

# Collectivity

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## Contents

<b>From rewiring to collectivity: a practical guide</b>	<b>1</b>
Model and notation . . . . .	2
Time-resolved recoverability . . . . .	2
Why collectivity matters . . . . .	2
Two kinds of change under rewiring . . . . .	2
Decomposing the effect on $\tilde{R}_{\text{med}}(t)$ . . . . .	3
Non-normality and why mid- $t$ is special . . . . .	3
Recovery window and the $2t \tilde{R}_{\text{med}}(t) \approx -\log P$ heuristic . . . . .	3
What to visualise in a separate check . . . . .	4
The experiment we will run . . . . .	4
Structure gradient . . . . .	4
What would falsify the story . . . . .	4
Practical notes on transformations . . . . .	5
Outputs to include in the figures . . . . .	5
What this buys us conceptually . . . . .	5

## 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*  $\sigma$  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  $\tilde{A}'$  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  $\rho$  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  $J$ :  $\|J^\top J - JJ^\top\|_F$ .
- 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  $\rho/C$ .

## 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**  $t_P^{\text{flat}}$  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.  **$\rho$ -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  $\rho$  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  $\rho$ -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.
- **$\rho$ -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  $t_P^{\text{flat}}$ .

## 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  $\rho$ -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.