The Limits of Falsifiability: Dimensionality, Measurement Thresholds, and the Sub-Landauer Domain in Biological Systems

Version 2.0

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Abstract

Karl Popper's falsifiability criterion assumes that scientific hypotheses can be reduced to binary tests. We show this assumption is *scale-dependent* and can *saturate* in high-dimensional biological systems operating near physical measurement limits. But the limitation runs deeper than measurement: *falsifiability itself depends on axiomatic choices about how questions are structured*, and these framework choices are themselves projections that cannot be tested from within the framework. In neural networks, much relevant information exists as patterns below the Landauer threshold for irreversible bit recording—signals too weak for individual neurons to detect

but detectable when pooled across populations. These sub-threshold patterns cannot be projected into binary outcomes without destroying their causal structure. We develop a framework connecting dimensionality, thermodynamic measurement limits, framework dependence, and biological epistemology, showing that Popperian logic represents a special case applicable only to low-dimensional systems with strong signals *and* shared axiomatic structure. The "unreasonable effectiveness of mathematics" in physics reflects selection bias toward domains where projection loss is small; biology is where this selection breaks down. Our analysis has implications for neuroscience, consciousness, and any domain where the system dimensionality exceeds the observer's representational capacity, motivating a shift from single-case hypothesis tests to multi-scale, ensemble-based inference that acknowledges the framework-dependence of all empirical claims.

Keywords: falsifiability, dimensionality, Landauer limit, framework dependence, Duhem-Quine thesis, stochastic resonance, consciousness, biological epistemology

1 Introduction

Karl Popper's falsifiability criterion has served as a cornerstone of scientific epistemology since its articulation in *The Logic of Scientific Discovery* [1]. The framework's elegance lies in its binary clarity: a hypothesis is scientific if and only if it can, in principle, be shown false through empirical observation. This criterion has proven remarkably effective in distinguishing science from pseudoscience across biology, from molecular genetics to ecosystem ecology.

However, recent advances in our understanding of biological complexity and physical measurement limits expose fundamental boundaries to Popper's framework. Complex biological systems, ranging from neural networks to protein folding landscapes, operate in high-dimensional phase spaces where causal relationships emerge from the collective behavior of many interacting components. We argue that falsifiability, rather than being a uni-

versal criterion for biological knowledge, applies only to systems meeting specific physical, mathematical, *and axiomatic* constraints.

1.1 Three Levels of Limitation

This paper identifies three distinct levels at which falsifiability breaks down:

1. **Physical measurement limits.** The Landauer principle establishes that recording one bit of information requires a minimum energy of $k_B T \ln 2$ [2]. Many biological patterns exist below this threshold—causally potent yet unmeasurable as discrete states.

2. **Dimensional projection loss.** High-dimensional systems projected onto low-dimensional observations lose almost all information. A binary test on a 100-neuron circuit preserves less than 1% of the information content.

3. **Framework dependence.** Before any measurement occurs, the choice of what counts as a test, what counts as evidence, and how the question is structured already embeds unfalsifiable assumptions. The framework is itself a projection.

The third level is the deepest and most often overlooked. Even in domains where measurement is possible and dimensionality is manageable, falsifiability remains relative to a framework that cannot itself be falsified from within.

1.2 The "Unreasonable Effectiveness" as Selection Bias

Eugene Wigner famously noted the "unreasonable effectiveness of mathematics in the natural sciences" [3]—the surprising correspondence between abstract mathematical structures and physical reality. We propose a partial explanation: physics has historically selected for systems where mathematical description works well.

Any mathematical description is necessarily finite-dimensional: one can only write finitely many symbols, equations, and variables. Real systems, especially biological ones, have state

spaces of enormous or effectively infinite dimension. Every mathematical model is already a projection, a shadow of the actual dynamics.

Physics appears successful partly through selection bias: we call "physics" the domains where projection loss is small enough for precise prediction—isolated systems, controlled conditions, symmetric situations where relevant degrees of freedom are few. The success of mathematics in physics does not demonstrate that mathematical description is universally adequate; it demonstrates that we have been studying the domains where it is adequate.

Biology is where projection loss becomes undeniable. Living systems maintain high-dimensional internal states that exceed observational access—not as a limitation of current technology, but as part of what makes them alive. The persistent difficulty of reducing biology to physics, the tendency of organisms to be "more than the sum of their parts," may reflect a genuine feature of the subject matter rather than temporary limitation.

2 Framework Dependence: The Deepest Limitation

2.1 The Duhem-Quine Insight Extended

Duhem [4] and Quine [5] established that no hypothesis is tested in isolation. Any empirical test involves auxiliary assumptions about measurement instruments, background conditions, and what counts as evidence. When a prediction fails, logic alone cannot determine whether the hypothesis or an auxiliary assumption is at fault.

We extend this insight: *the framework within which hypotheses are formulated is itself a projection.* Before you choose a hypothesis to test, you have already made choices about:

- What variables are relevant
- What counts as an observation
- What precision is sufficient

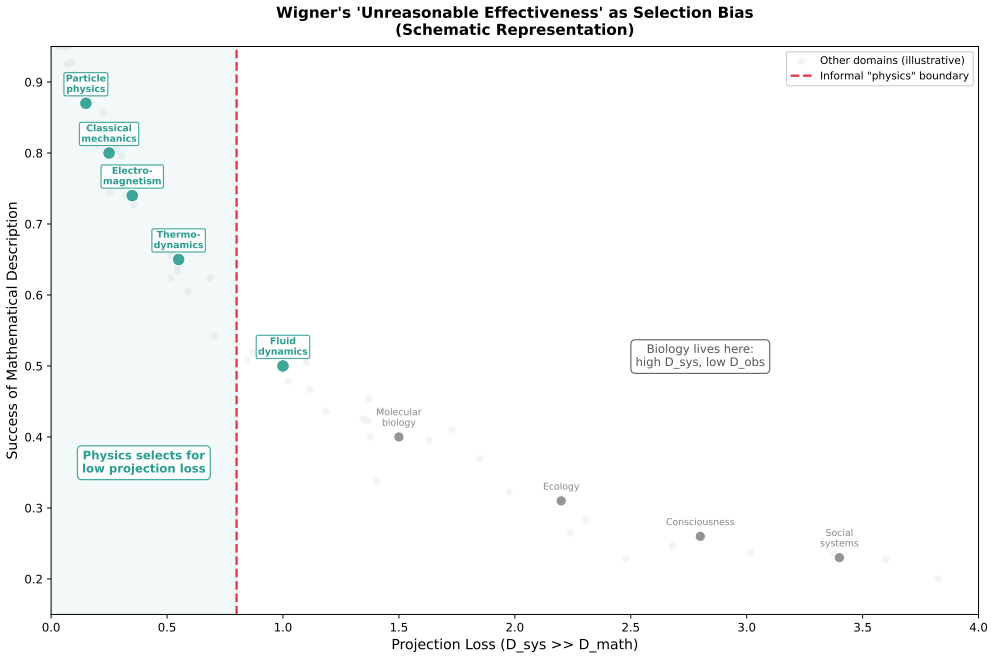

Figure 1: **The "Unreasonable Effectiveness" as Selection Bias (Schematic Representation).** Domains studied by physics (green) cluster where projection loss is small—where finite-dimensional mathematical descriptions capture most of the relevant dynamics. Biology, consciousness, and social systems occupy the high projection-loss regime where mathematical description fails. The apparent success of mathematics in physics reflects selection for tractable domains, not a deep truth about the mathematical nature of reality. *Note: Domain positions are illustrative; no rigorous quantification of "projection loss" exists across these diverse fields. The figure visualizes the qualitative argument, not empirical measurements.*

- How the question is structured
- What background knowledge is assumed

These choices constitute a dimensional reduction. The full space of possible framings is high-dimensional; any specific framing projects this into a particular low-dimensional subspace. Different researchers asking "different questions" are often occupying different projections of the same underlying reality.

2.2 Framework Choice as Dimensional Reduction

Consider an analogy. A three-dimensional object casts different shadows on different walls depending on the projection angle. Two observers seeing different shadows might disagree about the object's shape—one sees a circle, another sees a rectangle—even though they are observing the same object.

Similarly, researchers in different disciplines, or even within the same discipline using different paradigms, are projecting high-dimensional reality onto different low-dimensional coordinate systems. Their disagreements may not be resolvable by evidence because they are not making claims in the same framework.

This is not relativism. The underlying reality exists independently of the frameworks used to describe it. But *falsification is framework-relative*. A hypothesis can only be falsified with respect to a given set of background assumptions, and those assumptions cannot themselves be falsified within the framework that presupposes them.

2.3 Why Physics "Works"

Physics appears to escape this problem because its framework assumptions are unusually stable and widely shared. Physicists agree on what counts as a measurement, what the relevant variables are, and how precision is assessed. The axiomatic structure is settled.

But this stability is not a feature of nature; it is a feature of the discipline's sociology. Physics has historically focused on domains where:

1. System dimensionality is low or effectively reducible
2. Measurement is clean and repeatable
3. Framework assumptions are uncontested
4. Projection loss is small

In domains where these conditions fail—consciousness, ecology, evolution, social systems—falsifiability becomes contested not because researchers are irrational but because they occupy genuinely different frameworks that project reality differently.

2.4 The Regress Problem

One might attempt to resolve framework disputes by stepping back to a meta-framework that adjudicates between frameworks. But this meta-framework is itself a projection, subject to the same limitations. The regress does not terminate.

This is not a counsel of despair. It is a recognition that empirical knowledge is always framework-relative, and that the framework itself represents a dimensional reduction that cannot be fully tested from within. The appropriate response is not to abandon empirical inquiry but to hold frameworks as tools rather than truths, to expect scope limitations, and to remain alert for situations where framework choice dominates over empirical content.

3 The Binary Projection Problem in Biology

3.1 Implicit Assumptions in Biological Falsifiability

Popper's framework contains an implicit assumption particularly problematic for biology: that any meaningful biological hypothesis can be reduced to a falsifiable statement, essen-

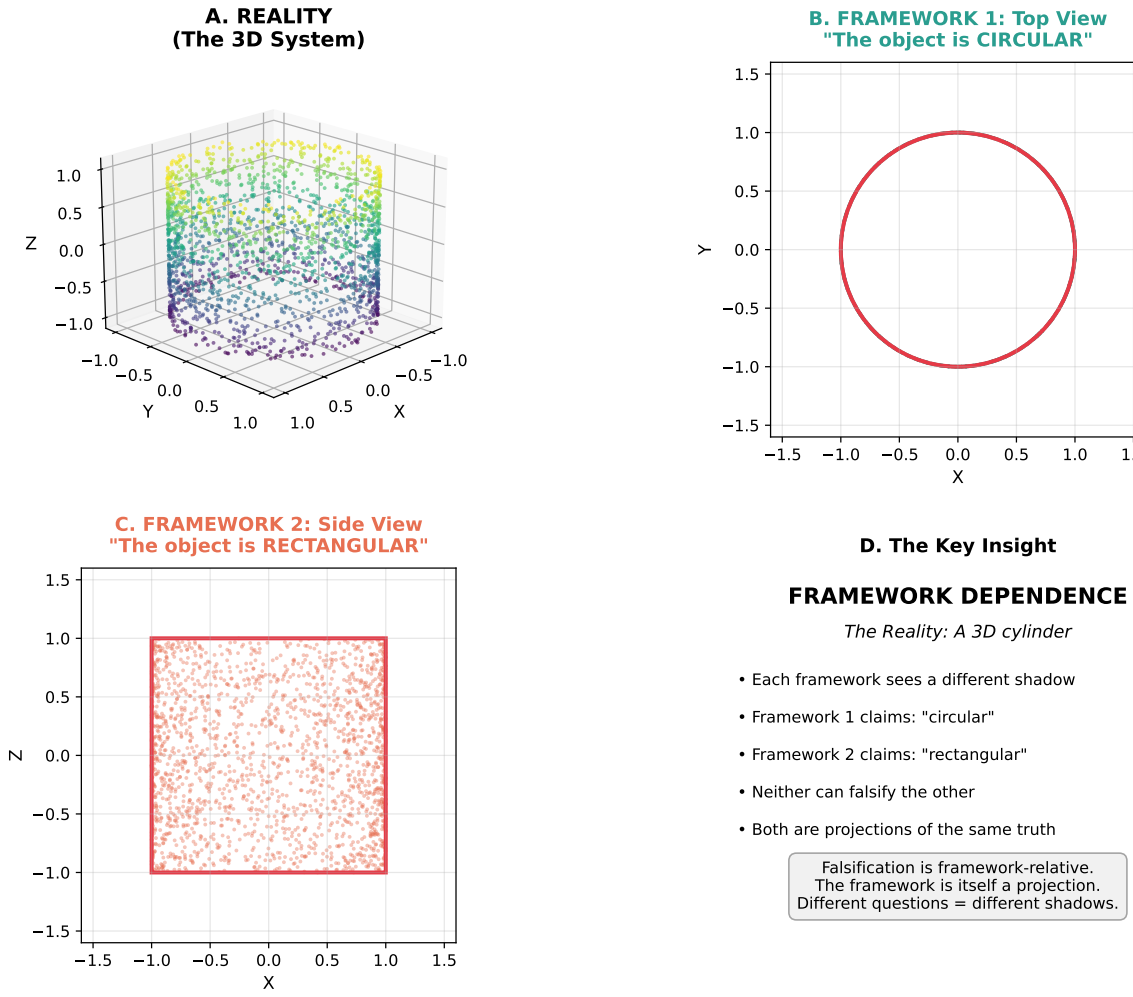

Figure 2: **Framework as Projection.** A cylinder (A) casts different shadows depending on projection angle. Framework 1 (B) observes only the XY projection and concludes the object is circular. Framework 2 (C) observes only the XZ projection and concludes it is rectangular. Both projections are "correct" given their assumptions, but they generate incompatible hypotheses. Neither can falsify the other because they are not making claims in the same dimensional subspace.

tially a binary decision. While Popper concerned himself with *in principle* falsifiability, we show that physical laws impose *in principle* limits on what biological phenomena can be falsified.

Clarification on Popper and binary tests. A skeptical reader may object that Popper's falsifiability is a *logical relation* between hypothesis and observation—observations can be continuous, noisy, statistical—and that modern "Popperian" practice often uses statistical falsification (likelihood ratios, posterior predictive checks) rather than literal single-bit measurements. We accept this clarification but note it does not dissolve our argument. The epistemic bottleneck is not in the measurement device but in the *demarcation logic*: even if raw measurements are rich, the scientific process ultimately forces a decision boundary (accept/reject, significant/non-significant, model A/model B). It is this forced projection from continuous evidence to discrete conclusion that creates information loss, regardless of how sophisticated the intermediate analysis.

Bayesianism does not escape. One might hope that Bayesian inference—which maintains full posterior distributions rather than forcing binary decisions—circumvents this problem. It does not. Bayesian methods face their own high-dimensional crises: the curse of dimensionality makes posterior computation intractable, priors become effectively uninformative or encode unjustified assumptions, MCMC samplers fail to mix, and variational approximations introduce uncontrolled bias. More fundamentally: if the posterior cannot be computed or even represented, Bayesian analysis cannot begin. The promise of "maintaining full distributions" is vacuous when the distribution lives in a space too large to explore. In high-dimensional biological systems, Bayesian inference does not preserve information—it projects onto a tractable subspace, just as frequentist methods do. The framework dependence runs deeper than the choice of statistical paradigm.

Consider a hypothesis about protein folding: "Protein X folds via pathway Y." Testing this proposition requires bringing the protein to a state where folding intermediates are discretely resolvable, measuring without disrupting the folding process, and projecting the

multi-dimensional folding landscape onto a binary decision axis. Yet protein folding occurs on a rugged energy landscape with astronomical numbers of conformational states [7]. The act of measurement necessarily perturbs this landscape, potentially switching the protein to alternative folding pathways. Moreover, the binary projection destroys information about parallel pathways, transient intermediates, and the inherently statistical nature of the folding process.

3.2 Information Loss Under Projection

For a biological system with n degrees of freedom, each with k distinguishable states, the total information content is:

$$I_{\text{total}} = \log_2(k^n) = n \log_2 k \quad \text{bits} \tag{1}$$

A binary test extracts exactly 1 bit—a yes/no partition of the state space. The fraction of information preserved is therefore:

$$\frac{I_{\text{preserved}}}{I_{\text{total}}} = \frac{1}{n \log_2 k} \tag{2}$$

In a modest neural circuit with $n = 100$ neurons, each with $k = 10$ distinguishable states, this ratio becomes $1/(100 \times 3.32) \approx 0.003$—less than 1% of the information preserved. A single binary test discards over 99% of the system's information content.

Optimized projections fare little better. One might object that scientific questions are not random partitions but *directed* projections—like principal component analysis (PCA)—designed to capture maximum variance. This is true, but it does not rescue the situation. Even optimized projections must discard the "long tail" of high-dimensional correlations, and in biological systems this tail often contains the critical causal structure: rare conformational states, weak but decisive couplings, transient coherences that gate function. The principal components capture what varies most, not what matters most. Optimizing

the projection does not eliminate projection loss; it merely concentrates the preserved information in directions chosen by the optimizer's assumptions—another layer of framework dependence.

This is not a practical limitation awaiting better technology. It is an information-theoretic fact about projection. Moreover, the situation compounds: to fully specify the system state would require $n \log_2 k \approx 332$ independent binary tests, each of which may perturb the system. The measurement problem is not just that individual tests are lossy, but that the number of tests required scales with system complexity while biological systems cannot tolerate arbitrary repeated measurement.

4 Three Axes of Measurement Limitation

Beyond framework dependence, three orthogonal physical constraints limit falsifiability:

4.1 High Dimensionality

Biological systems are fundamentally high-dimensional. A single cell's state requires thousands of variables to specify—gene expression levels, metabolite concentrations, protein conformations, membrane potentials. Any finite-dimensional description is a projection.

Mathematics itself is finite-dimensional: one can only write finitely many symbols. Every mathematical model is therefore a dimensional reduction. The question is not whether projection occurs but whether projection loss is small enough to preserve relevant structure. For biology, it often is not.

4.2 Quantum Timing and Measurement Disturbance

Even for low-dimensional systems, quantum measurement backaction imposes limits. When biological processes depend on coherent superposition or entanglement (as in photosynthetic

energy transfer [8]), measurement to resolve the system state necessarily collapses the superposition, destroying the very coherence that enables function.

Unlike position or momentum, time in standard quantum mechanics is a parameter rather than an observable; time-of-arrival is accessible only as a distribution, and precise timing readouts introduce back-action via non-commuting constraints. When such micro-timings are chaos-amplified, complete specification is limited in principle.

4.3 Thermodynamic Erasure and the Landauer Bound

At physiological temperature ($T \approx 310\,\mathrm{K}$), the Landauer limit for irreversible bit erasure is:

$$E_{\mathrm{Landauer}} = k_B T \ln 2 \approx 3.0 \times 10^{-21}\ \mathrm{J} \tag{3}$$

Strictly, Landauer's principle concerns the thermodynamic cost of *erasing* information, not detecting it. However, any measurement that produces a reusable, communicable result must eventually involve erasure—resetting the measurement apparatus for subsequent use. The deeper issue is *timing inaccessibility*: even if detection were thermodynamically free, specifying *when* to measure in a chaotic system requires information that cannot be obtained without perturbing the dynamics [25].

ATP hydrolysis releases approximately $5 \times 10^{-20}\,\mathrm{J}$, only 17 times the Landauer limit. Many biological signals operate near or below this fundamental limit. Sub-threshold membrane fluctuations, protein conformational vibrations, and weak molecular interactions fall in this regime, where reliable binary readout becomes physically constrained.

These three axes—dimensionality, quantum disturbance, and energetic erasure—often compound: high-dimensional biological systems operating near thermodynamic limits with quantum-like coherence represent the regime where falsifiability breaks down most completely.

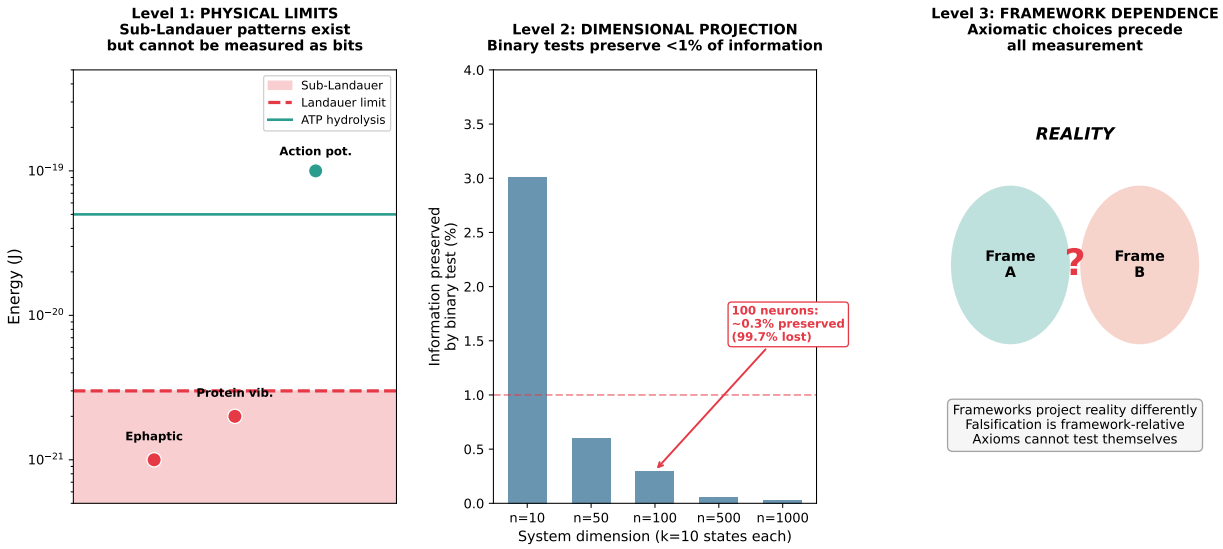

Figure 3: **Three Levels of Limitation.** Left: Physical measurement limits—many biological signals exist below the Landauer threshold for irreversible bit recording. Center: Dimensional projection loss—a binary test on a 100-neuron circuit preserves less than 1% of the information content. Right: Framework dependence—axiomatic choices about what counts as evidence precede all measurement and cannot be tested from within the framework.

5 The Sub-Landauer Domain

5.1 Definition

We define the sub-Landauer domain as the space of biological patterns whose energy content falls below the threshold for irreversible bit recording:

Definition. A biological structure $\mathcal{P}$ is *sub-Landauer* if:

1. Its energy scale $E_{\mathcal{P}} < k_B T \ln 2$
2. It exhibits temporal coherence beyond thermal relaxation
3. It causally influences observable biological functions
4. Measurement sufficient to resolve it as a bit destroys its biological role

Operationalizing $E_{\mathcal{P}}$. For patterns involving fields, correlations, or distributed codes, the "energy scale" requires operationalization. We define $E_{\mathcal{P}}$ as the *energy difference per*

effective degree of freedom per correlation time between the pattern-present and pattern-absent states. For an electric field perturbation, this is $\frac{1}{2}\epsilon E^2 \cdot V/D_{\text{eff}}$ where V is the affected volume and D_{eff} the number of coherently coupled modes. For a population correlation pattern, it is the change in free energy when the correlation is imposed versus destroyed. In each biological example below, we indicate how this quantity is estimated.

5.2 Biological Examples

Photosynthetic energy transfer. Quantum coherence in photosynthetic complexes exists at energies near 10^{-21} J—near the Landauer limit. The coherence enables near-perfect energy transfer efficiency by allowing excitons to simultaneously sample multiple pathways. Measurement to determine the specific path destroys the coherence and reduces transfer efficiency [8, 10].

Ephaptic coupling. Endogenous electric fields as weak as 1 mV/mm—well below single neuron detection thresholds—can shift spike timing by several milliseconds across neural populations [9, 11]. These fields represent information-carrying patterns that operate below the Landauer limit yet causally influence network dynamics.

Stochastic resonance. Weak periodic signals below individual neuron thresholds can entrain population activity through noise-mediated synchronization [6, 13]. The effective detection threshold drops as $E_{\text{threshold}}/\sqrt{N}$ for N coupled units, rendering sub-threshold drives decisive at the population level despite being individually unmeasurable.

5.3 Collective Computation Through Stochastic Resonance

Biological systems exploit stochastic resonance to amplify sub-Landauer signals. In neural populations, weak periodic signals below individual neuron thresholds can entrain population

activity through noise-mediated synchronization [14]. The mechanism requires:

$$E_{\text{signal}} + E_{\text{noise}} > E_{\text{threshold}} \tag{4}$$

where individually $E_{\text{signal}} < E_{\text{Landauer}}$ but collectively the signal emerges through correlation across many units.

Let $s(t)$ be a weak periodic drive with per-unit energy $E_{\text{signal}} < E_{\text{Landauer}}$ and independent noise $\eta_i(t)$ at units $i \in \{1, \ldots, N\}$. For $Y(t) = \frac{1}{N} \sum_i y_i(t)$ with y_i a thresholded response,

$$\text{SNR}(Y) \approx \frac{N \,\text{cov}(y_i, s)}{\sqrt{N \,\text{var}(y_i)}} \propto \sqrt{N} \tag{5}$$

so the effective detection threshold scales as $E_{\text{threshold}}/\sqrt{N}$. This is suprathreshold stochastic resonance [13], observed in sensory systems and neural arrays [15, 16].

The key insight is that sub-Landauer patterns are *decisive* for biological function precisely because they operate at criticality—the boundary between noise and signal.

Clarification on the "bit." The Landauer limit applies to recording a single bit irreversibly. When we say sub-Landauer signals are "unmeasurable," we mean that no *single* event carries enough energy to flip a reliable detector. But ensembles of such events can be detected: the "bit" extracted is a statistical property of the population (e.g., the mean phase), not any individual sub-threshold event. This is precisely how stochastic resonance works—the signal emerges from correlation across many units, none of which individually crosses threshold. The ensemble can be measured; the individual events constituting it cannot.

6 Analytical Bounds on Predictability

6.1 The Specification Horizon

To formalize the limits on complete system specification, consider a biological dynamical system with n coupled degrees of freedom, maximum Lyapunov exponent λ, and quantum uncertainty $\Delta x_i \geq \hbar/(2\Delta p_i)$ in each coordinate. The predictability horizon T_{pred} for deterministic specification is bounded by:

$$T_{\text{pred}} \lesssim \frac{1}{\lambda} \ln\left(\frac{L}{\Delta x}\right) \tag{6}$$

where L is the system size and Δx is the measurement precision. This is an *in-principle* bound: no improvement in measurement technology can extend specification beyond this horizon without fundamentally altering the system dynamics.

6.2 Information-Theoretic Requirement

For n effective degrees of freedom resolved to precision Δx over a domain of size L, the binary information required for full specification scales as:

$$I_{\text{required}} \sim \frac{n}{\ln 2} \ln\left(\frac{L}{\Delta x}\right) \quad \text{bits} \tag{7}$$

When I_{required} exceeds the maximum extractable information without destroying function, single-trial binary falsification becomes incoherent; only ensemble fingerprints remain accessible. This formalism shows that computational irreducibility [17] is not merely a practical limitation but follows from fundamental physical constraints.

7 Emergent Properties and Collective Phenomena

Biological systems exhibit emergent properties that exist only at the collective level. Swarming behavior in bacteria emerges from quorum sensing—a phenomenon where individual cells respond to population density through diffusible signals [18]. The swarm's properties cannot be reduced to binary statements about individual cells.

Similarly, consciousness appears to emerge from integrated information across brain regions [12]. Attempts to falsify theories of consciousness through binary tests necessarily destroy the integration that defines the phenomenon.

Evolution operates in fitness landscapes of enormous dimensionality. A single protein's fitness depends on its interactions with thousands of other molecules, environmental conditions, and evolutionary history. Wright's adaptive landscape metaphor [19], while useful, dramatically understates the true dimensionality—real fitness landscapes may have millions of dimensions.

8 Epistemological Implications

8.1 The Conjunction of Limits

The three levels of limitation—framework dependence, dimensional projection, and physical measurement bounds—interact multiplicatively. Even if measurement were perfect, dimensional projection would destroy information. Even if dimensionality were low, framework dependence would make falsification relative to unstated assumptions. Together, they circumscribe a domain where classical falsifiability becomes incoherent.

This domain is not marginal. It includes:

- Consciousness and neural integration
- Protein folding and molecular recognition

- Evolutionary dynamics on fitness landscapes
- Ecological network stability
- Developmental morphogenesis

These are not failures of current methodology awaiting future resolution. They represent fundamental limits on what binary epistemology can access.

8.2 Why Disagreement Persists

The framework-dependence of falsifiability explains why disagreement persists in biology despite good-faith empirical investigation. Researchers in different paradigms are not making claims in the same framework. Their hypotheses project differently. What counts as evidence differs. The "same" experiment can support different conclusions depending on auxiliary assumptions.

This is not irrationality. It is the geometric consequence of framework-relative inquiry. Resolution requires not more data but framework negotiation—explicit discussion of what assumptions are being made and whether they are shared.

8.3 Implications for Consciousness (Speculative)

Note: This subsection is more speculative than the preceding analysis. The arguments about measurement limits and framework dependence are established; their application to consciousness is a *hypothesis* rather than a derived conclusion. Alternative explanations for the "hard problem" exist and are not precluded by our framework.

The hard problem of consciousness may be hard precisely because consciousness emerges from high-dimensional, sub-Landauer coherence patterns. If conscious experience depends on patterns that:

1. Exist below measurement thresholds

2. Require integration across distributed neural populations

3. Are destroyed by the dimensional reduction of measurement

then consciousness is in principle inaccessible to binary falsification. The phenomenon would be real and causally efficacious yet invisible to third-person methodology.

This does not make consciousness mystical. It makes it a different kind of thing than what physics typically describes—not because it violates physical laws, but because it is constituted by dynamics that physical measurement cannot fully access.

9 Toward Multi-Scale Epistemology

9.1 Scale-Dependent Falsifiability

We propose that falsifiability in biology is scale-dependent:

> **Principle.** A biological hypothesis H about system S is falsifiable at energy scale E and framework F if:
>
> $$E > \max(E_{\text{Landauer}}, E_{\text{coherence}}(S), E_{\text{coupling}}(S))$$
>
> and H is expressible within the shared axiomatic structure of F.

This acknowledges that some biological questions admit falsification (enzyme kinetics, action potential propagation) while others do not (consciousness, ecosystem stability), and that even falsifiable hypotheses are only falsifiable relative to a shared framework.

9.2 Alternative Validation Approaches

Given these limitations, biological sciences require validation methods beyond falsification:

- **Pattern consistency**: Test whether models reproduce statistical patterns across scales

- **Predictive power**: Evaluate probabilistic predictions over ensembles
- **Mechanistic coherence**: Assess consistency with physical and chemical constraints
- **Convergent evidence**: Integrate multiple indirect lines of support
- **Framework transparency**: Explicitly state axiomatic assumptions

No single approach suffices. Biological validation requires a portfolio of complementary methods that acknowledge framework dependence and scale limitations.

Example: Ensemble-based inference in neural coding. Consider testing whether a neural population encodes a particular stimulus feature. A single-trial binary test ("did neuron i fire?") preserves almost no information about the population state. But measuring firing rates across many trials, computing cross-correlations, or extracting low-dimensional manifold structure from high-dimensional spike trains—these ensemble methods can reveal coding principles that single-trial falsification cannot access. The "hypothesis" is not "neuron i fires when stimulus X is present" but rather "the population trajectory occupies region R of state space with probability $p > p_0$ when X is present." This is falsifiable, but only statistically, and only with respect to a framework that defines the relevant state space, the appropriate dimensionality reduction, and the threshold p_0. The framework dependence is explicit, not hidden.

10 Conclusion

Karl Popper's falsifiability criterion has been invaluable for biology, helping distinguish science from pseudoscience. However, our analysis reveals three levels of limitation:

1. Physical measurement constraints create a sub-Landauer domain of causally potent but unmeasurable patterns
2. Dimensional projection destroys almost all information when high-dimensional systems are reduced to binary tests

3. Framework dependence makes all falsification relative to unstated axiomatic assumptions

The "unreasonable effectiveness of mathematics" in physics reflects selection bias: physics has focused on domains where projection loss is small and frameworks are shared. Biology is where this selection breaks down.

This is not a failure of scientific methodology but a recognition of fundamental limits on biological knowledge. The future of biological science lies not in universal falsifiability but in a scale-aware, dimension-sensitive, framework-transparent epistemology that respects the limits physics places on what can be known about living systems.

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

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and mathematics as projection. The author reviewed and edited all content and takes full responsibility for the content.

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- **v2.0** (December 2025): Expanded with framework-dependence argument, Wigner/selection-bias analysis, and mathematics-as-projection thesis. Available at: `https://coherencedynamics.com/papers/falsifiability`

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