Supplementary Information

Coupling-scale invariance and mode-selective critical slowing in reduced Wong–Wang networks

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Purpose and reproducibility status

This Supplementary Information (SI) provides the algebra omitted from the main text, including the extension from a reciprocal pair to connected symmetric regular networks, the numerical quality-control rules, and a complete deterministic and stochastic reproduction algorithm. The corresponding Python implementation is available at `https://github.com/thenewcomershk-lab/wong-wang-coupling` and archived at `https://doi.org/10.5281/zenodo.23495771`. No external empirical dataset is required. The literature is used only to source the reduced Wong-Wang form and its conventional parameterization (Wong and Wang, 2006; Deco et al., 2013; Castro et al., 2020). The numerical results are synthetic consequences of the stated equations and are therefore reproducible with the archived code.

The SI deliberately avoids claims of biological validation. The two-node reciprocal edge is normalized to one; it is not an anatomical tract weight. Likewise, the small-noise amplitude is selected to test the local linear theory and is not inferred from neural recordings. This distinction is important because large-scale implementations of the same model family use a structural connectivity matrix, a global gain and, in some applications, empirical fMRI or diffusion-MRI data (Deco et al., 2013; Castro et al., 2020). None of those datasets is needed for the theorem-level statements in the present manuscript.

1 Derivations and numerical identities

The deterministic drift is

$$F_1 = -\frac{S_1}{\tau_s} + (1 - S_1)\gamma H(J_N(wS_1 + GcS_2) + I_0)\,, \tag{1}$$

$$F_2 = -\frac{S_2}{\tau_s} + (1 - S_2)\gamma H(J_N(wS_2 + GcS_1) + I_0)\,, \tag{2}$$

with

$$H(x) = \frac{ax - b}{1 - e^{-d(ax-b)}}. \tag{3}$$

Let $z = ax - b$. Direct differentiation gives

$$H'(x) = a\,\frac{1 - e^{-dz} - dz\,e^{-dz}}{(1 - e^{-dz})^2}. \tag{4}$$

At $z = 0$, the apparent singularity is removable. The series

$$H(x) = \frac{1}{d} + \frac{z}{2} + \frac{dz^2}{12} - \frac{d^3z^4}{720} + \mathcal{O}(z^6) \tag{5}$$

shows that $H(b/a) = 1/d$ and $H'(b/a) = a/2$. The implementation below evaluates $1 - e^{-dz}$ with `expm1`; this matters because the fold solver can otherwise lose several digits when dz is small.

S1. Invariance and Jacobian diagonalization

Exchange symmetry implies $F_1(S_1, S_2) = F_2(S_2, S_1)$. Hence if $S_1(0) = S_2(0)$ in the deterministic system, the equality is preserved and the diagonal is invariant. At $S_1 = S_2 = S$, define

$$x = J_N(w + cG)S + I_0. \tag{6}$$

The Jacobian entries are

$$A = \frac{\partial F_1}{\partial S_1} = -\tau_s^{-1} - \gamma H(x) + (1 - S)\gamma H'(x) J_N w, \tag{7}$$

$$B = \frac{\partial F_1}{\partial S_2} = (1 - S)\gamma H'(x) J_N G c. \tag{8}$$

Therefore

$$J = \begin{pmatrix} A & B \\ B & A \end{pmatrix}, \qquad \lambda_+ = A + B, \qquad \lambda_- = A - B. \tag{9}$$

The normalized eigenvectors are $v_+ = (1, 1)^\top/\sqrt{2}$ and $v_- = (1, -1)^\top/\sqrt{2}$. The scalar derivative of the symmetric reduction equals λ_+ exactly. Since $B > 0$ for positive coupling, $\lambda_- < \lambda_+$ throughout the interior domain. This proves not only that the antisymmetric mode is stable at the fold but also that every stable symmetric equilibrium is stable to both linear modes.

S2. Fold normal form and prefactor

Let (S_c, G_c) be the upper fold. Set $s = S - S_c$ and $\mu = G_c - G$. Because $F = F_S = 0$ at the fold,

$$F(S, G) = -F_G\mu + \frac{1}{2}F_{SS}s^2 - F_{SG}s\mu + \frac{1}{6}F_{SSS}s^3 + \mathcal{O}(\mu^2 + |s|^4). \tag{10}$$

Balancing the first two terms yields $s = \mathcal{O}(\mu^{1/2})$ and

$$s_\pm = \pm\sqrt{\frac{2F_G}{F_{SS}}}\,\mu^{1/2} + \mathcal{O}(\mu). \tag{11}$$

For the upper fold $F_G, F_{SS} > 0$; the stable low branch uses $s_- < 0$. Differentiating the expansion with respect to S gives

$$\lambda_+ = F_S = F_{SS}s + \mathcal{O}(\mu) = -\sqrt{2F_G F_{SS}}\,\mu^{1/2} + \mathcal{O}(\mu). \tag{12}$$

Thus

$$\tau_{\mathrm{rec}} = \frac{1}{-\lambda_+} = \frac{1}{\sqrt{2F_G F_{SS}}}\,\mu^{-1/2} + \mathcal{O}(1). \tag{13}$$

For the declared parameterization, numerical differentiation at the upper fold gives

$$G_c = 0.8976692317486710, \tag{14}$$

$$S_c = 0.0801818817764104, \tag{15}$$

$$F_G = 0.4849137503404322, \tag{16}$$

$$F_{SS} = 105.0656724288501209, \tag{17}$$

$$K = (2F_G F_{SS})^{-1/2} = 0.0990654759377906 \text{ s}. \tag{18}$$

These values are printed by the code rather than copied into the computation.

S3. Linear stochastic covariance

Let $\delta S = (\delta S_1, \delta S_2)^\top$ be a perturbation about a stable symmetric equilibrium. To first order,

$$d\delta S = J\delta S\, dt + \sigma\, dW, \quad \mathbb{E}[dW\, dW^\top] = I\, dt. \tag{19}$$

The orthogonal matrix

$$Q = \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \tag{20}$$

diagonalizes J. Because Q is orthogonal, QdW is again a vector of independent standard Wiener increments. Therefore the two modal coordinates are independent Ornstein–Uhlenbeck processes. Their stationary covariance eigenvalues are

$$V_+ = \frac{\sigma^2}{-2\lambda_+}, \qquad V_- = \frac{\sigma^2}{-2\lambda_-}. \tag{21}$$

Transforming back gives

$$\mathrm{Var}(S_1) = \mathrm{Var}(S_2) = \frac{V_+ + V_-}{2}, \qquad \mathrm{Cov}(S_1, S_2) = \frac{V_+ - V_-}{2}, \tag{22}$$

and hence

$$\mathrm{Corr}(S_1, S_2) = \frac{V_+ - V_-}{V_+ + V_-}. \tag{23}$$

As the upper fold is approached from the stable side, $V_+ \to \infty$ in the linear approximation while V_- remains finite. Thus the correlation tends to one. This is a local critical-mode prediction, not a statement that the nonlinear bounded process has infinite variance.

S4. Exact connectivity-scale/global-gain invariance

For the N-node input

$$x_i = J_N \left(wS_i + G \sum_j C_{ij} S_j \right) + I_0, \tag{24}$$

let $\widetilde{C} = \alpha C$ and $\widetilde{G} = G/\alpha$ for any $\alpha > 0$. Then

$$\widetilde{G} \sum_j \widetilde{C}_{ij} S_j = \frac{G}{\alpha} \sum_j \alpha C_{ij} S_j = G \sum_j C_{ij} S_j. \tag{25}$$

Thus the full deterministic vector field is exactly invariant for every state, not merely on the synchronized branch. If the same additive-noise law is retained, the stochastic differential equation is also identical. This gives a structural non-identifiability: the equations determine GC, but not the overall scale of C and G separately.

For the two-node reciprocal edge, $C_{12} = C_{21} = c$, this reduces to the symmetric combination $w + cG$ and the fold gains obey $G_c(c) = G_c(1)/c$. The accompanying code includes a consistency check of the paired rescaling $C \mapsto \alpha C$, $G \mapsto G/\alpha$ for $\alpha \in \{0.5, 1, 2\}$.

S5. Symmetric regular networks and the graph spectrum

Let C be real, symmetric, nonnegative, connected and regular with zero diagonal and row sum r, so $C\mathbf{1} = r\mathbf{1}$. If all node states are equal to S, then

$$\dot{S} = -\frac{S}{\tau_s} + (1-S)\gamma H(J_N(w+Gr)S + I_0)\,. \tag{26}$$

Therefore the synchronized branch depends on the network only through rG.

At a synchronized equilibrium, define

$$a_0 = -\tau_s^{-1} - \gamma H(x) + (1-S)\gamma H'(x) J_N w, \tag{27}$$

$$\beta = (1-S)\gamma H'(x) J_N G. \tag{28}$$

The full Jacobian is

$$J^{\mathrm{lin}} = a_0 I + \beta C. \tag{29}$$

If ν_k is an eigenvalue of C, the corresponding neural eigenvalue is

$$\lambda_k = a_0 + \beta\nu_k. \tag{30}$$

For a connected regular graph, Perron–Frobenius theory gives the simple leading eigenvalue $\nu_1 = r$ with eigenvector $\mathbf{1}$. At a synchronized fold, $\lambda_1 = 0$, hence $a_0 = -\beta r$ and

$$\lambda_k = \beta(\nu_k - r) < 0, \qquad k \geq 2. \tag{31}$$

The slowest transverse eigenvalue is therefore

$$\lambda_{\mathrm{tr}} = -\beta_c\delta, \qquad \delta = r - \nu_2. \tag{32}$$

For fixed graph size this is strictly negative, so the synchronized Perron mode is the unique critical mode. Nevertheless, a family of graphs can have $\delta \to 0$, producing long stable transverse timescales.

With isotropic additive noise, the orthogonal eigenbasis of C also diagonalizes the linearized stochastic system:

$$du_k = \lambda_k u_k\,dt + \sigma\,dB_k, \qquad \mathrm{Var}(u_k) = \frac{\sigma^2}{-2\lambda_k}. \tag{33}$$

For a fixed connected regular graph approaching the fold, the covariance becomes dominated by the Perron mode. For regular graphs the Perron vector is uniform, so all pairwise local correlations approach one in the local OU approximation.

Two normalized graph families give useful exact benchmarks. For the complete graph $K_N/(N-1)$, the spectrum is 1 and $-1/(N-1)$ with multiplicity $N-1$, so

$$\delta_{K_N} = \frac{N}{N-1}. \tag{34}$$

For the cycle $C_N/2$,

$$\nu_k = \cos\left(\frac{2\pi k}{N}\right), \qquad \delta_{C_N} = 1 - \cos\left(\frac{2\pi}{N}\right) \sim \frac{2\pi^2}{N^2}. \tag{35}$$

At the reported upper fold, $\beta_c = 5.4288094032\ \mathrm{s}^{-1}$, so the slowest transverse recovery time of normalized cycles grows asymptotically as

$$\tau_{\mathrm{tr}} \sim \frac{N^2}{2\pi^2\beta_c}. \tag{36}$$

This synthetic calculation requires no anatomical or physiological dataset; it isolates the role of graph spectrum while holding the synchronized fold fixed.

2 Reproducibility algorithms

Algorithm S1: deterministic fold and branch computation.

1. Fix the literature-derived transfer and kinetic parameters and the declared edge normalization $c = 1$.
2. Evaluate H and H' with numerically stable formulas, including the removable singularity at $ax = b$.
3. Solve the two equations $F(S, G) = 0$ and $F_S(S, G) = 0$ from multiple initial guesses; retain roots in $0 < S < 1$ and $G > 0$ whose residual norm is below 10^{-10}.
4. Sort the two unique roots by G and evaluate λ_-, F_G, F_{SS} and the critical-slowing prefactor.
5. For a branch plot, scan G on a grid, bracket all zeros of $F(\cdot, G)$ in $S \in (0, 1)$, and classify each root by the sign of $\lambda_+ = F_S$.

Algorithm S2: stochastic verification.

1. At each selected subcritical G, initialize all realizations at the deterministic low stable equilibrium.
2. Integrate the two-dimensional SDE by Euler–Maruyama with $\Delta t = 10^{-3}$ s and independent Gaussian increments scaled by $\sigma\sqrt{\Delta t}$.
3. Discard the first 5 s and sample the remaining trajectory every 10 ms for analysis. No clipping is applied in the verification; the code records whether a simulated state leaves $(0, 1)$, and no reported small-noise realization does so.
4. Form $u_+ = (S_1 + S_2)/\sqrt{2}$. Estimate the lag-10 ms autocorrelation $\widehat{\rho}$ and set $\widehat{\tau} = -0.01/\log\widehat{\rho}$ when $0 < \widehat{\rho} < 1$.
5. Compute the empirical variance of u_+ and the Pearson correlation between S_1 and S_2; compare with the OU predictions from $\lambda_\pm$.
6. Repeat with 32 realizations using master seed 20260927. Report means and standard deviations without discarding valid realizations on the basis of agreement with theory.

Algorithm S3: graph-spectral verification without empirical data.

1. Normalize each synthetic regular graph to row sum one, so the synchronized scalar equation and its folds are identical across graph families.
2. Compute the second adjacency eigenvalue ν_2 analytically for the two-node edge, normalized complete graphs and normalized cycles.
3. Set $\delta = 1 - \nu_2$ and evaluate $\lambda_{\mathrm{tr}} = -\beta_c\delta$ using the independently computed upper-fold value of β_c.
4. Report $\tau_{\mathrm{tr}} = -1/\lambda_{\mathrm{tr}}$ and compare normalized cycles with the asymptotic law $N^2/(2\pi^2\beta_c)$.
5. Treat these calculations as topology-only model consequences; they are not fitted to a connectome and should not be interpreted as measurements of a biological network.

Table 1: Full stochastic quality-control table. Theory is the local OU result; simulation entries are mean ± SD across 32 realizations.

G	τ_{th}	$\widehat{\tau}$	$V_{+,\mathrm{th}}$	$\widehat{V}_{+}$	$\rho_{12,\mathrm{th}}$	$\widehat{\rho}_{12}$
0.500	0.180655	0.181189 ± 0.024146	9.0327×10^{-8}	$(9.0939 \pm 1.1911)\times10^{-8}$	0.240908	0.251655 ± 0.068482
0.700	0.246258	0.245516 ± 0.034165	1.2313×10^{-7}	$(1.2387 \pm 0.1703)\times10^{-7}$	0.410920	0.412383 ± 0.056755
0.800	0.340256	0.320910 ± 0.063658	1.7013×10^{-7}	$(1.6101 \pm 0.3223)\times10^{-7}$	0.551192	0.522405 ± 0.072332
0.850	0.476819	0.462273 ± 0.079447	2.3841×10^{-7}	$(2.3165 \pm 0.4192)\times10^{-7}$	0.665103	0.636339 ± 0.059764
0.880	0.768124	0.716903 ± 0.144502	3.8406×10^{-7}	$(3.5728 \pm 0.7155)\times10^{-7}$	0.781859	0.764717 ± 0.044868
0.890	1.153921	0.984274 ± 0.271003	5.7696×10^{-7}	$(4.9215 \pm 1.3565)\times10^{-7}$	0.850485	0.820228 ± 0.045503
0.895	1.940037	1.392127 ± 0.500251	9.7002×10^{-7}	$(6.7865 \pm 2.0911)\times10^{-7}$	0.908793	0.862595 ± 0.040387

3 Full numerical diagnostics

Table 1 gives the values used to construct the condensed stochastic table in the main manuscript. The progressive difference between τ_{th} and $\widehat{\tau}$ near the fold is retained rather than hidden. The same finite-window effect is visible in the variance: as the true correlation time becomes a substantial fraction of the analyzed record, time-average variance estimates are biased downward and become more variable across realizations.

A separate deterministic fit over $G \in [0.80, 0.8975]$ gives

$$\log \tau_{\mathrm{rec}} = -0.489619 \, \log(G_c - G) - 2.232625, \tag{37}$$

where the slope is close to $-1/2$. This regression is a numerical confirmation only. The theoretical exponent follows from the fold expansion and does not depend on the selected fitting window.

4 Independent computational implementation

The complete executable implementation is supplied as a separate machine-readable file, `reproduce_all.py`, rather than duplicated inside this SI. This separation prevents the manuscript, SI and computational source from silently diverging. Running the script from the package root regenerates the deterministic folds, equilibrium branch, critical-slowing fit, connectivity-scale check, graph-spectrum calculation, stochastic verification, CSV outputs and all numerical figures. The package is available at https://github.com/thenewcomershk-lab/wong-wang-coupling and archived at https://doi.org/10.5281/zenodo.23495771.

The package dependencies are pinned in `requirements.txt` (see the Software and environment statement below). The fixed master seed is 20260927 and stochastic realizations are generated in the declared order of coupling values. The transfer function is evaluated with an expm1-based implementation together with the analytic removable-singularity expansion, so the fold calculation is not dependent on unstable subtraction near $ax = b$.

The numerical source of truth is therefore the Python package. The SI is a derivation and audit document, not a second implementation. The package README contains the exact execution command, and `outputs/SHA256SUMS.csv` records the identities of the generated files.

Numerical output manifest. The final package contains: `folds.csv` (fold coordinates and residuals), `branch.csv` (symmetric equilibrium branches and modal eigenvalues), `csd_deterministic.csv` (recovery-time scaling data), `stochastic_summary.csv` (Monte-Carlo verification), `spectral_cycles.csv` (topology-only transverse recovery), and

`manuscript_numeric_audit.csv` (crosswalk from manuscript numerical claims to generated outputs). Numerical figures are emitted in two forms from the same source: publication-ready vector PDF files under `figures/publication/` and reproducibility PNG files under `figures/reproducibility/`. A SHA-256 manifest records the final file identities.

5 Sensitivity and falsification checks

A reproducibility supplement should not contain only the calculation that supports the preferred interpretation. The following checks are therefore prespecified as ways the main conclusion could fail or require qualification. These checks are not executed by the accompanying package; they are listed as prespecified tests of the main conclusion.

Time-step convergence. Repeat the stochastic calculation with $\Delta t = 0.5$ ms and 0.25 ms while keeping physical duration, burn-in, noise convention and analysis sampling interval fixed. The reported mechanism is supported if the estimated means change by less than their Monte Carlo standard error away from the immediate fold neighborhood. A systematic drift with Δt would indicate discretization error.

Record-length sensitivity. Repeat the analysis with 15, 30, 60 and 120 s post-burn records. The theory predicts that the deterministic $-1/\lambda_+$ does not change; the empirical correlation-time bias should shrink with longer records, especially at $G = 0.89$ and 0.895. If it does not, the local OU approximation rather than record length is the likely limitation.

Noise sensitivity. Repeat with $\sigma \in \{2.5 \times 10^{-4}, 5 \times 10^{-4}, 10^{-3}, 2 \times 10^{-3}\}$. In the strictly local regime the correlation time is independent of σ and the modal variance scales as σ^2. Departure from that law identifies the onset of nonlinear or basin-escape effects.

Connectivity rescaling. Repeat the deterministic fold solve after uniformly multiplying the connectivity matrix by $\alpha \in \{0.5, 1, 2\}$ and dividing G by the same factor. Every deterministic and stochastic input term should be unchanged to numerical precision. This is a direct unit test of the exact scale invariance proved in the main text.

Graph-spectrum check. For normalized cycles $C_N/2$, verify numerically that the synchronized fold does not move with N while the slowest transverse time agrees with $[\beta_c(1-\cos(2\pi/N))]^{-1}$. If the fold location changes, the row-sum normalization or synchronized reduction has been implemented inconsistently.

Symmetry breaking. A scientifically informative extension is to set $I_{0,1} = I_0 + \epsilon$ and $I_{0,2} = I_0 - \epsilon$. The exact $v_\pm$ eigenvectors then disappear. The appropriate question is not whether the theorem survives verbatim, but how the critical eigenvector rotates and whether its spectral gap from the second mode remains large. This extension should be treated as a new result rather than silently folded into the symmetric theorem.

6 Why no external dataset is required for this article

The manuscript is a theorem-and-model paper. Its claims are of three types: algebraic identities of the stated equations, numerically solved properties of those equations, and controlled stochastic simulations of those equations. None of these claims requires an empirical dataset. Adding an unrelated public EEG, MEG or fMRI dataset would not validate the coupling parameter unless the experiment supplied an independently justified mapping between the manipulation and G. The responsible data statement is therefore that no empirical dataset was analyzed, while the literature-derived model constants are cited at their original modeling lineage (Wong and Wang, 2006; Deco et al., 2013; Castro et al., 2020).

If a later version adds empirical validation, the dataset should be chosen only after defining: (i) the observable corresponding to the model state, (ii) a perturbation or covariate that can be mapped to coupling independently of the outcome statistic, (iii) preprocessing and sampling-rate rules, and (iv) an analysis plan separating confirmation of the $-1/2$ recovery scaling from exploratory time-series summaries. This prevents the empirical example from being selected merely because it resembles the simulated curve.

Software and environment statement

The reference implementation uses only widely available scientific Python packages. The reported values were reproduced with Python 3.12, NumPy 2.4.4, SciPy 1.17.1, pandas 3.0.2 and Matplotlib 3.10.8, as pinned in `requirements.txt`. Monte Carlo results should be rechecked if these versions change. No proprietary solver is used. The fold equations are solved by SciPy's hybrid root method and checked by an explicit residual threshold; branch roots are independently bracketed with Brent's method. Randomness enters only the Euler–Maruyama verification and is controlled by the stated NumPy seed sequence. The deterministic folds, eigenvalues and scaling law contain no stochastic randomness.

References

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