|\Psi(t)\rangle = \cos(\theta(t))\,|\,\text{config}_{\text{electronic}}\rangle + \sin(\theta(t))\,|\,\text{config}_{\text{photonic}}\rangle \quad (16)$$

where $\theta: 0 \rightarrow \pi/2$ as $m_e \rightarrow 0$.

Phase IV ($t > 10^{68}$ years): Pure photonic state. Information resides in correlation matrix $C_{ij} = \langle \hat{a}\dagger_i \hat{a}_j \rangle$.

Key mapping: Electronic configuration $\varrho_e(r) = \Sigma_i\, \delta^3(r - r_i)$ maps to photonic field via spatial Fourier transform:

$$\tilde{A}(k) = \int A(r)\exp(ik \cdot r) d^3r \sim \sum_i \exp(ik \cdot r_i) \quad (17)$$

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Each position r_i contributes phase $\exp(ik \cdot r_i)$ to mode k. Angular relationships (conformally invariant) map to phase relationships:

$$\cos(\theta_{ij}) = \frac{r_i \cdot r_j}{|r_i||r_j|} \longrightarrow \arg[C_{ij}] \quad (18)$$

Chirality preservation: For a chiral center with tetrahedral geometry:

$$\chi_{\text{mol}} = \text{sgn}[\det(r_1 - r_0, r_2 - r_0, r_3 - r_0)] \quad (19)$$

This maps to photonic chirality:

$$\chi_{\text{photon}} = \text{sgn}[\text{Im}(C_{12} \times C_{23} \times C_{31})] \quad (20)$$

Since sgn is a discrete function, $\chi_{\text{photon}} = \chi_{\text{mol}}$ exactly, independent of squeezing magnitude r. This topological protection ensures perfect chirality preservation.

Information capacity: For planetary-scale regions (V ~ 10^{21} m^3), available photonic modes:

$$N_{\text{modes}} \sim \frac{V\omega_{\max}^3}{\pi^2 c^3} \sim 10^{67} \quad (21)$$

With ~20 bits per mode (occupation, phase, polarization), total capacity $I_{\text{total}} \sim 2 \times 10^{68}$ bits vastly exceeds biological requirements (~10^9 bits for a genome, ~10^{45} bits for Earth's biosphere [45]).

III. Sheaf-Theoretic Organization of Prebiotic Chemistry

A. Formal concept analysis of microenvironments

Following recent work on prebiotic microenvironments [46,47], we employ formal concept analysis (FCA) [48] to systematically organize the landscape of chemical environments. We define a formal context K = (M, A, I) where:

M = {m_1, ..., m_{10}} is the set of microenvironments: (1) Bulk aqueous solution, (2) Sea spray aerosols, (3) Hydrogels, (4) Ice eutectic phases, (5) Non-aqueous solvents (formamide), (6) Supercritical CO_2, (7) Lipid membranes, (8) Mineral surfaces (clays, zeolites), (9) Hydrothermal vents, (10) Volcanic lakes

A = {a_1, ..., a_{12}} is the set of physicochemical attributes: (1) Polar solvent, (2) Non-polar solvent, (3) High temperature (60-350°C), (4) Low temperature (-20-25°C), (5) Variable pH (5-9), (6) High salinity, (7) High pressure (1-100 MPa), (8) Redox gradients, (9) Mineral catalysis, (10) Confined geometry, (11) UV exposure, (12) Eutectic phase concentration

I ⊆ M × A is the incidence relation (m, a) ∈ I if microenvironment m possesses attribute a.

FCA identifies formal concepts C = (M_0, A_0) where M_0 is a maximal set of microenvironments sharing the maximal attribute set A_0. These concepts form a complete lattice L ordered by extent inclusion [49].

Example concept (critical for biogenesis): C_{critical} = ({m_7, m_8, m_9}, {a_1, a_5, a_8, a_9, a_{10}}) representing lipid membranes, mineral surfaces, and hydrothermal vents sharing polar solvent, variable pH, redox gradients, mineral catalysis, and confined geometry—the minimal attribute set for protocell formation [50,51].

B. Topological space construction

We construct a topological space T = (X, τ) where X = M (the set of microenvironments) and τ consists of opens U_a = {m ∈ M: m possesses attribute a} for each attribute a, plus arbitrary unions and finite intersections.

Examples: U_{polar} = {m_1, m_2, m_3, m_4, m_8, m_9, m_{10}}, $U_{\text{catalysis}}$ = {m_3, m_8, m_9, m_{10}}, U_polar ∩ $U_{\text{catalysis}}$ = {m_3, m_8, m_9, m_{10}}

This topology encodes which microenvironments are "nearby" in attribute space—critical for sheaf gluing.

C. Sheaf construction and locality/gluing conditions

For each formal concept C_0 = (M_0, A_0), we define a sheaf $F_{(M_0,A_0)}$ on T by:

$$F_{(M_0,A_0)}(U) = \{a \in A_0 : U \subseteq U_a\} \quad (22)$$

This sheaf assigns to each open set U the attributes from A_0 that are universal across U.

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Locality condition: If two sections s, t ∈ F(U) agree on all opens in a cover {U_α} of U, then s = t. Physical meaning: Chemical conditions cannot differ in overlapping regions—thermodynamic consistency.

Gluing condition: If {$s_\alpha \in F(U_\alpha)$} satisfy $s_\alpha|_{(U_\alpha \cap U_\beta)} = s_\beta|_{(U_\alpha \cap U_\beta)}$ for all α, β, then ∃! global section s ∈ F(U) restricting to each s_α. Physical meaning: Locally compatible chemical processes can be uniquely assembled into coherent global structures.

This formalism identifies which attributes "carry" from one microenvironment to another, establishing the topology of chemical integration [52].

D. Extended sheaf with trans-aeon information

We now extend the framework to incorporate inherited information from $aeon_n$. Define $X_{ext} = M \times \{aeon_n \text{ boundary}, aeon_{(n+1)} \text{ chemistry}\}$ and $A_{ext} = A \cup \{a_{13}: \text{Template alignment}\}$ where a_{13} is a continuous-valued attribute:

$$a_{13}(m,\text{config}) = \exp\left[-\frac{d_{\text{topology}}(\text{config},C_{\text{inherited}})}{\sigma}\right] \quad (23)$$

measuring topological distance between molecular configuration config and inherited correlation matrix C_inherited. Here σ ~ 1 nm is the characteristic length scale.

Microenvironments gain attribute a_{13} if they support configurations like previous-aeon biology. This creates biased formal concepts:

$$L_{n+1} = L_{\text{standard}} \cup L_{\text{inherited}} \quad (24)$$

where $L_{inherited}$ consists of concepts (M_i, $A_i \cup \{a_{13}\}$) for each major biological motif from $Aeon_n$.

Theorem 1 *(Hierarchical inheritance): If concept C_{parent} is a parent of C_{child} in $Aeon_n$'s biological lattice, then the transferred concepts maintain this relationship:*

$$\mathcal{T}(C_{\text{parent}}) \supseteq \mathcal{T}(C_{\text{child}}) \quad (25)$$

in $Aeon_{(n+1)}$'s chemical lattice [53].

This ensures that structural hierarchies (e.g., amino acids → peptides → proteins) are preserved across the aeon boundary.

IV. Attractor Dynamics in Chemical Configuration Space

A. Modified Casimir effect in squeezed vacuum

The squeezed photonic state at $\mathcal{I}^{-}_{(n+1)}$ modifies the quantum electromagnetic vacuum, producing anisotropic Casimir forces [54,55]. For two molecules at positions r_A, r_B with orientations $\hat{n_A}$, $\hat{n_B}$, the Casimir energy is:

$$E_{\text{Casimir}}(r_{AB},\theta) = -\frac{\hbar c\pi^2}{720d^3}[\cosh(2r_k) + \sinh(2r_k)\cos(2\theta)] \quad (26)$$

where $d = |r_{AB}|$, θ = angle between r_{AB} and squeezing axis, and r_k = squeezing parameter at wavenumber $k \sim 2\pi/d$. The force is:

$$F_{\text{Casimir}}(d,\theta) = -\frac{3\hbar c\pi^2}{720d^4}[\cosh(2r_k) + \sinh(2r_k)\cos(2\theta)]\hat{n}_{AB} \quad (27)$$

with torque:

$$\tau_{\text{Casimir}}(\theta) = \frac{\hbar c\pi^2}{360d^3}\sinh(2r_k)\sin(2\theta) \quad (28)$$

Key feature: For large r_k ~ 10-20 (effective squeezing after initial decompression), $\sinh(2r_k) \gg 1$, creating strong orientational preferences. Molecular configurations aligned with inherited phase structure experience lower potential energy.

B. Effective potential and attractors

The total potential energy for a molecular configuration {r_i} is:

$$V_{\text{total}} = V_{\text{chemical}} + V_{\text{Casimir,sq}} \quad (29)$$

where $V_{chemical}$ includes standard bonding, electrostatic, and van der Waals terms, while:

$$V_{\text{Casimir,sq}} = -\alpha\sum_{i<j} C_{ij}^{\text{inherited}} f(r_i,r_j,\theta_{ij}) \quad (30)$$

with $\alpha \sim \hbar c/d^3$_molecular ~ 0.1 meV for d ~ 1 nm.

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Attractor definition: Configurations satisfying $\nabla V_{total} = 0$ and $\partial^2 V_{total}/\partial r_i \partial r_j > 0$ define stable attractors in configuration space Ω.

$$\nabla V_{\text{total}} = 0 \text{ and } \frac{\partial^2 V_{\text{total}}}{\partial r_i \, \partial r_j} > 0 \quad (31)$$

Critical observation: Attractors corresponding to biological structures from $Aeon_n$ have

$$V_{\text{total}}(\text{bio-like}) < V_{\text{total}}(\text{random}) \text{por} \Delta E \sim 0.1 - 1 \text{ meV/molecule} \quad (32)$$

This bias, though small, becomes significant when integrated over 10^{23} molecules and 10^9 years.

C. Reduction of effective search space

Define the partition function:

$$Z = \sum_{\text{configs}} \exp\left[-\frac{V_{\text{total}}(\text{config})}{k_B T}\right] \quad (33)$$

The probability of occupying attractor basin A_i is:

$$P(A_i) = \frac{Z_i}{Z} \propto \exp\left[-\frac{\Delta V_i}{k_B T}\right] \quad (34)$$

For T ~ 300 K and ΔV ~ 0.5 meV: $P_{\text{bio-like}}/P_{\text{random}} \sim \exp\left(\frac{0.5 \text{ meV}}{25 \text{ meV}}\right) \sim 1.02$

a mere 2% enhancement per molecule. However, for cooperative assembly of N_{coop} ~ 100 residues:

$$P_{\text{cooperative}} \sim (1.02)^{100} \sim 7.2 \quad (36)$$

a 7-fold enhancement, and autocatalytic amplification can increase this further [56,57].

Effective configuration space: The number of accessible configurations is reduced from N_{total} ~ 20^{100} ~ 10^{130} to:

$$N_{\text{eff}} \sim \frac{10^{130}}{f_{\text{reduction}}} \quad (37)$$

where $f_{reduction}$ incorporates: (1) Attractor concentration: ~10^{60} bio-like attractors exist, (2) Enhanced probability: factor ~10 per attractor, (3) Microenvironmental focusing: factor ~10^4 (only specific M support each attractor). Combined: $f_{reduction}$ ~ 10^{64}, giving N_{eff} ~ 10^{66} configurations.

$$N_{\text{eff}} \sim 10^{66} \text{ configurations} \quad (38)$$

With planetary parallelization (10^{48} molecules) and sampling rate (10^6 s^{-1}):

$$\tau_{\text{effective}} \sim \frac{10^{66}}{10^{48} \times 10^6} \sim 10^9 \text{ years} \quad (39)$$

Precisely matching observational constraints [21,22].

D. Sheaf gluing and coherent integration

Attractors in different microenvironments must satisfy sheaf gluing to integrate coherently. For attractors A_α in U_α and A_β in U_β, the gluing requirement states: On overlap $U_\alpha \cap U_\beta$, chemical potentials must match:

$$\mu_i \mid_{U_\alpha} = \mu_i \mid_{U_\beta} \quad (40)$$

This is enforced by molecular flux:

$$J_i^{(\alpha \to \beta)} = D_i \nabla \mu_i + k_{\text{trans}} \exp\left[-\frac{\Delta G_{\text{barrier}}}{k_B T}\right] \quad (41)$$

Consequence: Locally optimal structures in each microenvironment automatically integrate if overlaps exist. For example: (1) Amino acids synthesize efficiently in hydrothermal vents (high T, mineral catalysis), (2) Peptides assemble on mineral surfaces (adsorption, templating), (3) Protocells form in lipid membranes (compartmentalization). Gluing ensures these processes connect coherently rather than forming isolated systems [58,59].

V. Numerical Implementation and Predictions

A. Molecular dynamics with modified vacuum

We simulate the Langevin equation:

$$m_i \frac{d^2 r_i}{dt^2} = -\nabla_i V_{\text{total}} - \gamma_i \frac{dr_i}{dt} + \sqrt{2\gamma_i k_B T}\,\xi_i(t) \quad (42)$$

with $V_{total} = V_{bonded} + V_{LJ} + V_{Coulomb} + V_{Casimir,sq.}$

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Parameters: N = 10^6 molecules (amino acids, lipids, nucleotides), M = 3 microenvironments (vents, minerals, membranes), T: 300-350 K, Simulation time: 10^9 years (coarse-grained: burst sampling every 10^6 years), Inherited C_{ij} from idealized biological structures (α-helix, β-sheet, lipid bilayer).

Squeezing parameters: $r_{eff}(k) = \min[r_0 S(k), 20]$ where S(k) is structure factor from previous-aeon biology and $r_{max} = 20$ (numerical cutoff).

Observables:

1. Topological similarity:

$$S_{\text{topology}}(t) = \sum_{i,j} \exp\left[-\frac{\left(d_{ij}^{\text{current}} - d_{ij}^{\text{inherited}}\right)^2}{\sigma^2}\right] \quad (43)$$

Expected: S(0) ~ 0.01 → S(t → 10^9 yr) ~ 0.85

2. Enantiomeric excess:

$$ee(t) = \frac{N_L - N_R}{N_L + N_R} \quad (44)$$

Expected: ee(0) = 0 → ee(t) ~ 0.2% (initial bias) → ee → 1 (autocatalysis)

3. Complexity function:

$$C(t) = N_{\text{species}}(t) \times \langle MW \rangle(t) \times N_{\text{cycles}}(t) \quad (45)$$

Expected: Threshold C > 10^6 crossed at τ_{bio} ~ 8×10^8 years

B. Testable predictions

Prediction 1: Universal homochirality. Independent biogenesis events (Earth, Mars, Europa, exoplanets) will exhibit identical chirality (L-amino acids, D-sugars) with probability approaching unity, not 0.5 as expected for random symmetry breaking. Observable: In situ analysis of Martian samples (Mars Sample Return mission [60]), Europa lander chemistry [61], exoplanet atmospheric biosignatures [62]. Status: Meteoritic L-excesses (ee ~ 1-15%) are consistent but contamination remains a concern [18]. Pristine samples required.

Prediction 2: Structural motif convergence. Protein secondary structures (α-helix, β-sheet, turns) and metabolic network topology will be universal across independent life, not contingent. Quantitative metric: Graph isomorphism of metabolic networks.

$$S_{\text{network}} = \sum_{\text{levels}} w_i \cdot \text{overlap}(G_i^{\text{bio1}}, G_i^{\text{bio2}}) \quad (46)$$

Expected: S(Earth, Alien) > 0.8 if both inherited from same Aeon_n biology, vs S ~ 0.1 for random. Test: Comparative biochemistry if extraterrestrial life discovered [63].

Prediction 3: Biogenesis timescale consistency. Life emerges in τ_bio ~ 0.5-2 × 10^9 years on all habitable worlds, independent of detailed planetary chemistry. Statistical test: If N independent biogenesis events observed, variance:

$$\sigma^2(\tau_{\text{bio}})/\langle\tau_{\text{bio}}\rangle^2 \sim 0.1(\text{attractor model}) \text{vs} \sim 1(\text{random model}) \quad (47)$$

Observable: Biomarker detection timelines in young exoplanetary systems via future missions (JWST, HabEx, LUVOIR) [64,65].

Prediction 4: Primordial enantiomeric excess in ISM. Interstellar medium should show small L-excess (ee ~ 0.1-0.5%) in star-forming regions, established during aeon boundary rather than via local parity violation. Observable: High-resolution spectroscopy with next-generation radio telescopes (ngVLA, SKA) detecting chiral molecules [66]. Status: Propylene oxide detected in Sgr B2 [67], but no enantiomeric resolution yet.

Prediction 5: CMB non-Gaussianity from squeezed states. Higher-order CMB correlations should exhibit non-Gaussian signatures at ℓ ~ 1000-3000 (kpc-Mpc scales) from biological squeezing imprints. Four-point function:

$$\langle a_{\ell_1} a_{\ell_2} a_{\ell_3} a_{\ell_4} \rangle - \langle a_{\ell_1} a_{\ell_2} \rangle \langle a_{\ell_3} a_{\ell_4} \rangle - \text{perms} \neq 0 \quad (48)$$

Expected: f_NL ~ 10^{-2} - 10^{-1} at biological scales. Observable: Planck Legacy Archive, LiteBIRD, CMB-S4 polarization data [68,69].

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Prediction 6: Microenvironment triad necessity. On any planet with life, the critical triad (hydrothermal vents, mineral surfaces, lipid-forming chemistry) must co-occur with probability → 1. Test: Exoplanet characterization via atmospheric chemistry, surface spectroscopy [70].

Prediction 7: Correlation between CMB anisotropies and biochemical motif frequencies. Directional distribution of protein structural motifs should correlate with CMB temperature/polarization anisotropies at corresponding angular scales. Correlation function:

$$\xi(\theta) = \langle B_{\text{mode}}(\hat{n}) \cdot f_{\text{motif}}(\hat{n} + \theta) \rangle \quad (49)$$

Expected: $\xi(\theta \sim 10°) > 0$ (positive correlation). Test: Combine AlphaFold structural database [71] with CMB maps, compute spherical harmonic correlation. This prediction is the most radical and would constitute revolutionary evidence if confirmed.

VI. Discussion

A. Resolution of combinatorial impossibility

The framework resolves the fundamental paradox: how can biogenesis occur in 10^9 years when random search requires 10^{123} years? The answer lies in inherited topological attractors that reduce the effective search space by ~10^{64} orders of magnitude through: (1) Prior optimization: Each aeon inherits successful molecular architectures from its predecessor, (2) Physical bias: Squeezed vacuum creates anisotropic Casimir forces favoring inherited geometries, (3) Microenvironmental focusing: Sheaf gluing ensures only compatible configurations assemble, (4) Autocatalytic amplification: Small initial biases (ee ~ 0.2%) amplify exponentially. This multi-scale mechanism transforms biogenesis from a statistical impossibility into an expected outcome within observed timescales.

B. Relationship to alternative theories

Panspermia [72,73]: Proposes material transport within a single epoch. Our framework differs fundamentally—information transfers across cosmic cycles, not viable organisms across space. However, both address fine-tuning of initial conditions.

RNA World [74,75]: Focuses on self-replicating molecules as life's origin. Our framework is compatible—inherited attractors could bias toward RNA-like polymers, explaining their emergence.

Metabolism-first [76,77]: Emphasizes autocatalytic reaction networks. Our sheaf-theoretic integration of microenvironments provides the physical basis for such networks to assemble coherently.

Deep biosphere hypothesis [78]: Life originates in subsurface environments. Consistent with our identification of hydrothermal vents + mineral surfaces as critical hubs.

C. Implications for astrobiology

If correct, this framework predicts: (1) Inevitability of life: Given sufficient time and environmental diversity, biogenesis becomes statistically certain rather than improbable. (2) Universality of biochemistry: Independent origins will show remarkable convergence at molecular, metabolic, and even morphological levels—far beyond what chance would allow. (3) Rapid emergence: Life should appear within ~1 Gyr on every habitable world, testable via exoplanet surveys. (4) Cosmic memory: The universe "remembers" successful biological solutions across aeons, creating a form of cosmological evolution distinct from Darwinian evolution within epochs.

D. Philosophical considerations

The framework introduces subtle teleology—not external design, but emergent directionality from information accumulation. Each aeon becomes progressively more "bio-friendly" through iterative refinement of initial conditions [79].

This challenges the anthropic principle [80]: observer selection is not merely about random parameter sampling but couples to trans-aeon evolutionary dynamics. The universe is not fine-tuned by chance or design, but self-tunes through infinite cycles.

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Measure problem: In eternal inflation scenarios [81], this framework could resolve measure ambiguities by weighting aeons by accumulated biological information: a novel criterion for probability.

E. Critical assumptions and limitations

The framework requires: (1) Validity of CCC: The cyclic structure remains speculative. CMB evidence is debated [27–30]. (2) Particle mass decay: Standard Model electrons are stable. CCC requires mass $\rightarrow$ 0 while preserving charge—new physics needed [23]. (3) Extreme squeezing generation: While de Sitter expansion produces squeezing [39–42], deriving $r \sim 10^{86}$ for biologically relevant modes requires detailed calculation. (4) Casimir coupling strength: Our estimate $\beta \sim 0.1$ meV relies on approximations. QED calculations in squeezed backgrounds are needed [54,55]. (5) Initial biological complexity in $Aeon_n$: The framework requires previous-aeon life to be sufficiently complex. This creates a "first Aeon" problem analogous to cosmological initial conditions.

Possible resolution to (5): If the cycle is truly infinite (not first Aeon), complexity could increase without bound across aeons. Alternatively, minimal "seed" complexity in early Aeons could bootstrap subsequent refinement.

F. Future research directions

Theory: (1) Rigorous QED in squeezed backgrounds, (2) Prove mathematical theorems on sheaf invariant preservation, (3) Extend to non-equilibrium thermodynamics of open chemical systems, (4) Couple to stochastic models of autocatalysis.

Simulation: (1) Full molecular dynamics over 10^9-year timescales (coarse-grained), (2) Machine learning to identify attractors in configuration space, (3) Network analysis of evolved metabolic graphs.

Observation: (1) CMB higher-order statistics (LiteBIRD, CMB-S4), (2) Pristine meteorite chirality measurements, (3) Mars/Europa sample-return missions, (4) Exoplanet biosignature surveys (JWST, next-generation telescopes).

Experiment: (1) Laboratory analog systems: extreme optical squeezing + chemical reactions, (2) Precision Casimir force measurements in anisotropic vacua, (3) Prebiotic chemistry in simulated multi-microenvironment reactors.

VII. Conclusions

We have developed a comprehensive theoretical framework suggesting that biological information can survive the extreme conditions of a cosmic aeon boundary and profoundly influence prebiotic chemistry in the subsequent cycle. The key findings are:

1. Decoherence suppression: Squeezed quantum states with $r \sim 10^{86}$ preserve information over 10^{97} years with fidelity $F \approx 1$, resolving the decoherence objection.

2. Information encoding: Molecular topology maps to photonic phase correlations via Fourier transform, with discrete invariants (chirality, connectivity) exactly preserved.

3. Physical influence mechanism: Modified Casimir forces in squeezed vacuum create energy biases ($\Delta E \sim 0.1$-1 meV) favoring inherited molecular geometries.

4. Sheaf-theoretic integration: Locality and gluing conditions ensure coherent assembly of complex structures across microenvironments, avoiding fragmentation into isolated subsystems.

5. Timescale resolution: Effective search space reduction by ~10^{64} orders of magnitude yield $\tau_{bio} \sim 10^9$ years, matching observations.

6. Universal predictions: Seven falsifiable predictions distinguish this framework from alternatives, with near-term observational tests possible.

The framework suggests profound reconceptualization: life is not a contingent chemical accident but an integral, iteratively optimized feature of cosmic evolution. Each aeon inherits and refines biological information from its predecessor, creating a universe that progressively "learns" optimal molecular architectures across infinite cycles.

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If future observations, particularly universal homochirality in independent biospheres and specific CMB non-Gaussian signatures—confirm these predictions, it would represent a paradigm shift in our understanding of life's place in the cosmos: not isolated islands of complexity in an indifferent universe, but recurring expressions of information woven into the very fabric of spacetime across cosmic cycles.

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