

Arnold tongue of two coupled PING circuits

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Abstract

Reciprocal excitation should synchronize two PING circuits over a wider natural-frequency mismatch as coupling increases, while preserving the rule that the intrinsically faster circuit leads in phase [1]. We test that claim in a graph-native sweep over measured detuning and coupling. The 80 E / 20 I network recovers a centred Arnold tongue that widens across 4 successive coupling steps, and all 715 primary trials are valid. One near-resolution cell violates the strict phase-sign criterion, so the 80 E / 20 I reproduction failed despite 98.7% sign agreement. A focused 800 E / 200 I confirmation resolves that exception: all 40 coupled trials lock with the expected phase sign.

Methods

1. **Fix the graph and coupling intervention.** Each circuit contains 80 conductance-based excitatory neurons and 20 inhibitory neurons. A private 80-channel Poisson population drives each excitatory population. Local E-to-I AMPA and I-to-E GABA-A projections generate PING activity. Four reciprocal AMPA projections share coupling weight K : E_A projects to E_B and I_B , and E_B projects to E_A and I_A . The graph and network seed remain fixed. Figure 1 shows the intervention; the evidence-scale result verifies the realized parameter tensors.
2. **Construct and measure the natural-detuning axis before coupling.** First, both circuits receive the same Poisson input rate with $K = 0$. Five trials at each rate measure how uncoupled gamma frequency changes with drive. The longest interval that is fully valid, monotonic, and has a within-rate frequency interquartile range (IQR) no greater than 0.8 Hz is retained.

The retained curve maps an input rate to its median uncoupled gamma frequency. Second, this mapping is used in reverse to construct the drive for each of 13 requested signed frequency differences d . The midpoint of the retained output-frequency range is $f_c = 40.8$ Hz. For each d , circuit A is assigned the desired frequency $f_A^* = f_c + \frac{d}{2}$, while circuit B is assigned $f_B^* = f_c - \frac{d}{2}$. Linear interpolation on the measured curve then gives the input rates r_A and r_B expected to produce those two frequencies. For example, $d = +4$ Hz requests $f_A^* = 42.8$ Hz and $f_B^* = 38.8$ Hz, which map to $r_A = 106.0$ and $r_B = 86.36$ Hz per channel. Those two rates form one A/B input-rate pair.

Third, each pair is run with $K = 0$ using five matched seeds. For each seed, the measured natural detuning is

$$\Delta f_0 = f_A^0 - f_B^0, \quad (1)$$

where f_A^0 and f_B^0 are the gamma peak frequencies measured under the unequal drives while the circuits remain uncoupled. This seed-specific measured value, not $r_A - r_B$ and not the requested target, is the natural- detuning coordinate assigned to the corresponding coupled trial. Figure 2 shows both the equal-drive calibration and the resulting unequal-drive detuning measurements.

3. **Measure phase and concentration.** Excitatory spikes are converted to population rates with a fixed 5 ms Gaussian kernel. Gamma frequency comes from the post-transient spectrum. A zero-phase 25–90 Hz band-pass filter and analytic signal define relative phase

$$\varphi(t) = \text{unwrap}(\theta_{A(t)} - \theta_{B(t)}), \quad (2)$$

where $\varphi(t)$ is unwrapped relative phase at time t , and $\theta_{A(t)}$ and $\theta_{B(t)}$ are instantaneous phases. Phase concentration is

$$R = \left| \frac{1}{T} \sum_{t=1}^T \exp(i\varphi(t)) \right|, \quad (3)$$

where R is phase-locking value (PLV), T is the number of analysed time samples, and i is the imaginary unit. Figure 3 shows their time-domain behaviour; Figure 4 maps them across the primary grid.

4. **Freeze the locking rule.** Repeated uncoupled equal-drive trials set the admissible emergent frequency difference, relative-phase slope, and phase-slip count. A valid trial is locked when

$$L = \mathbf{1}[|f_A - f_B| \leq \varepsilon_f] \mathbf{1}[|a_\varphi| \leq \varepsilon_\varphi] \mathbf{1}[N_{\text{slip}} \leq \varepsilon_{\text{slip}}], \quad (4)$$

where L is the binary locking label, $\mathbf{1}[\cdot]$ is an indicator, f_A and f_B are coupled gamma frequencies, ε_f is the frozen frequency-difference tolerance, a_φ is the fitted slope of Equation 2, ε_φ is its tolerance, N_{slip} is the complete phase-slip count, and $\varepsilon_{\text{slip}}$ is its tolerance. PLV from Equation 3 is descriptive, not part of L . Figure 4 reports the component estimators, and Figure 5 applies Equation 4 without post hoc threshold changes.

5. **Execute the frozen primary grid.** Thirteen target detunings cross eleven coupling levels with 5 paired input seeds per cell. Each trajectory lasts 3000 ms at a 0.1 ms timestep; the first 500 ms are discarded. A trial is invalid if recorded state is non-finite, any E or I firing rate is below 1 Hz, or either E population lacks a resolved 25–80 Hz peak. Figures 3–5 report this frozen grid.
6. **Apply the registered verdict.** Geometry passes only if the locked region is contiguous, centred near zero detuning, and widens across at least three successive nonzero coupling levels. Every grid cell must contain a valid trial. In every locked nonzero-detuning cell, the circuit with greater natural frequency in Equation 1 must lead in phase under Equation 2. The verdict subsection applies these clauses literally.
7. **Run a focused finite-size confirmation.** Because only one phase-sign cell fails at 80 E / 20 I, the follow-up increases each population tenfold and tests mirrored target detunings at the uncoupled, disputed, and stronger coupling levels. It retains E-population spikes and summary observables, uses ten paired seeds per cell, and lengthens the post-transient window to 5 s. Figure 6 reports the result without reopening the primary grid.

The evidence archive bit-packs exact input and population spikes for every primary and follow-up cell. The primary archive also retains population-mean voltage and projection conductance at 1 ms resolution, compiled bundles, input hashes, seed ledger, and one realized parameter set per coupling level.

Results

The authored graph isolates reciprocal coupling

Method 1 varies only the four cross-circuit AMPA projections. The local PING loops, private drives, graph topology, and seed are fixed, so a change across K is attributable to the registered coupling intervention.

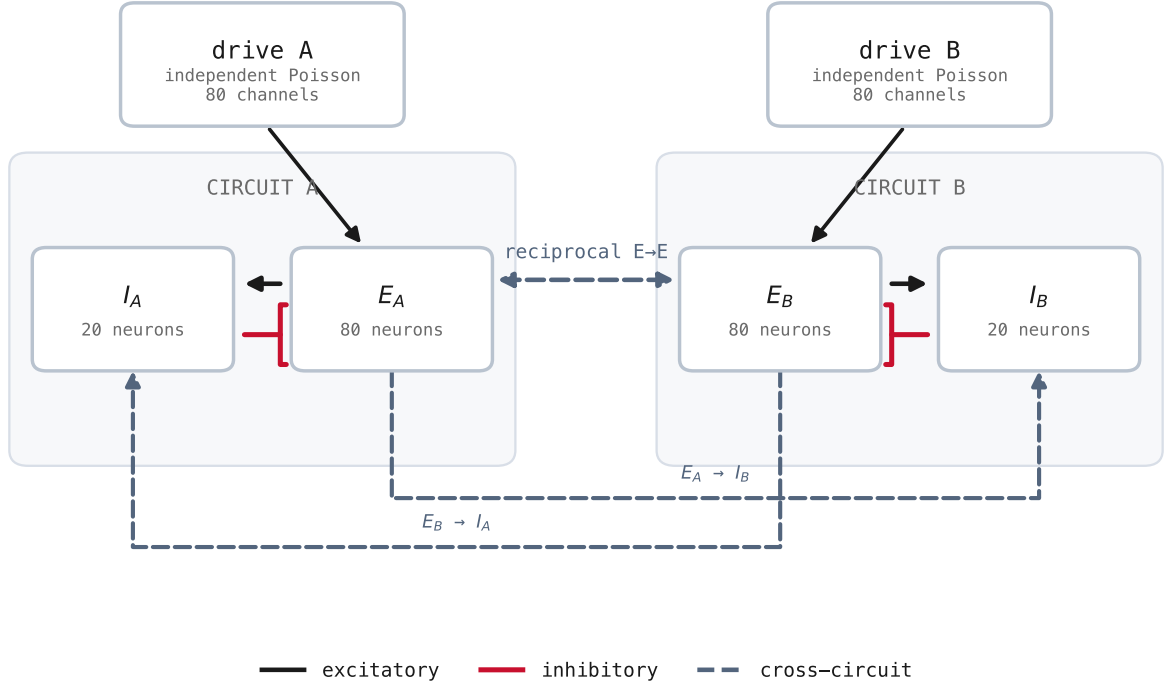


Figure 1: Two-circuit coupling intervention. Each private Poisson input drives a local E-to-I-to-E PING loop. Dashed pathways are the four reciprocal AMPA projections varied together by coupling weight K ; red bar-headed pathways are local GABA-A inhibition. Only the dashed pathways vary across the primary grid.

The realized parameter archive confirms that all non-coupling tensors remain invariant across 11 coupling levels, as required by Method 1.

Calibration defines a stable detuning axis

Method 2 yields a stable monotonic interval from 70 to 130 Hz per input channel. This interval supplies 13 paired A/B input-rate conditions. Measuring those conditions without coupling produces the natural-detuning coordinate used in the primary map.

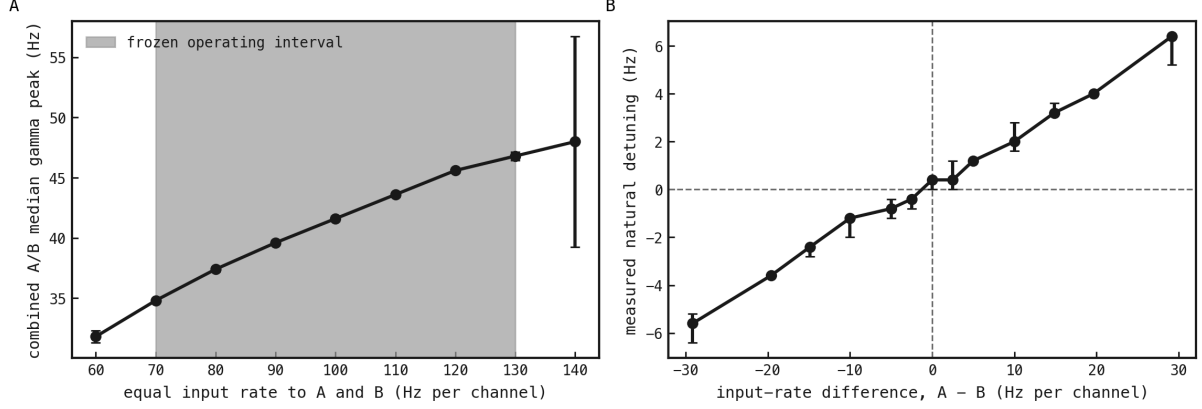


Figure 2: Construction of the natural-detuning axis before coupling. (A) Both circuits receive the same input rate with $K = 0$. Each point is the median of 10 gamma-frequency measurements: circuits A and B in each of five trials. Bars show half their interquartile range. The shaded 70–130 Hz interval is retained because its frequency response is valid, stable, and monotonic. The 60 Hz condition is rejected for excessive within-rate spread; the 140 Hz condition is rejected because the frequency estimator switches between two spectral modes across seeds. (B) For each requested frequency difference, two desired frequencies are placed symmetrically around the 40.8 Hz centre of the retained range. Interpolation on Panel A converts each desired frequency into a drive rate, producing 13 A/B input-rate pairs. These pairs are then run with $K = 0$. The horizontal axis shows the applied input-rate difference $r_A - r_B$. The vertical axis shows the median measured natural detuning $\Delta f_0 = f_A^0 - f_B^0$ from Equation 1; bars span the interquartile range across five matched seeds. These measured values, rather than the input-rate differences or requested targets, become the detuning coordinates in Figures 4 and 5. Dashed lines mark zero.

The frozen thresholds used in Equation 4 are 0.8 Hz for frequency difference, 11.53 rad/s for absolute phase slope, and 4 complete slips. The grid is identified by checksum 8813df0395d0aeb00eb4613d28f776cc09cb4ff783694a7c7603e749c79f3c0f.

Representative trajectories distinguish locking from drift

Conditions selected before inspection show the transition in time: relative phase remains bounded after locking and drifts at the immediately preceding coupling.

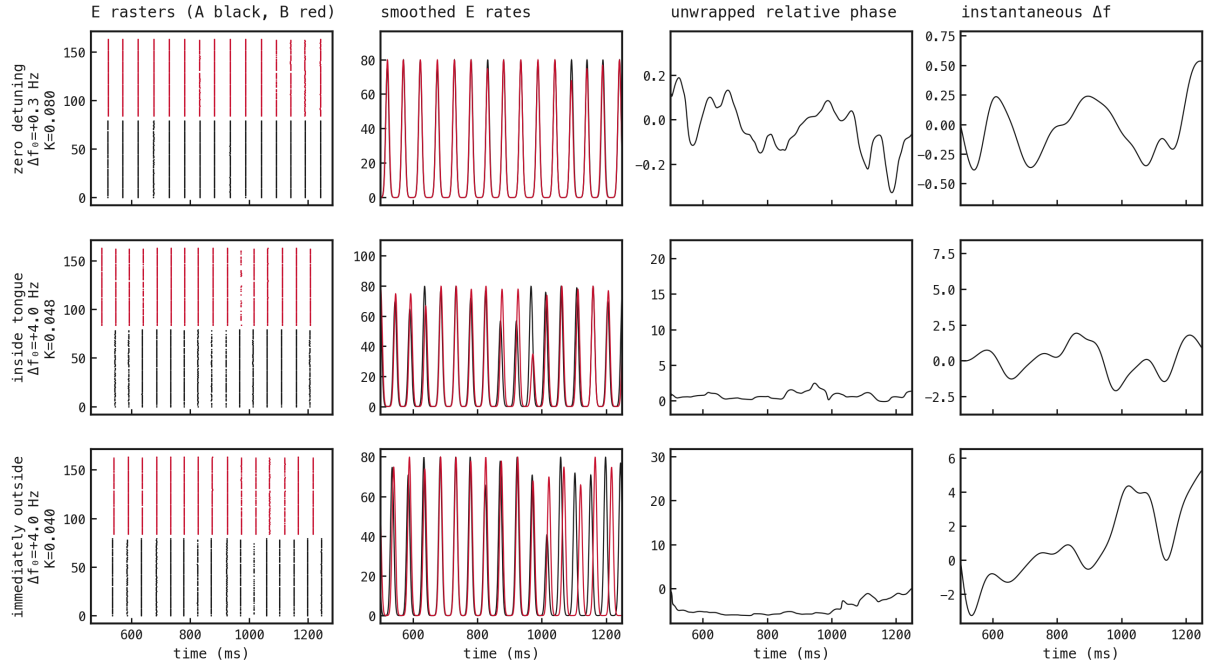


Figure 3: Predetermined time-domain checks. Rows show zero detuning at maximum coupling, the first locked positive-detuning condition, and the same detuning at the immediately preceding coupling. Columns show E rasters, 5 ms-smoothed E rates in hertz, unwrapped relative phase $\varphi(t)$ from Equation 2 in radians, and instantaneous frequency difference in hertz. Relative phase is bounded in the locked conditions and drifts immediately outside the boundary.

Component estimators localize the locking transition

All 715 primary trials are valid. Across the grid, low coupled-frequency difference, low relative-phase drift, few phase slips, and high phase concentration emerge together as coupling increases.

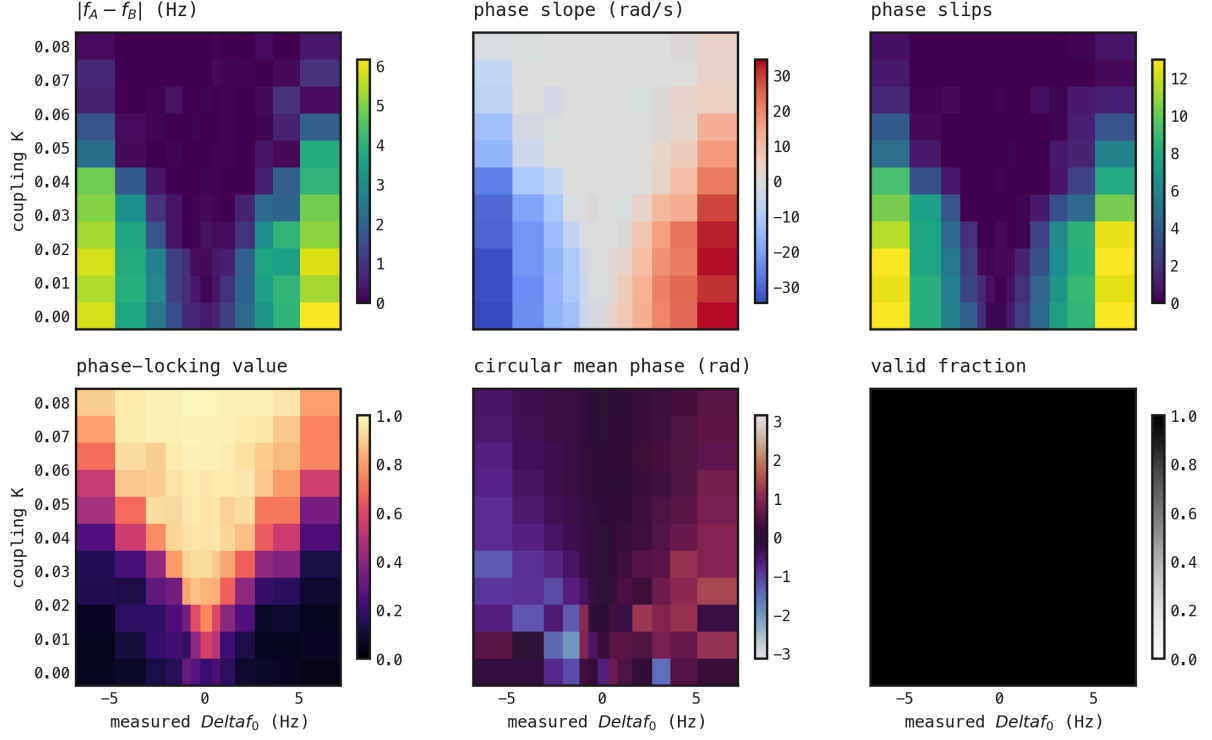


Figure 4: Component estimators on the primary grid. All panels share measured natural detuning in hertz horizontally and coupling K vertically. Panels report coupled frequency difference in hertz, fitted slope of Equation 2 in radians per second, complete phase slips, PLV R from Equation 3, circular mean phase in radians, and valid-trial fraction. Validity is 100% across the grid, while low frequency difference, low phase drift, few slips, and high PLV coincide in the region subsequently classified as locked in Figure 5.

Coupling produces a widening Arnold tongue

Applying Equation 4 to the component estimators produces a contiguous locked region centred near zero detuning. Its width reaches 11.92 Hz at the largest coupling and increases across 4 successive coupling steps.

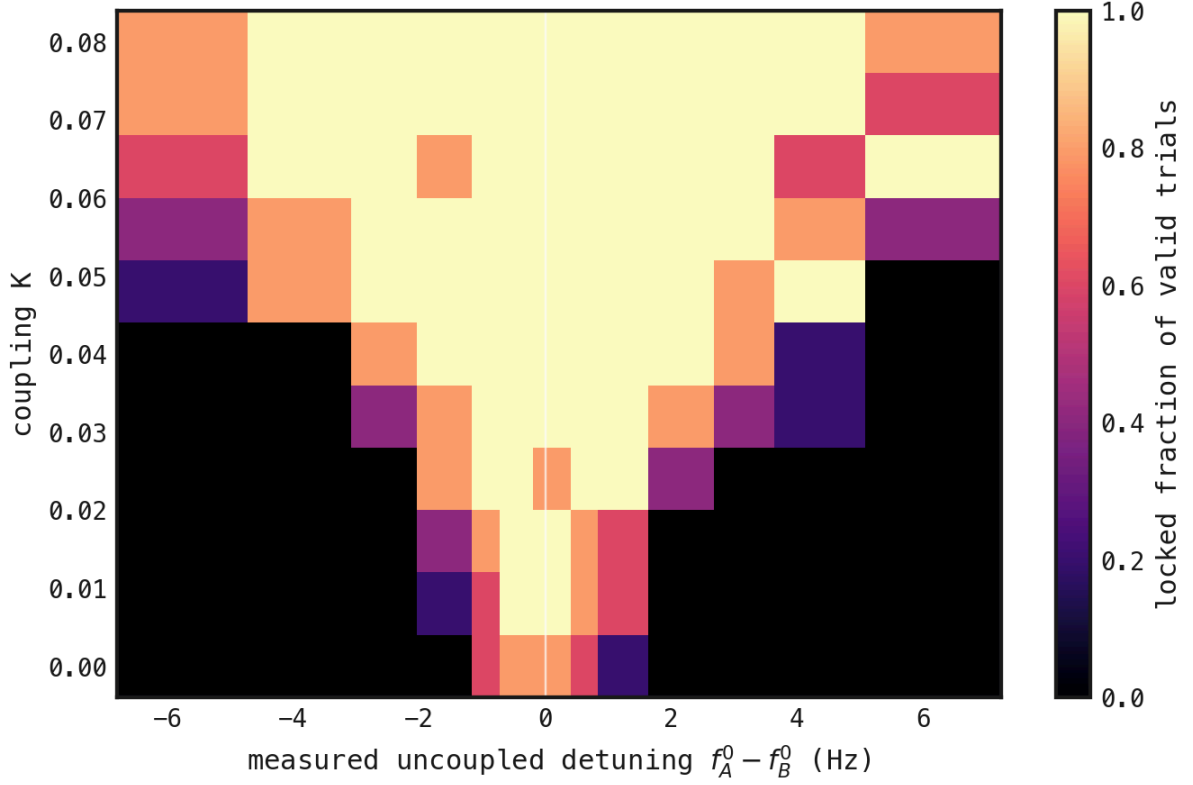


Figure 5: Primary Arnold tongue. Measured natural detuning Δf_0 from Equation 1 is on the horizontal axis in hertz; reciprocal coupling K is on the vertical axis; colour is the fraction of valid trials that satisfy Equation 4. The centred locked region widens with coupling, satisfying the registered geometric clause.

The strict 80 E / 20 I verdict fails one phase-sign cell

Method 6 gives a split result. Geometry and validity pass, but one qualifying cell has the wrong phase sign. Agreement is 98.7%, while the registered clause requires every qualifying cell to agree. The overall 80 E / 20 I reproduction therefore failed. The exception lies near the estimator's registered resolution, so Method 7 tests that boundary rather than repeating the full grid.

The 800 E / 200 I confirmation resolves the exception

The focused confirmation passes: all 40 coupled trials are valid and locked under Equation 4, and all 40 have the phase sign required by Equation 1 and Method 6. At the disputed negative-detuning cell, all 10 seeds have the correct sign with mean phase -0.543 rad. The mirrored positive condition gives 0.526 rad.

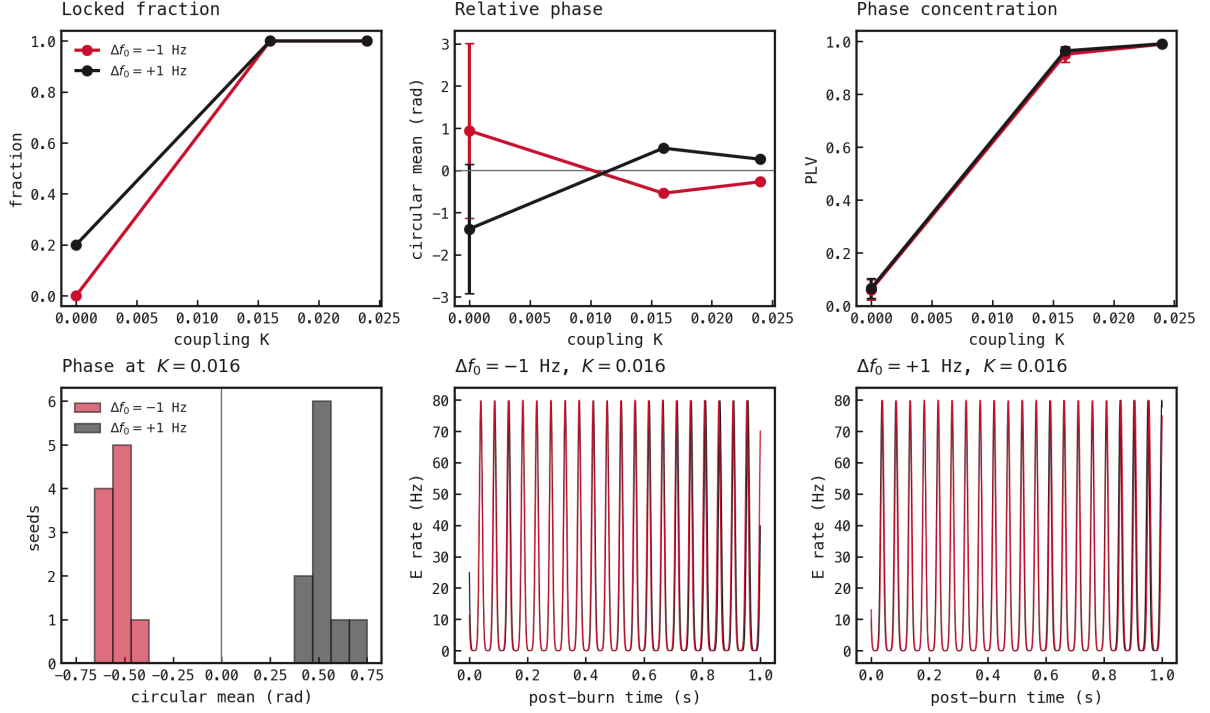


Figure 6: Focused 800 E / 200 I finite-size confirmation. Top panels show locked fraction, circular mean relative phase in radians, and PLV R from Equation 3 over coupling K for mirrored natural detunings; error bars are one standard deviation across 10 paired seeds. The lower-left panel isolates phase at the disputed coupling. The remaining panels show post-burn E-population rates in hertz (circuit A black, circuit B red). Both detuning signs lock with mirrored phase ordering, resolving the lone 80 E / 20 I exception.

The follow-up supports finite-size or estimator-resolution noise, rather than a systematic phase-ordering contradiction, as the cause of the original exception.

Evidence scale

Dense primary retention would occupy 27.82 GB. The published exact-event and state-summary archive occupies 165.5 MB, a 168.1-fold reduction. The 143 primary cells required a median 19.03 s each locally.

References

1. Lowet, Roberts, Hadjipapas, Peter, van der Eerden & De Weerd (2015): *Input-Dependent Frequency Modulation of Cortical Gamma Oscillations Shapes Spatial Synchronization and Enables Phase Coding*. PLOS Computational Biology. doi:10.1371/journal.pcbi.1004072