

Collectivity

Nico, Núria & Jeff

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From rewiring to collectivity: a practical guide

We want to separate two distinct ways rewiring changes dynamics:

- it can change the *collective scale* of biotic interactions (the spectral radius of the interaction matrix);
- it can change the *shape* of interactions (how that strength is distributed across modes and pathways), which is especially relevant in non-normal systems.

Our aim is to build a pipeline that detects, visualises, and interprets the respective contributions to predictability loss across time.

Model and notation

We work with a Generalised Lotka–Volterra (GLV) linearisation around a feasible equilibrium. Write the Jacobian as

$$J = D + A,$$

where $D = -\text{diag}(\tau_1^{-1}, \dots, \tau_S^{-1})$ encodes time scales and A is the interaction matrix with zero diagonal.

It is often convenient to factor out the overall *collective scale* σ of A and a unit-radius shape \hat{A} :

$$A = \sigma \hat{A}, \quad \rho(\hat{A}) = 1, \quad J(\sigma, \hat{A}) = D + \sigma \hat{A},$$

where $\rho(\cdot)$ denotes the spectral radius. We will call $\sigma = \rho(A)$ the *collectivity*.

Time-resolved recoverability

For a chosen perturbation ensemble (e.g., biomass-weighted), define the time-dependent effective return rate $\tilde{R}_{\text{med}}(t)$. As $t \rightarrow \infty$, $\tilde{R}_{\text{med}}(t) \rightarrow -\max \Re \lambda(J)$ (the asymptotic resilience). Small- t is controlled by D (time scales), while intermediate t is where non-normal structure can dominate.

Why collectivity matters

The Neumann series of indirect effects $(I - A)^{-1} = I + A + A^2 + \dots$ converges when $\rho(A) < 1$. Larger $\rho(A)$ implies stronger amplification of indirect paths. For normal matrices,

$$\rho(A) \leq \|A\|_2 \leq \|A\|_F,$$

and there is a tight lower link to May’s complexity $C = \|A\|_F / \sqrt{S}$. For non-normal matrices the lower bound fails: triangular or highly directional structures can have $\rho(A)$ much smaller than $\|A\|_F$, while anti-symmetric or strongly aligned structures can push $\rho(A)$ upwards. This gap between $\rho(A)$ and summary norms is exactly where *structure* (beyond mere magnitude) lives.

Two kinds of change under rewiring

Consider a rewiring $A \rightarrow A'$ with D fixed.

1. **Collectivity drift.** The spectral radius changes by $\Delta\sigma = \rho(A') - \rho(A)$. This alters the net size of the space of indirect pathways.
2. **Shape change.** Even after we rescale to match collectivity,

$$\tilde{A}' = \frac{\rho(A)}{\rho(A')} A', \quad \rho(\tilde{A}') = \rho(A),$$

the alignment of \hat{A}' with D , and its non-normal geometry, can change transient behaviour and mid- t recoverability.

Our goal is to measure both contributions separately and ask when mid- t peaks persist after collectivity is matched.

Decomposing the effect on $\tilde{R}_{\text{med}}(t)$

Given $J = D + A$ and $J' = D + A'$:

- **Raw change**

$$\Delta R_{\text{raw}}(t) = \tilde{R}_{\text{med}}(J', t) - \tilde{R}_{\text{med}}(J, t).$$

- **Collectivity-matched change**

$$\Delta R_{\text{shape}}(t) = \tilde{R}_{\text{med}}(D + \tilde{A}', t) - \tilde{R}_{\text{med}}(J, t).$$

- **Implied collectivity contribution**

$$\Delta R_{\sigma}(t) = \Delta R_{\text{raw}}(t) - \Delta R_{\text{shape}}(t).$$

If $\Delta R_{\text{shape}}(t)$ shows a mid- t hump even after ρ is matched, the signal is genuinely structural (non-normal geometry, misalignment with time scales). If the hump disappears, the earlier peak was mostly collectivity drift.

Non-normality and why mid- t is special

When J is non-normal, eigenvectors are non-orthogonal, and the Schur basis can carry strong feedforward/feedback couplings. Consequences:

- Small t : dominated by D (sum of individual time scales). Matching D pins this regime.
- Large t : driven by $-\max \Re \lambda(J)$. If a manipulation pins the edge mode, large- t differences collapse.
- Intermediate t : sensitive to eigenvector geometry and to $[D, A] \neq 0$. That is where non-normal transient amplification and mode mixing create the “mid- t gap”.

Useful diagnostics to track alongside curves:

- Non-normality of J : $\|J^\top J - J J^\top\|_F$.
- Misalignment with time scales: $\|[D, A]\|_F$.
- Schur basis conditioning $\kappa(Z)$ (overlap of invariant subspaces).
- Participation ratios (how concentrated eigenvectors are).
- Collectivity vs norms: $\rho(A)$, $\|A\|_F$, ratios $\rho/\|A\|_F$ and ρ/C .

Recovery window and the $2t \tilde{R}_{\text{med}}(t) \approx -\log P$ heuristic

Define the recovery fraction $P \in (0, 1)$ as the target level of remaining perturbation energy in the chosen ensemble. Exact evaluation involves $\text{tr}(e^{tJ} C e^{tJ^\top})$ (with perturbation covariance C).

A convenient *scalar* proxy comes from treating $\tilde{R}_{\text{med}}(\cdot)$ as roughly constant on $[0, t]$:

$$2t \tilde{R}_{\text{med}}(t) \approx -\log P.$$

This is accurate when $\tilde{R}_{\text{med}}(s)$ is flat on $[0, t]$ (weak non-normal transients). It **overestimates** the recovery time if there is early transient amplification (mid- t hump), and becomes **asymptotically exact** as $t \rightarrow \infty$.

What to visualise in a separate check

For representative ER, trophic, and niche cases:

- Plot the **exact** t_P from the criterion on $\text{tr}(e^{tJ} C e^{tJ^\top})$.
- Plot the **proxy** t_P^{flat} from $2t \tilde{R}_{\text{med}}(t) = -\log P$.
- Show their ratio vs P and relate the discrepancy to non-normality diagnostics.

The experiment we will run

We compare three manipulations of A while keeping D fixed:

1. **Raw rewire** $A \rightarrow A'$ (e.g., degree-preserving pair swaps, or spectrum-preserving eigenvector shuffle).
2. **ρ -matched rewire** $A' \mapsto \tilde{A}' = \frac{\rho(A)}{\rho(A')} A'$.
3. **A-space spectrum-preserving shuffle** (scramble eigenvectors of A while preserving its full spectrum), used as a control that isolates eigenvector geometry.

For each case we compute $\Delta R_{\text{raw}}, \Delta R_{\text{shape}}, \Delta R_{\sigma}$ across t , and aggregate across replicates.

Structure gradient

We repeat along a discrete path:

- ER (no degree heterogeneity, zero sign/magnitude correlation)
- degree-heterogeneous ER
- add magnitude correlation
- trophic signs
- niche model

This spans from “random” to “structured”. We expect:

- In ER-like systems, after ρ matching, $\Delta R_{\text{shape}}(t)$ is small and mostly long- t (edge-mode) driven.
- In trophic/niche systems, $\Delta R_{\text{shape}}(t)$ retains a mid- t hump whose size tracks non-normality and $\|[D, A]\|_F$.

What would falsify the story

- If ρ -matching removes mid- t peaks even in strongly structured networks, then the earlier peaks were collectivity drift, not structural shape.
- If $\Delta R_{\text{shape}}(t)$ is large at small t while D is identical, we failed to pin the time-scale regime (a bug in the transformation).
- If diagnostics (non-normality, $[D, A]$, $\kappa(Z)$) do not correlate with mid- t excess, the interpretation needs revisiting.

Practical notes on transformations

- **A-space shuffle.** Work in the real-Schur basis of A : write $A = ZTZ^\top$. Apply a block-orthogonal rotation U on the *bulk* Schur subspace, then reconstruct $A' = Z(U^\top TU)Z^\top$. This preserves the *spectrum of A* exactly and leaves D unchanged.
- **ρ -matching.** After any rewire A' , compute $\rho(A')$ and rescale by $\rho(A)/\rho(A')$. This matches collectivity but allows other eigenvalues and eigenvectors to move—precisely what we want to attribute to “shape”.
- **Why not J-space when we study structure?** Shuffling directly in J ’s Schur basis mixes D and A and inevitably perturbs time-scales or the edge mode; that is fine as a *control*, but A-space is the clean place to isolate biotic structure.

Outputs to include in the figures

For each level and manipulation:

- Curves of $|\Delta R_{\text{raw}}(t)|, |\Delta R_{\text{shape}}(t)|, |\Delta R_{\sigma}(t)|$.
- Mean $\tilde{R}_{\text{med}}(t)$ for the original and transformed systems to show small/mid/large- t anchoring.
- Scatter of mid- t excess vs diagnostics $\{\rho(A), \|A\|_F, \rho/\|A\|_F, \|[D, A]\|_F, \kappa(Z)\}$.
- Recovery-time comparison: exact t_P vs proxy t_P^{flat} .

What this buys us conceptually

- It turns “scrambling eigenvectors” into a **controlled partition**: how much change is due to *how much biotic strength exists* (collectivity), and how much is due to *where that strength lives* (shape).
- It makes structured vs random comparisons meaningful: if structure elevates $\rho(A)$, the ρ -matched analysis asks whether there is *anything left* that cannot be explained by a mere change in collective scale.
- It connects directly to the theory of indirect effects and to non-normal transient growth, clarifying why mid- t is the natural place where structure should appear.