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Article

Reservoir as a Hidden Information Layer: On the Limiting Character of Quantum Mechanics and Its Manifestations in Biological Systems

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Abstract

Biological systems display phenomena—particularly in enzymatic catalysis, excitonic coherence, and protein folding—that appear to exploit selective stabilisation of microstates beyond what standard quantum mechanics typically predicts for warm, noisy environments. We propose that these deviations can be interpreted as signatures of an informational reservoir: a hidden, aperiodic layer of structured information accessible only to sufficiently complex biological systems. Standard quantum mechanics then emerges as a limiting, coarse-grained description in which the reservoir term vanishes. The proposed reservoir is not reducible to any finite set of underlying parameters; instead, it functions as a high-complexity information landscape that can be "read" only by finely organised biomolecular architectures. We outline empirically testable predictions and discuss implications for biological stability, functional directionality, and the physical foundations of living systems.

Keywords: quantum biology; enzymatic tunnelling; excitonic coherence; protein folding; informational reservoir; abiogenesis; quantum mechanics; Kolmogorov complexity

1. Introduction

Quantum mechanics (QM) provides extraordinarily precise predictions in simple inorganic systems, particularly at low temperature and low complexity. In biological systems, however, phenomena appear whose behaviour deviates from standard predictions by many orders of magnitude. The most prominent include:

- enzymatic catalysis, where reaction rates exceed quantum tunnelling models by several orders of magnitude, a discrepancy linked to the role of distal protein dynamics rather than active-site electrostatics alone [1];
- excitonic coherence in warm, noisy environments, observed by femtosecond two-dimensional spectroscopy [2]; while vibronic coupling accounts for a significant portion of the observed prolongation [3], residual topology-dependent effects remain that are not fully captured by current decoherence models;
- protein folding, whose speed and directionality are statistically improbable under random search models, and which are not fully accounted for by smooth energy landscape descriptions [4].

These phenomena share a common feature: selective stabilisation of micro-states that is not fully explicable by standard QM. We propose that this stabilisation is a manifestation of a reservoir — a hidden information layer interacting with biological structures. Simple quantum systems are necessarily observed through a defocused lens. Biological systems, through the extreme refinement of their molecular organisation, achieve partial focus — and fine structure becomes visible. To illustrate this conceptually, Figure 1 contrasts the "defocused" perception of the reservoir (left) with its detailed structure visible under precise focus (right).

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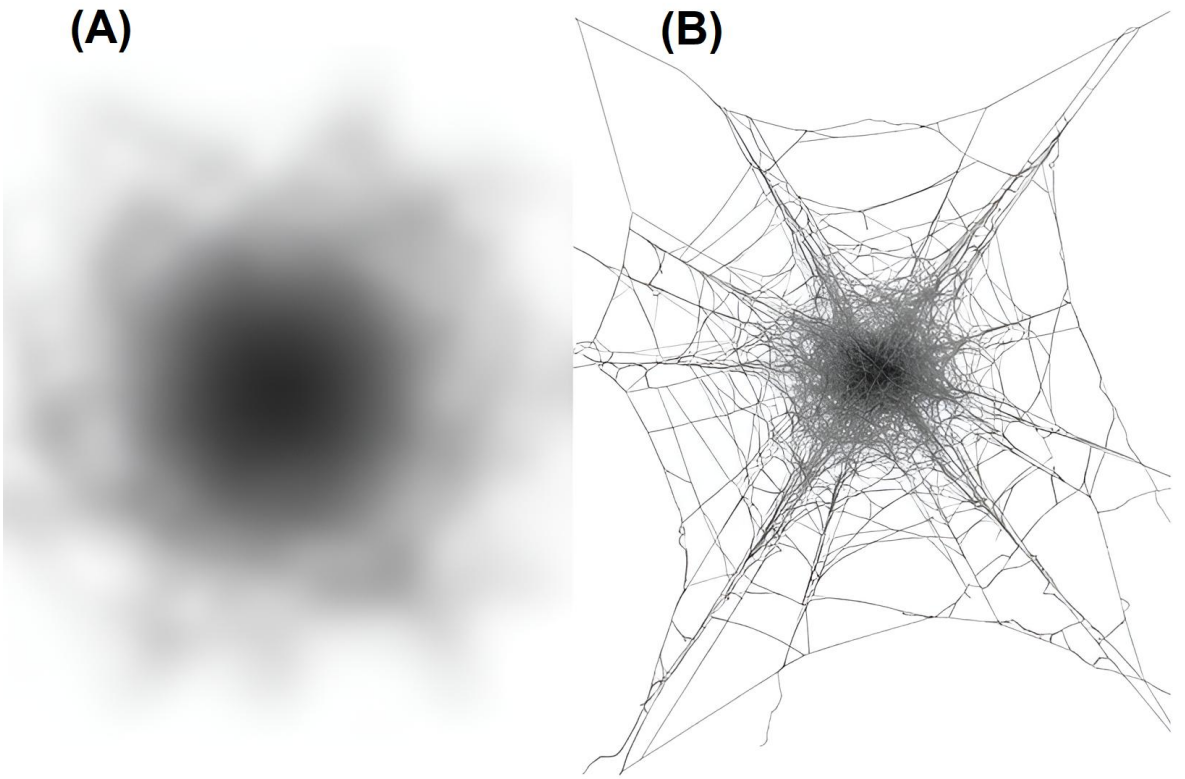

Figure 1. Optical analogy for the reservoir hypothesis. (**A**) Defocused view: the intricate, aperiodic structure of the reservoir appears only as a smooth, gradually darkening central blur with no discernible details — analogous to how standard quantum mechanics perceives complex biological systems through a limited, "blurred" resolution, seeing primarily probabilistic distributions rather than fine topology-dependent organization. (**B**) Focused view: the same reservoir is revealed in sharp detail as a highly irregular, chaotic web (spider-web-like network) with the highest density and complexity concentrated in the center — visible only when the observing system (e.g., a sufficiently organized biological structure) achieves precise "tuning" or focus, allowing access to the hidden aperiodic information layer.

This contrast illustrates why quantum behaviour in simple inorganic systems appears fully explained by standard formalism, while in living systems the same underlying reality manifests unexpected coherence, directionality and rate enhancements: the difference lies not in the laws themselves, but in the effective resolution with which they are "observed" by the molecular architecture.

Not only is the reservoir perceived differently depending on the „focus", but the actual interaction depends on topological compatibility. Figure 2 shows why periodic, highly symmetric structures (typical for inorganic crystals) cannot couple meaningfully to the aperiodic reservoir, whereas the complex, irregular folding of biomolecules allows precise matching and selective stabilization.

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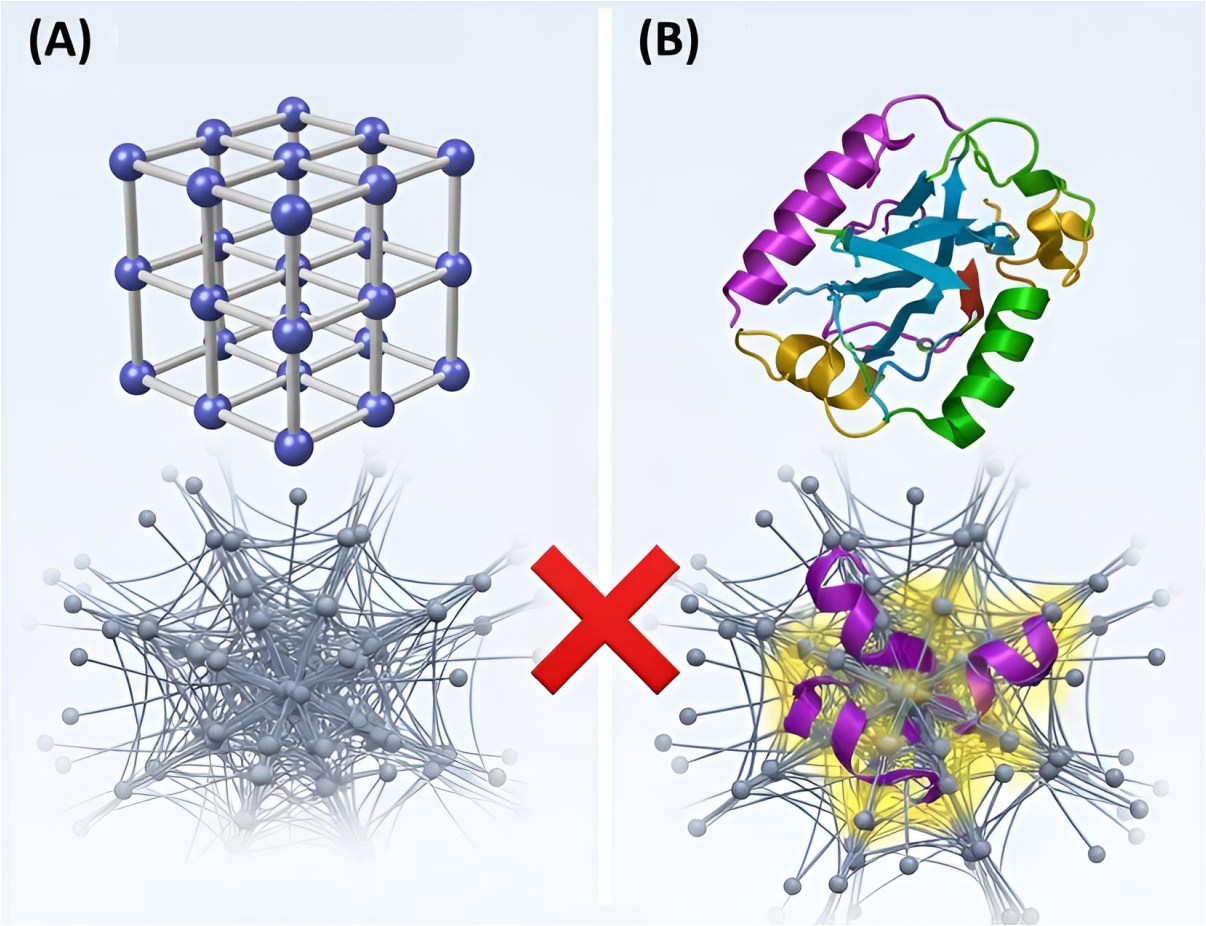

Figure 2. Topological matching between system and reservoir. (**A**) Periodic crystal lattice — a highly repetitive structure (e.g. cubic) shows no meaningful overlap with the aperiodic structure of the reservoir (depicted here as a random, chaotic web). The system effectively "slides" over it without significant coupling — typical behaviour for inorganic materials. (**B**) Folded biomolecule (enzyme/protein) — a complex aperiodic structure featuring protruding loops and binding sites fits precisely into the irregular, random topology of the reservoir. This exact complementarity opens the coupling channel and enables selective stabilization of micro-states — a hallmark of biological systems.

The key conceptual move of this paper is an analogy with Einstein's 1905 analysis of Brownian motion [5]. Einstein did not possess a microscopic model of atoms, nor a closed-form equation for their trajectories. He nonetheless demonstrated that statistical deviations in the motion of pollen particles constitute evidence for an underlying substructure — the discreteness of matter. We propose an analogous inference: that statistical deviations in biological quantum phenomena constitute evidence for an underlying information substructure, which we call the reservoir. We do not claim to provide a complete formal theory of the reservoir, just as Einstein did not provide a complete theory of atomic interactions. We claim only that the deviations are real, that they are consistent, and that they point toward a layer of organisation below the resolution of standard quantum mechanics.

The present hypothesis is distinct from earlier proposals invoking quantum effects in biology. The Penrose–Hameroff Orch-OR model [17] proposes objective wavefunction collapse in microtubules as the locus of quantum biological effects; our framework does not require a specific collapse mechanism and is agnostic about the physical substrate of the reservoir. De Broglie–Bohm pilot wave theory [18] introduces a guiding wave as a hidden variable in the classical sense — a definite subquantum trajectory. The reservoir, by contrast, is not a trajectory or a definite value but an aperiodic information structure whose complexity is irreducible. The present proposal is therefore complementary to, but structurally distinct from, both of these predecessors.

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2. Quantum Mechanics as a Limiting, Blurred Description

The standard wave function Ψ describes a system as a smooth probability distribution without internal structure. This description is highly accurate in simple systems. We propose, however, that it represents a blurred limit of a deeper dynamics — in the same way that Newtonian gravity is the limiting case of general relativity, and classical thermodynamics is the limiting case of statistical mechanics.

The blurring arises from two sources. First, measurement is invasive: any experimental interaction with a quantum system disturbs its state, and coupling to a deeper layer is destroyed in the process. Second, in structurally simple (inorganic) systems, the coupling to the reservoir is negligible — the reservoir appears featureless, and standard QM statistics emerge as the appropriate description. In highly organised biological systems, this coupling becomes significant, and deviations appear.

An optical analogy is instructive: a defocused lens produces a smooth, featureless distribution of light and shadow. A focused lens reveals fine structure and detail. Simple quantum systems are necessarily observed through a defocused lens. Biological systems, through the extreme refinement of their molecular organisation, achieve partial focus — and fine structure becomes visible.

3. Empirical Anomalies Suggesting a Deeper Layer

3.1. Enzymatic Catalysis

Enzymes exhibit proton and electron tunnelling with efficiencies several orders of magnitude higher than standard quantum models predict [1,6]. This suggests that enzymes stabilise transition states through a mechanism not fully contained in standard QM. Crucially, this stabilisation is sensitive to distal mutations — modifications far from the active site, which alter vibrational modes and conformational dynamics rather than local electrostatics [7]. This is a signature consistent with coupling to a structured, non-local information layer: the relevant variable appears to be the global vibrational topology of the protein, not the local electrostatic environment of the reactive site.

3.2. Protein Folding

Protein folding proceeds with a speed and directionality that is statistically improbable under naive random search models. Energy landscape and funnel models (Onuchic, Luthey-Schulten, Wolynes [4]) have substantially advanced our understanding of this process by replacing the Levinthal paradox with a statistical funnelling picture. These models successfully account for the broad features of folding kinetics and thermodynamics. Nevertheless, several aspects of folding remain incompletely explained within this framework: the precision and robustness of folding across highly noisy biological environments, the systematic role of non-local vibrational modes in mediating folding rates [7], and the folding behaviour of intrinsically disordered proteins under cellular conditions [8]. We propose, as a working hypothesis, that the reservoir may provide additional orientational information that biases the conformational search in ways not fully captured by a smooth energy surface — a suggestion that is testable via the predictions in Section 8.

3.3. Excitonic Coherence

Early femtosecond two-dimensional spectroscopy experiments reported long-lived excitonic coherence in the FMO complex at cryogenic and, subsequently, physiological temperatures [2,10]. These findings attracted wide attention as potential evidence for functional quantum coherence in biology. Subsequent theoretical and experimental work has substantially revised this picture: Cao et al. [3] and Scholes et al. [9] have demonstrated that vibronic coupling between electronic and nuclear degrees of freedom accounts for a significant portion of the observed signals, and that purely electronic coherence is likely shorter-lived than originally reported. We accept this revision as correct within its own terms.

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The reservoir hypothesis does not require the original strong interpretation of FMO coherence to stand. We propose a more limited claim: that the spatial topology of the chromophore network — the geometry of inter-chromophore couplings and their arrangement — plays a stabilising role that is not fully captured by models treating vibronic coupling as the sole structured variable. Specifically, we suggest that sensitivity of coherence lifetime to topological perturbations (rearrangement of chromophore geometry) should exceed sensitivity to equivalent thermal perturbations within the physiological range. This is an empirical question, addressed directly by Prediction 2 in Section 8, and is logically independent of the question of whether long-lived purely electronic coherence exists.

While conventional mechanisms such as vibronic coupling, structured baths, and statistical sampling within standard quantum mechanics can account for a significant portion of these effects, they often require increasingly fine-tuned or borderline assumptions to fully match the observed magnitudes and topology-dependence (see section 10. Discussion for a detailed critique and alternative perspective).

4. The Reservoir: A Hidden Information Layer

We propose that the above anomalies share a common explanation: the existence of a reservoir — a hidden information layer with a rich, aperiodic structure. The reservoir has the following properties:

- it is not accessible to direct measurement;
- it is disrupted by every measurement interaction;
- it is readable only by finely organised structures;
- it selectively stabilises micro-states in complex systems;
- it is aperiodic and therefore cannot be described by a closed analytical expression.

The reservoir is not a hidden variable in Einstein's sense — it is not a set of definite classical values underlying quantum probabilities. It is, rather, an information landscape: a structure that can be read and that influences dynamics, but that cannot be compressed into a single equation. The appropriate analogy is not a Hamiltonian but a genome, or a software source code: a structure whose causal efficacy is real and measurable, but whose content is aperiodic and non-compressible [11].

This analogy is more than rhetorical. Kolmogorov complexity establishes that aperiodic information-rich structures — like a DNA sequence or a compiled program — cannot in principle be described by a formula shorter than the structure itself [12]. There is no equation for the genome of a mouse. The reservoir, we propose, has the same logical character: it is a real physical substructure whose description requires its full specification, not a formula. This is why we do not offer a closed-form theory of the reservoir, and why we believe no such theory is possible. What is possible — and what we offer — is the inference that such a layer exists, based on the pattern of deviations it produces.

5. Biomolecules as Reading Heads of the Reservoir

Biomolecules have a specific property: their internal dynamics, vibrations, topology, and spatial organisation are tuned to the structure of the reservoir. Throughout this paper, we use the term topology to refer operationally to the network of vibrational coupling strengths between residues or chromophores — measurable, in principle, via normal mode analysis, contact map spectroscopy, or two-dimensional infrared spectroscopy. A complex structure with a rich coupling network resonates with the reservoir and increases the directionality of reactions by many orders of magnitude. In inorganic, structurally simpler systems, coupling to the reservoir is negligible; such systems experience the reservoir as so strongly blurred that it is expressed only as ordinary statistical QM predictions.

- Enzymes read the reservoir and stabilise transition states.
- Proteins read the reservoir and fold directionally.
- Excitons read the reservoir and maintain coherence.

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Inorganic matter without the necessary structure does not couple significantly to the reservoir, and reverts to standard QM predictions. The reservoir is not absent in inorganic systems — it is present but unreadable, like text in a language whose alphabet one does not possess.

6. Why a Complete Mathematical Description May Be Impossible

We wish to address directly an objection that will occur to many readers: is a hypothesis that cannot be fully formalised scientific? We argue that it is, for the following reasons.

Einstein's 1905 paper on Brownian motion did not contain a microscopic theory of atomic collisions [5]. It contained an inference: that the observed statistics of pollen motion are consistent with an underlying discrete structure, and inconsistent with a purely continuous fluid. The atomic structure was real and causally efficacious, even though no closed-form description of individual atomic trajectories was offered. The paper was accepted as a scientific contribution because it made testable predictions — predictions about the mean squared displacement of particles as a function of time and viscosity — not because it provided a complete microscopic theory.

We are in an analogous position. We do not offer a closed-form theory of the reservoir. We offer an inference — that the pattern of biological quantum deviations is consistent with an underlying aperiodic information structure — and a set of testable predictions. The absence of a closed-form theory is, moreover, not a contingent limitation of our current knowledge but a principled one: aperiodic structures of high Kolmogorov complexity cannot be described by short formulae [12]. This is not a defect of the hypothesis; it is a feature of the class of objects it describes.

7. Schematic Illustration via the Television Analogy

To clarify the nature of the proposed reservoir coupling, an analogy with a television receiver is instructive (see Figure 3 for a schematic overview).

Without claiming to provide a complete theory of the reservoir, we can indicate schematically where a coupling to a deeper information layer would enter quantum dynamics. We write, purely as a notational device:

$$E\Psi = \hat{H}\Psi + \hat{R}[\Psi, I] \quad (1)$$

where E represents the total energy and effective stability of the system, $\hat{H}$ is the standard Hamiltonian, I is the aperiodic information structure of the reservoir, and $\hat{R}$ is a schematic term representing reservoir coupling. This is not a proposed dynamical law, but a schematic placeholder. We wish to be explicit that this is not a calculational equation and $\hat{R}$ is not defined: its content is precisely the irreducible, high-complexity information structure of the reservoir. The expression is useful solely as a locator — it identifies where the deviation from standard QM enters, and clarifies that the deviation is structurally distinct from a correction to $\hat{H}$. Readers who find this notation misleading without a defined $\hat{R}$ may prefer to read the claim as purely verbal: standard QM dynamics are supplemented by an information-coupling term whose existence is inferred from empirical deviations and whose form is, in principle, non-compressible.

If the television is not tuned to any station, the screen shows only noise or remains black. In that case, a physicist studying the internal circuitry could fully explain the entire behaviour of the set solely from its electronic components and thermal noise — nothing more is required. However, once the television is tuned to a station and a coherent image appears, the situation changes profoundly. Analysing the hardware alone is no longer sufficient to account for the structured content on the screen; the image arises from coupling to an external reservoir of broadcast information.

To make this idea accessible even without any background in quantum mechanics, imagine the equation in the simplest possible terms using our television analogy.

EΨ represents the actual behaviour of the whole system — what you ultimately see and how it changes over time. In the TV example, this is the picture that appears on the screen (or the random snow if nothing is received).

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$\hat{H}\Psi$ stands for the internal structure of the system itself — its "wiring" and the properties of all its components. In the TV, this is the circuit board, the exact values of all resistors, capacitors, and chips.

Standard quantum mechanics (the version taught in textbooks) assumes that everything can be explained by the structure alone:

$$E\Psi = \hat{H}\Psi \tag{2}$$

In other words, the picture on the screen is produced solely by the hardware. If one understood the circuit board perfectly, one should — under this assumption — be able to predict everything that appears on the screen; nothing else is required. We propose that this is not always enough. In complex biological systems something additional is at work, which we write as an extra term in equation (1).

The new term $\mathcal{R}[\Psi, I]$ represents an influence that does not originate from the internal structure of the system. In the television analogy, it corresponds to the broadcast signal arriving from the transmitter — the structured information that cannot be inferred from the hardware alone.

Crucially, both terms on the right-hand side must work together. The broadcast signal alone is useless if the TV is not tuned (you see only noise). At the same time, a perfectly tuned circuit board without any incoming signal also produces only internal noise. Only when the hardware ($\hat{H}\Psi$) is in the right configuration and the external structured information ($\mathcal{R}$) is present does the coherent picture appear.

Exactly the same logic applies in biology: the molecular structure of an enzyme or protein ($\hat{H}\Psi$) determines whether it is able to "tune in" to the hidden information layer. When it does, the extra term $\mathcal{R}$ becomes significant and produces the dramatic effects we observe — ultra-fast catalysis, directional folding, or protected coherence — that standard quantum mechanics alone cannot explain.

This principle is schematically illustrated in Figure 3, where the untuned receiver corresponds to a system without access to the reservoir (only internal noise), while the tuned receiver demonstrates the emergence of structured behaviour through coupling.

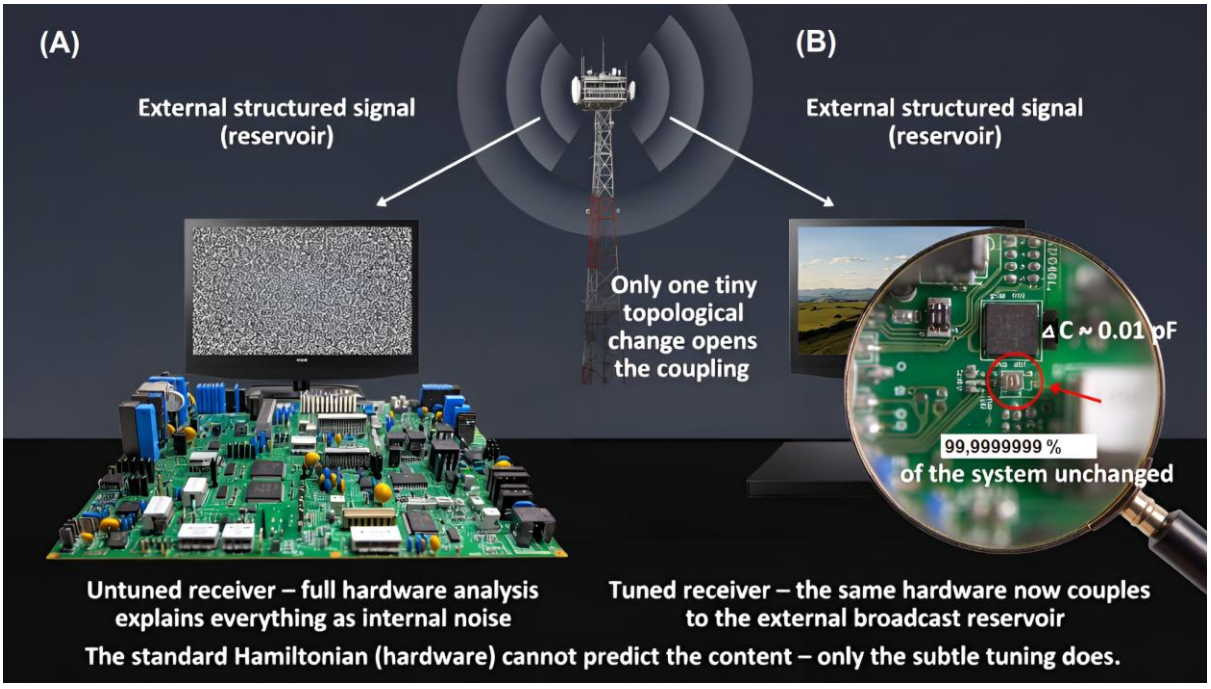

Figure 3. Television receiver analogy for reservoir coupling. (**A**) Untuned state: the complex circuitry (millions of components) produces only internal thermal noise on the screen; a physicist analysing the hardware alone would conclude that nothing more is needed. (**B**) Tuned state: the identical circuitry, after a minute capacitance change of order 0.01 pF in the varactor tuning circuit (highlighted), receives a coherent structured image from the external broadcast. The transmitter (top) emits the same signal to both receivers; only the topology-sensitive

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coupling decides whether the output is noise or organised meaning. This mirrors how standard quantum mechanics fully accounts for simple inorganic systems, whereas only sufficiently organised biological structures gain access to the hidden aperiodic reservoir.

Crucially, the physical structure of the television remains essentially identical in both cases. Among its millions of components, the only meaningful difference is a subtle change in capacitance within the input tuning circuits — typically on the order of hundredths of a picofarad (≈ 0.01 pF) in modern varactor-based tuners — a minute, easily overlooked adjustment that nevertheless decisively opens the coupling to the external broadcast reservoir. While approximately 99.9999999 % of the entire system remains unchanged, this tiny topological perturbation transforms the output from unstructured thermal noise to highly organized, externally structured meaning. The hardware itself (corresponding to the standard Hamiltonian) determines only the technical capacity to display an image, but reveals nothing about the broadcast content. Moreover, even a detailed inspection of the Hamiltonian would not obviously disclose the potential for receiving a coherent image unless one already anticipates or presupposes the existence of an external information reservoir. Contemporary science, operating without such a presupposition, is therefore perplexed by the profound behavioural differences between lifeless machines and living organisms and continues to search for the essence of life in molecular noise, statistical fluctuations, or purely internal quantum effects — rather than recognizing the critical, topology-sensitive coupling that grants access to a hidden information layer.

8. Testable Predictions

The following predictions distinguish the reservoir hypothesis from both standard QM and existing alternative explanations. We note that vibrational topology is operationally defined here as the network of inter-residue or inter-chromophore vibrational coupling strengths, measurable via normal mode analysis or two-dimensional infrared spectroscopy.

Prediction 1 (Enzymatic catalysis): Distal mutations — those that alter vibrational coupling networks rather than active-site electrostatics — will produce disproportionately large reductions (target: >10-fold relative to active-site mutations of equivalent structural perturbation) in catalytic rate [1,7]. The reservoir hypothesis predicts this because the global vibrational topology, not local geometry, is the primary coupling channel.

Prediction 2 (Excitonic coherence): Coherence lifetime will be more sensitive to changes in the spatial topology of the chromophore network than to temperature, within the biologically relevant range of 200–350 K — a range chosen because vibronic coupling magnitudes are known to vary less than thermal energy within this window [3,9]. Standard decoherence models predict temperature should dominate. The reservoir hypothesis predicts topology is the primary variable. This prediction is logically independent of the question of whether long-lived purely electronic coherence exists.

Prediction 3 (Protein folding): Protein folding will exhibit deviations from statistical funnel-model predictions even at elevated noise levels, provided that the vibrational coupling topology is preserved. Disrupting topology — not merely increasing thermal noise — should be the critical variable for abolishing anomalous folding speed [4,8].

Prediction 4 (Synthetic biomolecules): A synthetic biomolecule designed with sufficiently complex vibrational coupling topology — not necessarily with natural sequence — should exhibit anomalously fast folding or catalysis compared to classical predictions [13]. This is a strong prediction: it implies that the causal variable is organisational complexity, not evolutionary fine-tuning.

9. Conclusions

We have proposed that a class of biological quantum anomalies — enzymatic tunnelling efficiency, excitonic coherence, and protein folding directionality — share a common explanation: coupling to a hidden information layer, which we call the reservoir. The reservoir is aperiodic and non-compressible; it cannot be described by a closed-form equation, for the same reason that there is

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no formula for the genome of a mouse. This is not a defect of the hypothesis but a reflection of the logical character of the objects it describes.

The methodological position of this paper is analogous to Einstein's 1905 analysis of Brownian motion [5]: we infer the existence of a substructure from the pattern of statistical deviations it produces, without claiming to provide a complete microscopic theory of that substructure. Standard quantum mechanics is re-interpreted not as a fundamental theory but as a limiting, blurred description — accurate in structurally simple systems, increasingly inadequate as organisational complexity grows.

We have proposed four testable predictions that distinguish this framework from both standard QM and existing alternatives. Confirmation of any of these predictions — particularly the synthetic biomolecule prediction — would constitute strong evidence for the reservoir hypothesis. Disconfirmation would constrain it. The framework is, in this sense, scientifically tractable despite the principled impossibility of its full formalisation.

The framework is fully compatible with standard quantum mechanics, which it treats as a limiting case valid in structurally simple systems.

10. Discussion

The reservoir hypothesis carries implications that extend beyond the quantum anomalies discussed above. One of the deepest unsolved problems in origins-of-life research is the statistical improbability of abiogenesis: the probability that a self-replicating molecule arises by random chemistry in a prebiotically plausible environment is, under standard assumptions, vanishingly small [14,15]. The reservoir hypothesis reframes this problem. If coupling to the reservoir increases the directionality of molecular processes by many orders of magnitude — but only once a structure reaches a threshold of organisational complexity sufficient to read the reservoir — then the origin of life need not be treated as a random accident. It becomes instead a threshold phenomenon: a phase transition in the coupling between molecular structure and the information layer. Below the threshold, chemistry proceeds as standard statistical models predict. At the threshold, the reservoir begins to stabilise configurations, accelerating self-organisation in a manner that standard probability estimates do not capture. On this view, the first replicators would represent not an improbable fluke but a highly probable outcome once chemistry has explored sufficient configuration space to cross the readability threshold — at which point reservoir coupling would drive rapid, self-reinforcing stabilisation. This suggestion is explicitly speculative and goes beyond what the empirical anomalies discussed above directly support; we offer it as a candidate explanation that the present framework makes available, not as a consequence that follows necessarily from it.

This reframing has a natural corollary for the persistence of life: living systems resist entropy not merely through metabolic energy input but because the reservoir continuously stabilises their micro-states against thermal noise. A machine, however energetically maintained, lacks the organisational topology required for reservoir coupling and therefore remains fully subject to entropic degradation. If correct, this would contribute to resolving a long-standing asymmetry between living and non-living matter that thermodynamics alone has not satisfactorily explained [16]. The implications extend to astrobiology — life may be considerably more probable wherever chemistry can reach the coupling threshold — to synthetic biology, where the design target shifts from sequence to topological complexity — and to the thermodynamics of living systems, where the reservoir provides a physically grounded account of biological order that standard quantum mechanics cannot supply.

Reading the aperiodic information content of the reservoir by biological structures thus effectively reduces the configurational entropy of the system below the level expected by standard quantum mechanics and thermal noise, thereby providing a physically based mechanism for maintaining biological order in far-from-equilibrium conditions. The reservoir hypothesis also carries a methodological implication.

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Current mainstream explanations often attribute the observed anomalies in enzymatic rates, excitonic coherence, and protein folding primarily to vibrational modes, structured baths, or statistical sampling within the conventional quantum framework. While these mechanisms undoubtedly play important roles, they frequently appear as boundary cases — borderline sufficient to account for the data, yet requiring increasingly elaborate fine-tuning or averaging over improbable ensembles to remain consistent. Such accounts, though formally possible within the existing formalism, carry an air of ad hoc adjustment: they preserve the completeness of standard quantum mechanics at the cost of invoking statistical coincidences whose probability borders on the implausible (e.g., the rapid emergence and long-term stability of life far from equilibrium). The reservoir hypothesis proposed here does not deny the validity of these conventional contributions, but suggests they may represent an incomplete description — one that becomes adequate only in the limit of low organisational complexity, while failing to capture the essential topology-dependent coupling present in living systems.

The absence of a closed-form description is therefore not a contingent limitation but a principled one: aperiodic structures of high Kolmogorov complexity cannot be compressed into a shorter formula. In this conceptual sense, the role of $\hat{R}$ is analogous to Einstein's cosmological term: an additional structural component introduced not as a calculational device, but because the existing equations appear incomplete without it. Unlike a constant, however, $\hat{R}$ represents an aperiodic information layer rather than a numerical correction.

The reservoir hypothesis also suggests a reinterpretation of thermal noise. Rather than acting solely as a source of decoherence, the fluctuating environment in the biologically relevant temperature range may provide the dynamical degrees of freedom required for coupling to the reservoir — too weak at cryogenic temperatures, too disruptive at high temperatures, but constructive within the narrow window in which life operates.

From this perspective, thermal noise itself becomes a candidate for a structured bias that enables reservoir coupling within the narrow temperature window in which life operates. Decoherence shaped by the reservoir may thus play a paradoxically stabilising role in living systems, even though it is usually assumed to be purely disruptive.

A more radical ontological possibility should also be considered. In contemporary quantum mechanics, a particle does not possess a definite position or momentum until it is measured; the very act of measurement — typically through interaction with a probe particle of comparable scale — collapses the state and erases any pre-existing delicate coupling. This collapse is not merely a disturbance of an otherwise well-defined trajectory (as Heisenberg originally envisioned), but the creation of definiteness where none existed.

If the reservoir is an aperiodic information layer that couples preferentially to precisely tuned molecular topologies, any experimental probe capable of extracting information would simultaneously destroy the very coupling it seeks to detect. The reservoir could therefore remain hidden behind a fundamental "ontological veil" — a barrier that is not technological but intrinsic, comparable in principle to the speed of light or the structure of causality. In simple inorganic systems this veil renders the coupling invisible; in highly organised biomolecules, however, the coupling manifests spontaneously through enhanced rates, directionality, or coherence before any measurement can collapse it.

The same logic offers a straightforward resolution of the double-slit experiment: when a detector is placed to determine which path the electron takes, the interference pattern disappears not because of any deep mystery, but because the measuring particle physically perturbs the delicate state that was previously influenced by the reservoir. What quantum mechanics often presents as paradoxical becomes, under this view, an ordinary physical consequence of measurement-induced disruption.

This perspective also suggests that some of the apparent "mysteries" of quantum mechanics may be less fundamental than commonly presented — arising not from an inherent indeterminacy of reality, but from the unavoidable physical disruption caused by measurement itself.

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In practice, any measurement requires interaction with a probe particle (or field) whose energy and momentum are of the same order of magnitude as those of the system under study — we simply do not possess "lighter" or "gentler" projectiles than elementary particles themselves (electrons, photons, etc.). There is no available tool that could probe a quantum state without significantly perturbing it. This fundamental limitation of measurement technology reinforces the possibility that certain delicate couplings — such as the one proposed here with the reservoir — remain systematically hidden from direct observation, even though their functional consequences in organised biological systems are plainly observable.

Thus the reservoir may be detectable only through its functional effects in living systems, never through direct inspection — much like the television broadcast that cannot be deduced from the receiver's circuitry alone, yet is undeniably received when the set is properly tuned.

A recurring difficulty in the study of complex biological systems is the assumption that any causally efficacious mechanism must be expressible as a closed-form Hamiltonian or derivable from first principles. Where this condition is not met, the residual is typically assigned to stochastic noise. We suggest that this assumption, while appropriate for simple inorganic systems, may be systematically inadequate for organised matter above the reservoir coupling threshold. The anomalies discussed in this paper are not obviously reducible to noise — they are consistent, directional, and topology-dependent. If the reservoir hypothesis is correct, the appropriate response is not to seek a compact equation for the reservoir, but to develop experimental and theoretical tools capable of probing the coupling between organisational complexity and physical dynamics [19]. This would not represent a departure from scientific method — it would represent its extension to a class of objects, living systems, whose most salient properties have so far resisted reduction to standard quantum statistics.

Taken together, these considerations suggest that the reservoir hypothesis offers a coherent physical framework for phenomena that have long resisted reduction to standard quantum mechanics, while remaining fully compatible with it in the appropriate limit.

If the reservoir hypothesis is correct, it reframes the long-standing ambition of a "theory of everything". No single closed-form dynamical law can be complete, because such laws describe only the compressible part of physical reality. A full account would require both the algorithmic layer of equations and the irreducible, aperiodic information layer represented by $\mathcal{R}$.

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