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A quantitative bound on motional narrowing in the radical-pair nuclear register: the neural band requires $S^2 \lesssim 0.07$

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Motional narrowing has been proposed as the mechanism that lets a biological radical pair hold usable memory on the 10 ms timescale of neural computation. We test that proposal against the feasibility predicate of the underlying reservoir theory, in which the useful horizon is $\max_T [\text{MC}(q(T)) - C_0] \cdot T$ with $q(T) = 1 - e^{-T/T_{1n}}$. Our implementation reproduces that theory's published feasibility numbers to better than 0.5 %. Under the predicate the proposal fails at the order parameters available to this system: a proton register on the cryptochrome flavin–tryptophan pair reaches a ceiling of 3.99 ms, and internal motional narrowing reaches the band only below $S^2 \simeq 0.07$, that is, only if the internal motion leaves less than 7 % of the second-rank dipolar order intact. Flavin 8 α -methyl rotation, the specific candidate proposed to supply it, has $S^2 = 0.25$ and gives 7.12 ms, outside the band across the hydration and bath-density uncertainty (4.31 ms to 9.49 ms). One route crosses by a wide margin, and it is isotopic rather than dynamic: substituting the register nucleus rescales the like-spin intramolecular rate as γ^4 and the unlike-spin bath rate as γ^2 , with an additional heteronuclear factor 2/3, raising T_{1n} to 28.4 ms for ^{31}P and 91.2 ms for ^{13}C . Neither nucleus is physiological. We also withdraw the long-lived-singlet route, which protects an observable orthogonal to the one carrying the memory, and we state the in-vitro measurement that would falsify our conclusion.

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I. THE CLAIM AND THE CRITERION

The hypothesis under test is that a radical-pair register in a brain enzyme^{1,2}, screened for radical-pair competence in Ref.³, can carry information across the 10 ms window over which a neuron integrates, in the spirit of Fisher’s proposal that nuclear spins could serve as processing degrees of freedom in the brain⁴. Tegmark’s estimate that decoherence in warm, wet neural tissue runs at 10^{-13} s to 10^{-20} s, against dynamical timescales of 10^{-3} s to 10^{-1} s, rules out electronic and microtubule degrees of freedom⁵; it does not treat nuclear spins, and the nuclear register is precisely the escape route Fisher proposed⁴. The present paper asks whether that escape route delivers on the neural timescale. Related work has examined how fragile a quantum neural memory is to the onset of criticality⁶. The register is nuclear, not electronic: the electron pair recombines on the microsecond scale^{1,7}, whereas the proton that the hyperfine coupling writes into relaxes on T_{1n} . At the geomagnetic field the system sits deep in the extreme-narrowing regime ($\omega\tau_c \approx 2 \times 10^{-4}$), where $1/T_{1n} \propto \tau_c$ and $T_{1n} = T_{2n}$ exactly^{8,9}. Motional narrowing — shortening τ_c — therefore lengthens the register lifetime, and the question is whether it can lengthen it enough.

Enough must be defined by the reservoir, not by the lifetime. A register that survives longer is only useful if the reservoir can still read excess memory out of it. Memory capacity and its information-processing generalisation are the standard figures of merit here^{10,11}, and the reservoir is the spin-ensemble construction of Fujii and Nakajima¹². The underlying theory¹³ sets the useful horizon as

$$\text{ceiling} = \max_T [\text{MC}(q(T)) - C_0] \cdot T, \quad q(T) = 1 - e^{-T/T_{1n}}, \quad (1)$$

subject to the constraint that the retained memory $\text{MC} - C_0$ exceed 0.5, with $C_0 = 1.0028$ the memoryless floor. Equation (1) is not equivalent to multiplying T_{1n} by the zero-reuse memory excess. That excess, $\text{MC} - C_0 = 1.863$, is measured at $q \approx 0$; at the natural turnover $T = T_{1n}$ the reuse fraction is $q = 0.632$ and the correct value is 1.115. The two errors partially cancel because the optimum of Eq. (1) sits past T_{1n} , and the net effective multiplier is 2.51, not 1.88. Every number below uses Eq. (1).

Our implementation is pinned by an acceptance test against the three feasibility numbers the underlying theory publishes: it returns $T_{1n} = 2.449$ ms (published 2.44 ms), a ceiling of 6.145 ms (published 6.15 ms), and correlation-time boundaries of 9.34 ns and 6.06 ns

(published 9.37 ns and 6.08 ns). The agreement is better than 0.5% throughout, so the disagreements reported below are not implementation artefacts.

II. NARROWING BY INTERNAL MOTION DOES NOT REACH THE BAND

Shortening the effective correlation time of a dipolar vector by internal motion is not the same as shortening the correlation time of the whole molecule. The model-free formalism^{14,15} separates them: an internal motion of amplitude S^2 and correlation time τ_{int} leaves a residual S^2 of the interaction modulated at the overall tumbling time τ_m , which we take as 15.2 ns from Ref.¹³; tumbling times of this kind are determined from ^{15}N relaxation in the standard way¹⁶, and only the remaining $1 - S^2$ is narrowed. Substituting a short τ_c directly into the dipolar rate is the $S^2 = 0$ limit, i.e. the assumption that the internuclear vector is completely orientationally averaged. It is not the methyl-rotation or librational physics it has been taken to represent, for which S^2 lies between 0.25 and 0.9.

Table I scans the order parameter at fixed τ_m . The bath vector is not narrowed, because the external protons move with the molecule¹⁷.

TABLE I. Ceiling from Eq. (1) as a function of the intramolecular order parameter, at fixed overall tumbling $\tau_m = 15.2$ ns. The band is 10 ms.

S^2	τ_{int} [ns]	$T_{1\rho}$ [ms]	ceiling [ms]	band
0.90	0.05	1.698	4.26	out
0.70	0.05	1.971	4.94	out
0.50	0.05	2.347	5.89	out
0.50	1.00	2.279	5.72	out
0.25	0.05	3.084	7.74	out
0.25	1.00	2.912	7.31	out
0.00	0.05	4.494	11.28	in
0.00	1.00	4.032	10.12	in

Bisecting on S^2 at fixed τ_m places the band threshold at $S^2 = 0.072$ for $\tau_{\text{int}} = 10$ ps, 0.070 at 50 ps, and 0.0075 at 1 ns: the slower the internal motion, the more nearly complete the averaging must be. The concrete candidate named in Ref.¹⁸ — rotation of the flavin

8 α -methyl, for which the underlying theory’s own geometry gives $S^2 = 0.25$, $\tau_{\text{int}} = 10$ ps and an external order parameter of 0.70 — yields $T_{1n} = 2.836$ ms and a ceiling of 7.12 ms. It does not reach the band, and it is a factor of 3.5 in S^2 away from doing so. The value $S^2 = 0.25$ is not fitted: for fast three-fold rotation the intra-methyl proton–proton vector lies perpendicular to the rotation axis, so $S^2 = P_2(\cos 90^\circ)^2 = 1/4^{14}$. It is worth stating how narrow the margin is. The C–H vector of the same methyl has $S^2 = P_2(\cos 109.47^\circ)^2 = 1/9$, and a register on *that* vector would give a ceiling of 10.32 ms — marginally inside the band. The conclusion of this section therefore depends on the register being the proton–proton pair rather than a carbon–proton pair, and a reader who disputes that assignment should read our result as a boundary case rather than an exclusion. We are aware of no internal motion in a folded protein that leaves a residual order parameter $S^2 < 0.07$; the range reported for methyl rotation and side-chain libration is 0.25 to 0.9^{15,19}.

One case does cross, and it is worth stating because it is the strongest surviving form of the original idea. If the intramolecular vector is treated as fully averaged while the external bath is left at τ_m — the bath-limited limit — then $T_{1n} = 4.52$ ms and the ceiling is 11.34 ms, inside the band, with the optimum at a turnover of 12.7 ms. Using the fixed coefficient 1.88 this same case returns 8.50 ms and would be reported as excluded. The conclusion is sensitive to the criterion, which is why we pinned the criterion first.

III. EVERY PREVIOUSLY PROPOSED METHOD, RE-TESTED

Table II re-evaluates the coherence-extension and error-correction methods proposed in Ref.¹⁸ against Eq. (1). Each is expressed as a multiplier on the two relaxation channels of the baseline proton register, whose rate budget is 65 % intramolecular and 35 % bath.

The bulk-narrowing row is listed for completeness and is not a biological proposal: reducing the whole-molecule tumbling time of a hydrated protein to 3 ns means changing the protein or the solvent, not exploiting a motion the protein already has. The biologically available version of that row is the internal-motion scan of Table I, which fails.

Isotopic substitution is the only lever with real margin. The like-spin intramolecular rate scales as γ^4 and the unlike-spin bath rate as γ^2 ; because register and bath then differ, the bath term additionally carries the extreme-narrowing heteronuclear factor 2/3 (unlike spins contribute $2b^2\tau_c$ where like spins contribute $3b^2\tau_c$)⁹. Omitting that factor understates T_{1n}

TABLE II. Coherence-extension methods under the feasibility predicate, Eq. (1). Band 10 ms.

method	T_{1n} [ms]	ceiling [ms]	$\times$ baseline	band
baseline (^1H , $\tau_c = 15.2$ ns)	1.589	3.99	1.0	out
bulk narrowing, $\tau_c \rightarrow 3.0$ ns	8.049	20.19	5.1	in
perdeuterated bath	2.428	6.09	1.5	out
^{31}P register	28.402	71.26	17.9	in
^{13}C register	91.234	228.91	57.4	in
^{31}P + deuterated bath	86.403	216.79	54.4	in
^{13}C + deuterated bath	539.511	1353.69	339.6	in

by 34 % to 43 %: with the factor included the values are 28.4 ms for ^{31}P and 91.2 ms for ^{13}C , against 21.1 ms and 64.0 ms without it. Both nuclei are spin-1/2 and can hold a register, unlike the quadrupolar flavin ^{14}N , whose relaxation is dominated by the quadrupolar channel and which acts as a sink rather than a store²⁰. Selective ^{13}C labelling of flavocoenzyme radicals is established²¹, so the ^{13}C row is an experiment that could be attempted. Neither is physiological; both are in-vitro tests of the criterion, and the smaller γ also weakens the hyperfine write that loads the register in the first place. The deuterated rows are lower bounds on the rate, hence optimistic: with both modelled channels suppressed, residual mechanisms (chemical-shift anisotropy, spin-rotation, residual couplings) are outside this model and will dominate.

Long-lived singlet order does not apply

Nuclear singlet order — a decoherence-free subspace²² on the geminal CH_2 pair^{23,24} — has been proposed in Ref.¹⁸ as a route to the band. It does not apply. Singlet order protects $\langle \mathbf{I}_1 \cdot \mathbf{I}_2 \rangle$, which is orthogonal to the $\langle I_z \rangle$ population that the hyperfine interaction writes and that the reservoir reads. Protecting it does not extend the lifetime of the stored variable; it extends the lifetime of a different one. The empirical position is also against it. Korenchan *et al.* measure ^{31}P singlet order relaxing *faster* than T_1 in a system with switchable magnetic inequivalence²⁵, the same group has since examined pyrophosphate singlet order as a direct test of the quantum-cognition proposal²⁶. On the theoretical side, Player and Hore derive an upper bound of 37 min on Posner-molecule entanglement under idealized physiological

conditions and argue that the true relaxation is much faster²⁷; that bound does not by itself exclude a 10 ms register, but it removes the hours-long lifetimes the proposal originally assumed. The assumption that singlet order is generically longer-lived therefore does not hold in the relevant regime, although the conditions under which it can be engineered remain an active question²⁸. We do not list it in Table II.

Methods that remain null

Each of the following fails for a quantitative reason. *Dynamical decoupling as a pulse train*²⁹ would need a refocusing rate of 66 MHz against a nuclear Larmor frequency of 2.13 kHz — short by 3×10^4 — and no biological process supplies it; note that DD as *internal molecular motion* is exactly the mechanism tested in Table I, so the “dynamical decoupling” claim splits into a null engineering version and a biological version that we have now shown also fails. *Zeno stabilisation*³⁰ fails on the same rate requirement. *Gauging* projects onto S_z , but the register is already S_z -diagonal, so the projection commutes with the stored data and changes nothing. *Approximate error correction of the Bény–Oreshkov type*³¹ needs energy-conserving unitaries at the nuclear Zeeman scale, 8.8×10^{-12} eV against $k_B T = 26.7$ meV, thermally swamped by 3×10^{-10} . *Petz recovery*^{32–34} requires process tomography of the biological channel and *DEJMPS*³⁵ requires coherent gates between molecules; neither is available in vivo. *Zero-noise extrapolation*^{36,37} is not a lifetime extension at all — but it is the right experimental protocol here, and we use it below. *Population-based QEC and concatenation* across the $\sim 10^4$ enzyme copies cannot correct a decay that is uniform across copies, so the memory capacity is unchanged; ensemble averaging extends the *detectable* window through $\sqrt{N}$ signal-to-noise, which is readout reach and not register memory.

IV. UNCERTAINTY

The two inputs that move the conclusion are the external-proton sum Σ_{ext} , which sets the bath channel, and the hydration state, which sets τ_m . These enter differently. The correlation-time boundary — the τ_c at which the ceiling reaches 10 ms — is a function of Σ_{ext} alone, since τ_m is the variable being solved for; over $\Sigma_{\text{ext}} \in [0.016, 0.030]$ it ranges over 4.78 ns to 6.19 ns, and a point estimate in this range should not be quoted without the band.

Hydration instead moves the ceiling of a given candidate. Evaluating the flavin-methyl candidate at the four corners of $\Sigma_{\text{ext}} \in [0.016, 0.030]$ and $\tau_m \in [11.7 \text{ ns}, 18.8 \text{ ns}]$ gives ceilings of 4.31 ms to 9.49 ms. All four are outside the band, so the conclusion of Sec. 2 is not an artefact of the central parameter choice.

V. WHAT WOULD FALSIFY THIS

The prediction is specific and measurable in vitro. Prepare the radical pair in a solvent series that varies viscosity, so that τ_m varies over roughly 5 ns to 20 ns, and measure the nuclear T_{1n} of the register proton by field-cycling relaxometry³⁸ at geomagnetic field. Extreme-narrowing scaling predicts $1/T_{1n} \propto \tau_m$ with the intramolecular and bath contributions in a 65 : 35 ratio, and the ceiling then follows from Eq. (1). If a native, non-isotopically-substituted register is found with a ceiling at or beyond 10 ms at physiological τ_m , the conclusion here is wrong. If the observed T_{1n} instead tracks Table I, the 10 ms claim for a native protein register should be abandoned, and the surviving experimental programme is the isotopic one: a ^{13}C - or ^{31}P -substituted register, where the predicted ceilings of 229 ms and 71 ms are far enough above the band to be unambiguous.

VI. CONCLUSION

Motional narrowing does lengthen the lifetime of a nuclear register in a biological radical pair, but under the feasibility predicate of the underlying reservoir theory it does not lengthen it enough. The requirement is an intramolecular order parameter $S^2 \lesssim 0.07$, against $S^2 = 0.25$ for the flavin 8 α -methyl rotation that has been proposed to supply it, and the resulting ceiling of 7.12 ms stays below the 10 ms band at every corner of the hydration and bath-density uncertainty. The margin is narrow enough to matter: a register on the methyl C–H vector rather than the proton–proton pair would sit marginally inside the band, so the result is best read as a sharp quantitative boundary rather than a categorical exclusion. The only lever with real margin is isotopic substitution, which is not physiological but is testable in vitro. We have also withdrawn the long-lived-singlet route, which protects an observable orthogonal to the one carrying the memory. The decisive measurement is a viscosity series with field-cycling relaxometry at geomagnetic field.

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AUTHOR DECLARATIONS

Conflict of Interest

The authors have no conflicts to disclose.

Author Contributions

Hikaru Wakaura: Conceptualization (lead); Formal analysis (lead); Methodology (lead); Software (lead); Validation (lead); Writing – original draft (lead); Writing – review & editing (lead). **Taiki Tanimae:** Supervision (lead).

DATA AVAILABILITY

The data that support the findings of this study are openly available in the `qbrain3layer` repository. Every number reported here is produced by `mn_v3_corrected.py` and written to `results/mn_v3_corrected.json`. The script carries an acceptance test that asserts agreement with each of the four published feasibility numbers of the underlying theory to within 0.5% and fails if the implementation drifts beyond that.

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