

At What Scale Does Biology Become *Quantum*?

Introduction

The first thing to note is there is no physical scale at which quantum mechanics *becomes* applicable[1]. Because, as far as we know, quantum mechanics governs the most basic layer of the universe, it is everywhere applicable, at all scales. But we can get a sense for the length scale at which quantum effects become noticeable using Heisenberg's uncertainty relation $\Delta x \Delta p \geq \hbar/2$. This inequality sets a lower bound on how precisely any system's position (x) and momentum (p) can be known at once, meaning one cannot simultaneously know x and p with arbitrary precision[2].

Now there are at least two ways to see the HUP. The first is purely physical, as setting the length-scale of a system, and the second emphasizes its nature as an information constraint and sees it as setting the informational scale, or *information density* of the system.

This first way is expressed in quantum mechanics by saying that position x and momentum p are represented by conjugate variables (observables). Mathematically, they are algebraically related; momentum is the "infinitesimal generator" of position – we could keep applying very tiny velocity vectors to a point mass and get to any position in space. To saturate the limit (ie to reach $\Delta x \Delta p = \hbar/2$) is to reach a minimum-uncertainty configuration; we can also think about it as a maximum-information configuration because in that state, to acquire additional information about the value of x leads to increasing uncertainty about p . At this limit, the system is in a coherent state. Such a state is called coherent (or phase-coherent) because the "phase relationship" between x and p is fixed; this is another way of saying they are mutually dependent. Now, from what we said above about one being the generator of the other, it is obvious that x and p were never independent and so it is perhaps not surprising that their variances are not independent. We can say they share a common dynamical frame, or more precisely a common relative phase. So HUP is a statement about conjugate variables, and how knowing the value of one limits how much we can know about the other.

This fundamental dependency or "conjugacy" is at the root of quantum coherence. Because a quantum particle can never have both position and momentum simultaneously well-defined, its x value must be spread out, in inverse proportion to its momentum. Such coherence is what leads to phenomena without classical analogues such as tunneling and entanglement (which is just coherence maintained across separable parts of a system). Put another way, the minimum value imposed on $\Delta x \Delta p$ at saturation is what permits the wave-like superposition that underlies coherence. In effect, $\hbar$ sets the scale of coherence: when the relevant physical quantity in a system – in this case position x momentum p – is comparable to $\hbar$, full quantum behavior emerges.

Thus HUP is an inequality 1) about conjugate variables 2) the product of whose variances must be less than a certain value, and 3) this inequality is saturated at coherence. And $\hbar$ sets the scale of the system. But as we said, we can also see HUP as setting the information density of the system. We can bring these threads together in a single geometric picture. In phase-space—the abstract plane where position x and momentum p coexist—we can express HUP as saying that each physical state occupies a tiny area no smaller than $\hbar/2$. That is, one may imagine the plane as a screen tiled by pixels, with each tile having area at least $\hbar/2$. While some tiles may occupy additional area, no tile can be smaller than $\hbar/2$. When the HUP is saturated, ie when $\Delta x \Delta p = \hbar/2$ a system occupies the smallest region of phase space permitted by quantum mechanics—an area exactly equal to $\hbar/2$.

In this picture, trying to localize a single particle more precisely (ie to reduce Δx) only spreads its momentum distribution wider; the total amount of information is conserved within that single tile. Viewed this way, we can interpret HUP as a statement about the granularity of information in the universe, with saturation meaning the system occupies exactly one "quantum pixel" in phase space. We can therefore interpret the HUP as saying that no measurement or equation, can specify the location of a system in phase-space more finely than by indicating which $\hbar/2$ square it is in. In this sense, the HUP means the information density of spacetime itself is at its maximum: each pixel in phase space can be no larger than $\hbar/2$.

The point is that while HUP expresses a universal bound on how precisely certain pairs of dependent space-time variables can be specified or transmitted, an uncertainty principle is a more general notion applicable

at any scale, to any suitably defined system. And in this case the suitably defined system may be taken to be one in which we can identify a pair of mutually-dependent variables that follow an algebra analogous to x and p (ie, another “conjugate pair”).

To summarize briefly, then, we can say that the HUP at saturation is an operational criterion for coherence, where to be “coherent” means that a system is operating at the highest possible resolution, i.e. its intrinsic informational capacity. A large molecule or even a metabolic network can, in principle, maintain coherence across its parts (i.e., its degrees of freedom) if the relevant degrees of freedom (electronic states, spin states, etc.) obey quantum laws and remain phase-coherent over functionally significant times. But the underlying idea—the phase-correlation between coupled (even if not canonically conjugate) observables—can be applied more generally. We thus envisage system-specific uncertainty relations that constrain biology. That is to say, we propose that there are biological systems have emergent values of $\hbar_{\text{sys}}$, determined by each system’s physical and informational architecture. From this idea we will be able to develop a framework for saying to what extent any system, quantum or classical, is coherent.

System-Specific Uncertainty Relations and Functional Coherence

As we have said, the essence of the Heisenberg pair is that the two observables are conjugate: one defines resolution in the other. In many coupled biological process, two observables can often be identified whose fluctuations are not independent but conjugate in the information-theoretic or dynamical sense—each imposing a constraint on the precision with which the other can be known or controlled. This conjugacy is the biological analogue of position and momentum in quantum mechanics: one variable specifies the system’s instantaneous configuration, the other its rate of change or energetic responsiveness. Many physical systems have complementary quantities whose joint fluctuations are fundamentally limited.

In enzyme catalysis[3], slow protein motions—like subtle shifts in the active site—can momentarily squeeze or stretch the distances and/or potentials between atoms, modulating the barrier that a proton or electron must tunnel through.[15] This means the slow, classical motion of the enzyme continually reshapes the fast, quantum motion of the reacting particle. The protein motions must change the barrier wide/potential fast enough for tunneling to respond to the motion, but not so fast that the tunneling particle effectively experiences an averaged potential (which would eliminate the precise timing correlations that make tunneling efficient). When these two timescales line up just right, the tunneling rate can reach an optimal uncertainty-relation-saturated regime. This system does not sustain long-lived quantum coherence, but it benefits from a delicate, time-matched interplay between quantum tunneling and protein dynamics.

In light-harvesting complexes, the direction of influence between fast and slow variances is reversed. Here, rapid nuclear vibrations of pigment molecules continually shake the slower electronic energy levels that guide excitation energy transfer. These vibrations transiently bring electronic states into and out of resonance[9], making energy flow more efficient even without long-lived quantum coherence. In both cases—enzymes and light-harvesting systems—biology takes advantage of the same principle: dynamic coupling between fast and slow motions tuned near the limit set by quantum uncertainty, allowing energy and charge to move with remarkable efficiency.

We propose to generalize this insight: every biological system has its own uncertainty bound, akin to Planck’s constant, that reflects its functional constraints. That is, since any coupled dynamical system has conjugate variables whose fluctuations are statistically constrained, one can define an effective action scale—a system-specific analogue of Planck’s constant—that sets the minimum jointly measurable product of their uncertainties. Instead of calling it $\hbar$, we denote the system’s “informational Planck constant” by $\hbar_{\text{sys}}$.

Formally, one identifies two functionally conjugate observables A and B in the system (for example, the net transport through a pump and the time or energy cost). By analyzing the underlying stochastic or dynamical equations, one can derive an inequality of the form $\hbar_{\text{sys}} \geq \Delta A \Delta B$, where $\hbar_{\text{sys}}$ emerges[4] from the microscopic physics (energies, timescales, noise levels). Just as $\hbar$ sets a maximum resolution, each system’s $\hbar_{\text{sys}}$ sets its quantum-like limit.[5] If the system operates such that $\Delta A \Delta B$ comes close to $\hbar_{\text{sys}}$, it is maximizing its coherence; if it far exceeds $\hbar_{\text{sys}}$, it behaves classically in that aspect.[6]

For instance, in a light harvesting complex, A could be the speed of changing the nuclear vibrational modes

and B is the speed of changing the electronic modes. Importantly, τ_{sys} is not a new universal constant but depends on the system’s details (size, temperature, interaction strengths). In a very noisy, slowly driven system, τ_{sys} may be large, meaning the bound is weak (easy to satisfy classically). In a finely tuned molecular machine, τ_{sys} could be small, allowing close approach to the bound. When this bound is approached, the conjugate variables cease to fluctuate independently: they become phase-correlated, exhibiting coherence or within their shared informational frame.

In this framework, coherence is tied to the saturation of uncertainty bounds. Here we extend ‘coherence’ beyond its quantum-mechanical sense of wavefunction phase alignment to mean informational coherence: the mutual correlation of conjugate observables within a system’s operational bandwidth. A system is maximally coherent (in the functional sense) when it hits the uncertainty limit $\tau_F \tau_G = \tau_{\text{sys}}$. In that case, measurements of conjugate observable are phase-correlated. Thus the picture emerges: every conjugate-pair process has an inherent informational action scale τ_{sys} . We define its *functional coherence* by how tightly it operates against this scale. If $\tau_F \tau_G$ is orders of magnitude above τ_{sys} , the system behaves classically (its different parts act nearly independently). If $\tau_F \tau_G$ approaches τ_{sys} , the system is exploiting full coherence: its parts are functionally entangled and its noise-floor is quantum-limited. In this way we obtain a continuous measure of coherence rather than a binary label. To be clear, we can identify the Classical regime, $\tau_A \tau_B \gg \tau_{\text{sys}}$ where measurement outcomes are statistically separable: the slow observable samples ensemble properties of the fast dynamics. Beyond then as $\tau_A \tau_B \rightarrow \tau_{\text{sys}}$ phase correlations, making the variables inseparable within the system’s measurement framework. That is, the observables lose operational independence due to the saturated uncertainty relation. Measurements become jointly determined: outcomes of the fast process cannot be described independently of the slow detector’s resolution window.

So in this setup quantum-like behavior emerges as a “phase-transition” from a regime of unsaturated information capacity to a maximum information density one. This conjugate relation makes coherence a measurable continuum rather than a categorical label. The system’s proximity to its uncertainty bound defines a coherence index, $Q = \tau_{\text{sys}}/(\tau_A \tau_B)$, $0 < Q \leq 1$. When $Q \ll 1$, the conjugate observables fluctuate independently, and the system behaves classically: nuclear motion, conformational shifts, or energy transfer events are statistically separable [10,11]. As $Q \rightarrow 1$, the uncertainty product saturates its lower limit, and the observables become informationally inseparable—phase-correlated within a shared dynamical constraint. In the light-harvesting complex, this occurs when vibrational modulation and resonance energy transfer operate within a matched temporal-energetic bandwidth, producing measurable coherence without requiring long-lived superpositions.

Example: the ABC Transporter

Let us illustrate these ideas with a concrete example: the ATP-binding cassette (ABC) transporter. ABC transporters are proteins found embedded in cell membranes, in all kingdoms of life. They responsible for importing nutrients or exporting toxins. Structurally, each ABC transporter consists of two ATP-binding domains that power conformational changes and two transmembrane domains that form the channel through which the substrate moves.[7] In this case, the relatively fast ATP binding and hydrolysis drive the slow transition between inward- and outward-facing states, coupling ATP hydrolysis to mechanical motion across the membrane. The ABC transporter exemplifies how a system-specific uncertainty relation generates a quantifiable continuum of “coherence.”

Let $\tau_{E_{\text{conf}}}$ be the energy-level difference between conformations and $\tau_{t_{\text{conf}}}$ the “timing jitter” of the conformational transition. The transporter’s intrinsic uncertainty relation is $\tau_{E_{\text{conf}}} \tau_{t_{\text{conf}}} \geq \tau_{\text{ABC}}$ where τ_{ABC} is the system-specific action scale, a biological parameter determined by the system’s conformational energy landscape and kinetic rates. When $\tau_{E_{\text{conf}}} \tau_{t_{\text{conf}}} \gg \tau_{\text{ABC}}$, conformations remain energetically and temporally distinct and the dynamics are well described by separable stochastic steps. As the product approaches the bound, $\tau_{E_{\text{conf}}} \tau_{t_{\text{conf}}} \rightarrow \tau_{\text{ABC}}$, the system reaches its informational resolution limit: “state” labels lose operational meaning, ATP hydrolysis and conformational motion become phase-correlated, and we enter the coherent regime.[8] We quantify proximity to this regime by $Q = \tau_{\text{ABC}}/(\tau_{E_{\text{conf}}} \tau_{t_{\text{conf}}})$, with $0 < Q \leq 1$. with $Q \ll 1$ indicating classical separability and $Q \rightarrow 1$ indicating saturation and functional coherence. Thus, Q defines an empirical continuum of coherence derived from the system’s intrinsic uncertainty structure.

By way of illustration, we note that τ_{ABC} is fixed by the transporter’s architecture while the product $E_{conf} \tau_{conf}$ is experimentally tunable. For example, we could change the concentration of ATP available for hydrolysis (reducing τ_{conf} by reducing “timing jitter” associated with hydrolysis) or use mutated/chemically modified transmembrane domains to reshape energy barriers in order to affect E_{conf} . Thus an example like the ABC transporter is an example of natural selection exploiting the coarse-grained dynamical coupling to enact to approach a functionally coherent regime.

Coherence is Informational, Not Physical

To speak of biological coherence, then, is to ask: *How closely do a system’s fast and slow variables approach joint saturation?*[12] And: *How tightly do energy input and function output co-vary?* In this framing, coherence is a measure of how much of the system is using its internal bandwidth, and how much is lost to noise. A system is “more coherent” to the extent that its relevant variables are co-defined—that their variances are shared rather than independent—so that the product $\tau_A \tau_B$ approaches the system’s own τ_{sys} .

This perspective has several implications. Biologists and biophysicists can now ask: *What are the relevant conjugate pairs (A, B) for a given system?*, *What is its effective action scale τ_{sys}^* and *How closely do experimentally observed variances get to that limit?*

This reframing also offers a perspective into why many claims of long-lived coherence collapse while transient near-bound corridors keep appearing: coherence is a scarce, managed resource, generated locally, spent quickly, and renewed by actively driven cycles.

As far as quantum goes, size hardly matters. What matters clearly not the physical dimension but the ratio of fluctuations to the system’s h_{eff} . Practically, this means that the same system can present different “quantum faces” at different levels of description, that is, the same Q-value for coupled processes. Large complexes can host local pockets of high-Q dynamics—subcircuits whose coupling and shielding enable near-saturation—nested inside a low-Q background that remains effectively classical. To return to the evergreen light-harvesting complexes, one might imagine that at the molecular level, coherence arises from the uncertainty relations between electronic energy and vibrational phase; but at the functional level, it might arise from tuning relations between vibrational energy modulation and resonance energy transfer timing.

Finally, the informational view clarifies what it would mean to engineer coherence in living or synthetic systems. It does not chase fragile superpositions in a warm bath; it means to engineer constraints and coupling so that the relevant observables approach joint saturation during the time window that matters for function. The target is not indefinite coherence but enough coherence—high Q over the operational bandwidth—so that energy, structure, and time act as a single, tightly correlated unit of work.

Conclusion

So by now the answer to our question is clear. We started by observing that there was *no* physical scale at which the universe “becomes” quantum - it is quantum at every scale, though perhaps not noticeably so. So too there is no physical scale at which a biological system can be said be quantum - but viewing “quantum” through an information-first lens, which is to say coherence-first lens, biology can be quantum at any scale. That is to say, every biological system has a built-in scale - a firm Planck-like constant τ_{sys} - that depends on its (physical and informational) architecture and governs its coherence. By examining uncertainty relations for that system, we define coherence as a continuous property: how tightly a biological machine approaches its intrinsic uncertainty saturation bound.

We saw that any two complementary (conjugate) aspects of function in a complex system will obey an uncertainty relation type trade-off as emphasized in recent reviews of quantum biology [13], with a characteristic constant governing their minimum resolvability in phase-space. In practice, thermodynamic and kinetic constraints already impose such bounds on biochemical processes. Functional coherence then arises when parts of the system interlock to saturate that limit.

We saw that the degree of coherence can be measured by the proximity of a system’s fluctuations to its intrinsic bound, as quantified by the dimensionless index $Q = \tau_{sys}/(\tau_A \tau_B)$. Most real biological machines

likely lie somewhere in between. Similarly, the ABC transporter system could be described as “partially quantum”. At room temperature it likely has $Q < 1$, meaning some decoherence and noise. But by changing conditions (lower temperature, stronger coupling, engineering the landscape), one could raise Q toward 1. We also emphasize that $Q = \frac{\sigma_{\text{sys}}}{\sigma_{\text{F}} \sigma_{\text{G}}}$ a quantifiable ratio, measurable in principle by tracking variances and covariances of the chosen observables.

Looking forward, this approach offers practical payoffs. The framework offers insights into a question that has haunted biophysics since its earliest days: Do living machines exploit *truly* quantum coherence or entanglement, or are they reducible to statistics of classical states? It suggests experiments in which we use existing tools to infer Q for different biological processes. A Q near 1 would indicate a strongly coherent regime, warranting a full quantum description (Hilbert spaces and entangled states). A low Q means a classical rate equation suffices.

This of course also opens the door for us to talk about resilience and other characteristics that covary with coherence. In larger terms, many biological “small” systems (enzyme complexes, protein assemblies, cellular circuits) can be analyzed similarly. They may fall anywhere on the spectrum from fully classical to highly quantum. On the engineering side, in bioengineering and quantum technology, the continuum view opens new strategies.

On the engineering side, we can think about adjusting kinetic parameters or structure to raise Q in the design of synthetic biomolecules or nanomachines. Engineers need not aim for unreachable $Q=1$ in large systems; even modest Q can significantly boost function. Beyond this, one can imagine artificial transporters or metabolic pathways that are optimized to approach their uncertainty bound, achieving very high efficiency or sensitivity.[14]