

# Proof

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2025-11-13

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## R<sub>med</sub>, rewiring, and where structure matters

This documentatoins lays out the methods and evidence behind our findings about the median return rate  $R_{\text{med}}(t)$ , why early and late times are predictable from simple summaries, and why the mid-time window is where network structure does the work.

### What $R_{\text{med}}(t)$ measures

Consider the linearized dynamics around equilibrium with Jacobian  $J \in \mathbb{R}^{S \times S}$ . A small shock with covariance  $C \succeq 0$  evolves as  $e^{tJ}$ . We summarize the typical energy of the deviation at time  $t$  by

$$\Phi(t) = \text{tr}(e^{tJ} C e^{tJ^\top}).$$

The median return rate is the effective exponential rate at which this typical deviation shrinks between 0 and  $t$ :

$$R_{\text{med}}(t) = -\frac{1}{2t} \log \frac{\Phi(t)}{\Phi(0)}.$$

Two perturbation models:

- Uniform:  $C = I$ . Every species is shocked equally.
- Biomass-weighted:  $C = \text{diag}(u^2)$ . Larger  $u_i$  implies larger typical shock to species  $i$ .

Intuition:  $R_{\text{med}}(t)$  averages decay rates of the dynamical modes, with weights coming from both the perturbation  $C$  and how the modes sit in state space.

### Endpoint anchors (small $t$ and large $t$ )

A short-time expansion gives

$$R_{\text{med}}(t) = -\frac{\text{tr}(JC)}{\text{tr}(C)} + \mathcal{O}(t).$$

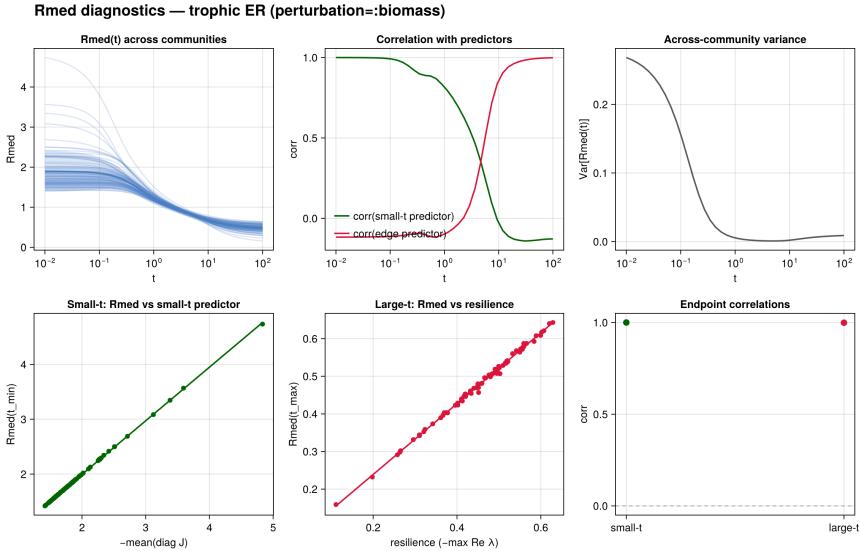
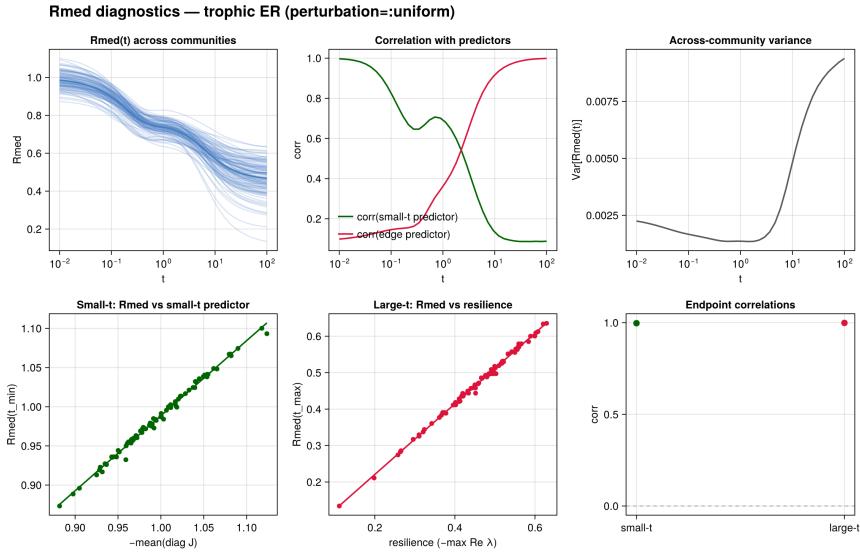
So:

- Uniform:  $R_{\text{med}}(0^+) \approx -\text{mean}(\text{diag } J)$ .
- Biomass-weighted:  $R_{\text{med}}(0^+) \approx -\sum_i u_i^2 J_{ii} / \sum_i u_i^2$ .

At large  $t$ , a single slow mode dominates:

$$R_{\text{med}}(t) \rightarrow -\max \Re \lambda(J) \quad (t \rightarrow \infty).$$

These two anchors explain why we can predict  $R_{\text{med}}(t)$  at the extremes with minimal structure-specific detail.



## How we build the Jacobians

- Draw  $u$  with mean  $u_{\text{mean}}$  and coefficient of variation  $u_{\text{cv}}$ .
- Build  $A$  as trophic ER: fixed size  $S$ , connectance conn, mean absolute interaction mean\_abs, magnitude CV mag\_cv, and symmetry control  $\rho_{\text{sym}}$ .
- Form  $J = -\text{diag}(u) + A$ .

## Small- $t$ and large- $t$ predictors

- Small- $t$  predictor.

Uniform:  $\hat{R}_{\text{small}} = -\text{mean}(\text{diag } J)$ .

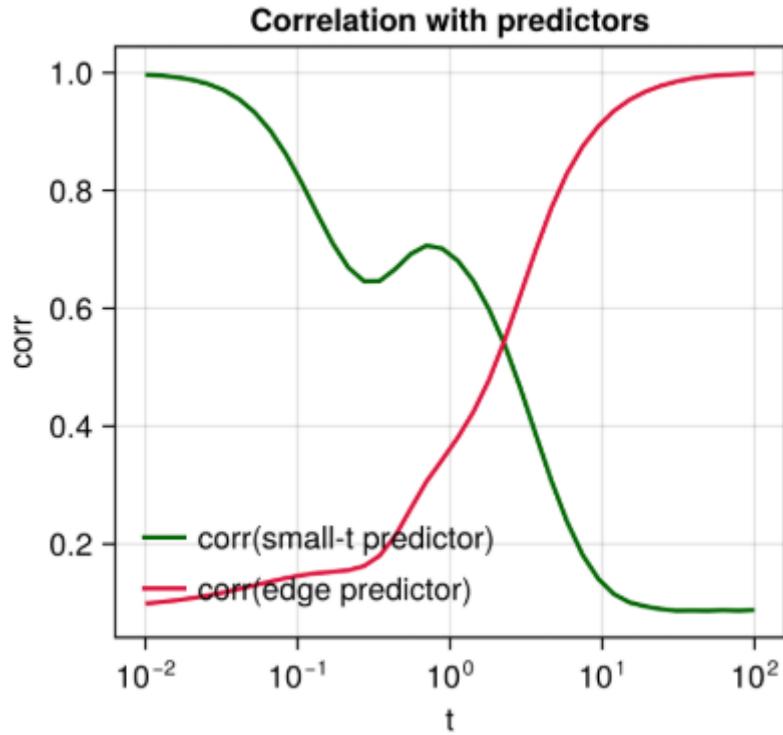
Biomass:  $\hat{R}_{\text{small}} = -\sum_i u_i^2 J_{ii} / \sum_i u_i^2$ .

- Edge predictor (large- $t$ ).

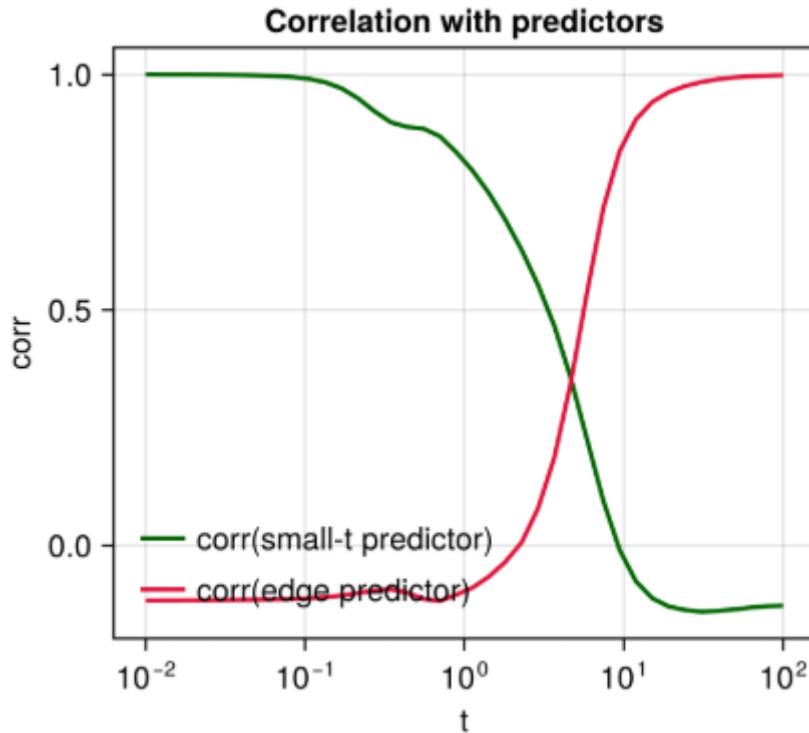
$$\hat{R}_{\text{edge}} = - \max \Re \lambda(J).$$

In the figures below, we can see how the correlation of  $R_{\text{med}}(t)$  across communities switches from the small- $t$  predictor to the edge predictor as  $t$  grows. **The crossover marks the mid-time zone.**

### Correlation Uniform



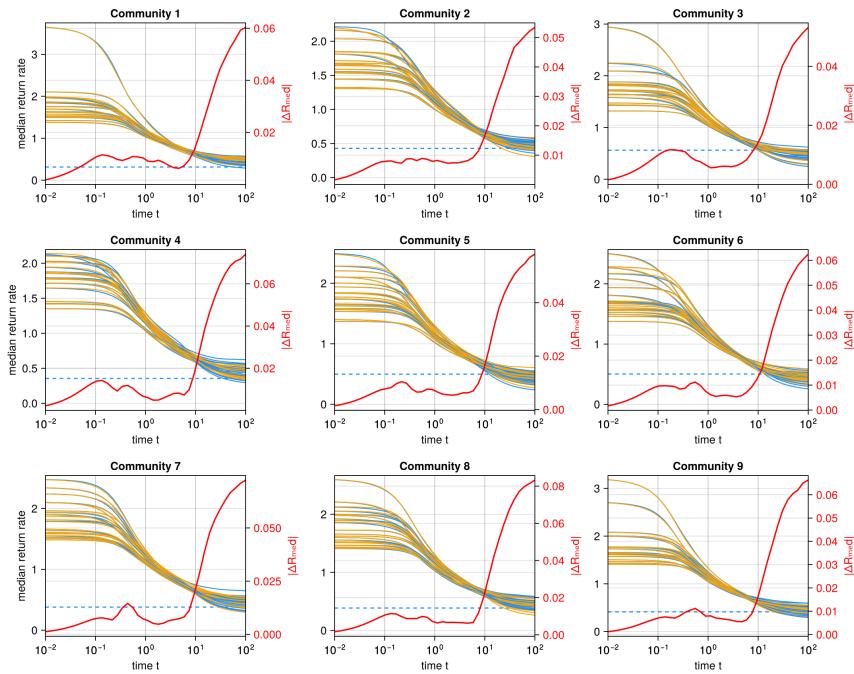
## Correlation Biomass



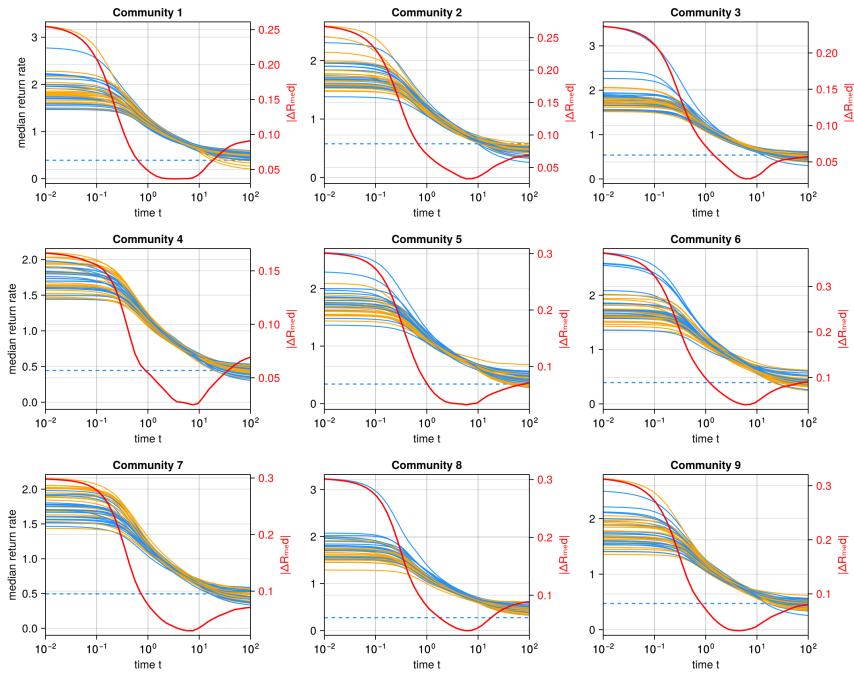
Why the rewire results behave differently whether we maintain TimeScales  $u$  or we redraw them

- Keeping  $u$  the same (or even reshuffling  $u$ 's) and rewiring  $A$ :
    - Early-time values barely move (they depend on the diagonal).
    - Late-time values can diverge (slow mode shifts).
    - $|\Delta R_{\text{med}}(t)|$  tends to grow with  $t$ .
  - Redrawing  $u$ :
    - Early-time shifts are large (the diagonal changes).
    - Mid-time compresses (many modes contribute, geometry averages).
    - Late-time may rise depending on the slow mode shift.
- With  $C = I$ , late times emphasize the edge; with  $C = \text{diag}(u^2)$ , early times are more sensitive to the diagonal and to mode orientation.

Random ER communities — Convergence toward resilience; SINGLE COMMUNITY = false & ABSDIFF = true, same\_u = true, perturbation\_type = biomass

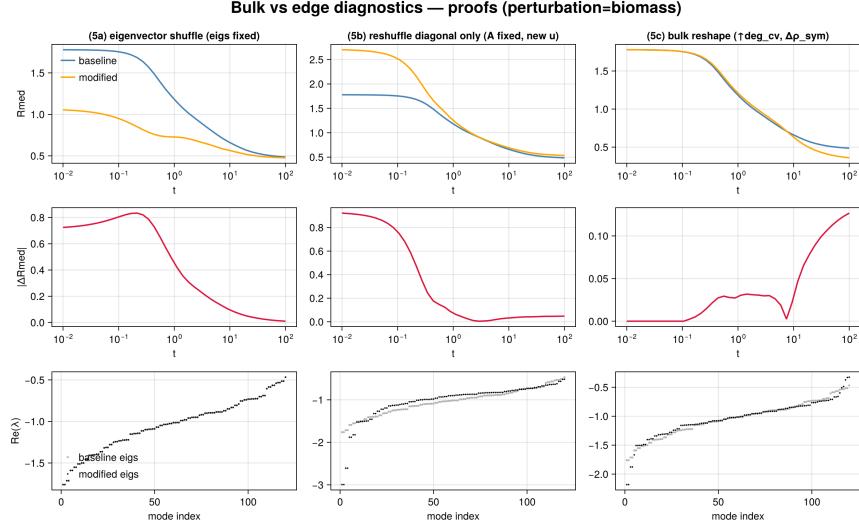


Random ER communities — Convergence toward resilience; SINGLE COMMUNITY = false & ABSDIFF = true, same\_u = false, perturbation\_type = biomass



## Proof experiments

### Full results



We ran three tests to isolate bulk vs edge vs orientation effects.

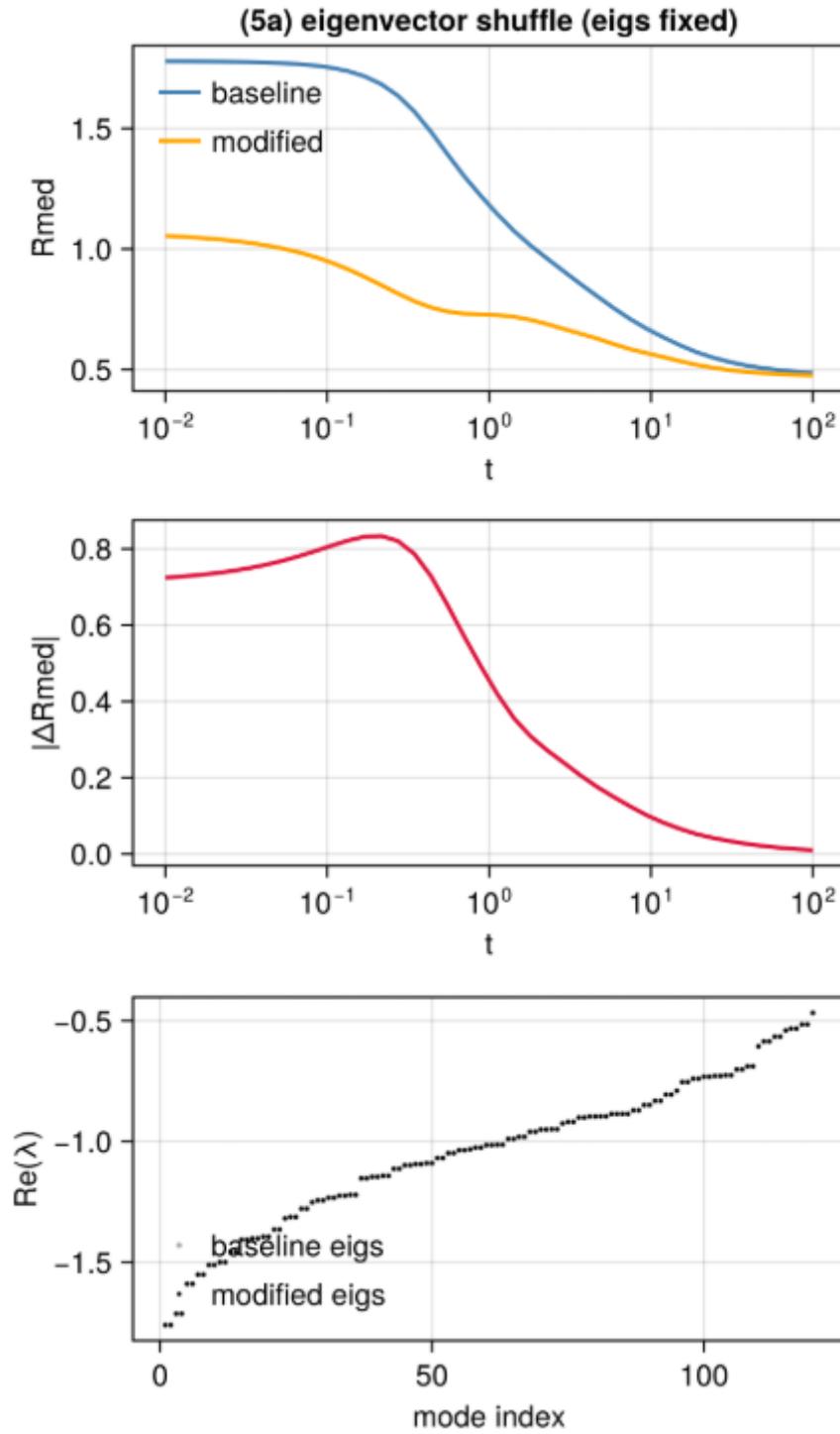
#### 5a) Fix eigenvalues, shuffle eigenvectors

Take the real Schur form  $J = ZTZ^\top$  (quasi-upper triangular  $T$ ). Draw a random orthogonal  $Q$ , build

$$\tilde{J} = QTQ^\top.$$

Eigenvalues are preserved; eigenvectors are randomized.

- Expectation: small- and large- $t$  barely change (anchors fixed), mid- $t$  compresses because orientations average out.
- Observation: exactly this, especially under biomass weighting where  $C$  couples more to orientations.

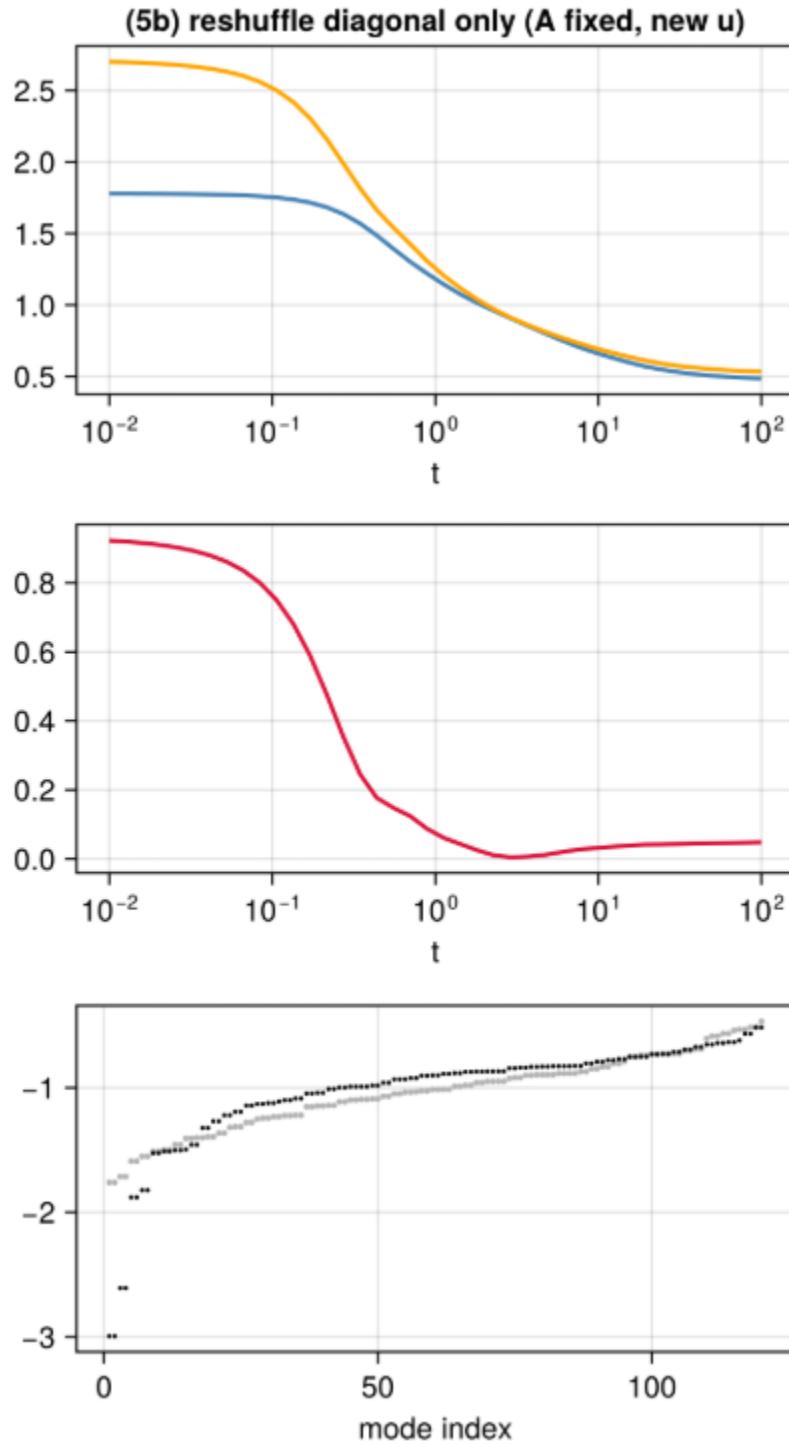


### 5b) Change only the diagonal (new $u$ ), keep $A$ fixed

Replace  $u$  by a new draw (**a reshuffle does not work!**), keep  $A$  unchanged, so only  $-\text{diag}(u)$  moves.

- Expectation: early  $R_{\text{med}}(t)$  shifts a lot; edge can move a bit; a mid- $t$  valley appears for  $|\Delta R_{\text{med}}|$ .

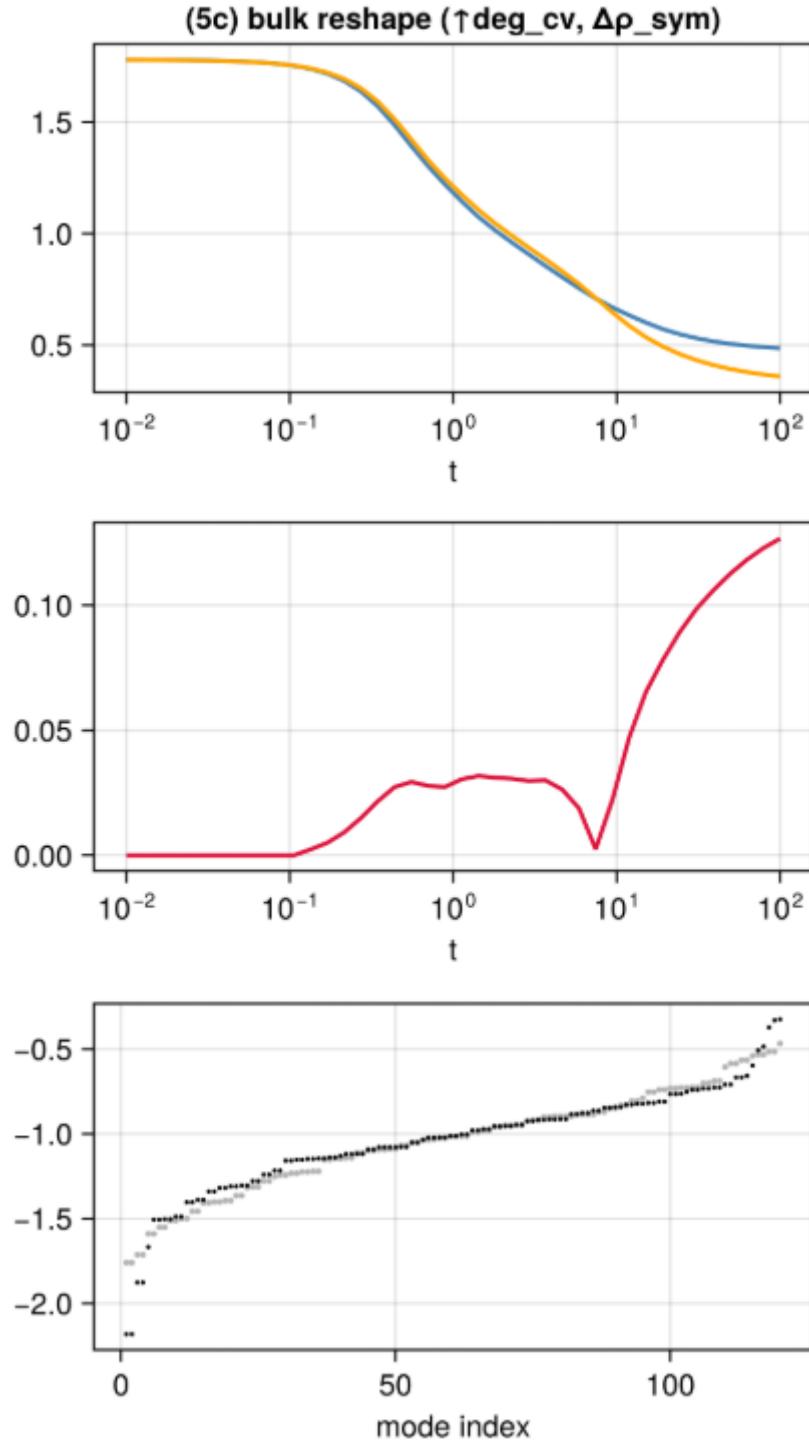
- Observation: valley present, stronger when perturbations are biomass-weighted.



### 5c) Reshape the bulk (degree CV, sign and magnitude structure)

Increasing degree heterogeneity, introducing sign/magnitude correlations, or adjusting symmetry moves many eigenvalues (bulk).

- Expectation: mid-time becomes more discriminative, while endpoints remain anchored (**it does not happen!**  $|\Delta R_{\text{med}}(t)|$  (**pink line**) **increases kind of monotonically with  $t$** ).
- Observation:  $|\Delta R_{\text{med}}(t)|$  rises at intermediate and large  $t$  while invariant at low  $t$ .



## Explanation for me

### What does it mean to shuffle the eigenvectors?

Write  $J = V\Lambda V^{-1}$  in the simple diagonalizable case or  $J = ZTZ^\top$  in real Schur form. Each column of  $V$  or  $Z$  gives a direction in state space in which perturbations evolve as a single exponential (or a 2D rotation–decay for a  $2\times 2$  block). The perturbation covariance  $C$  assigns weights to these directions.

Shuffling eigenvectors means keeping the decay speeds (eigenvalues) but rotating the preferred directions randomly. The shock energy spreads more evenly across directions, so the mid-time region — where many modes compete — compresses. The endpoints do not rely on those orientations: small  $t$  cares about the diagonal average; large  $t$  cares only about the slowest decay rate.

### Claims I can make “confidently”

- Early time is predicted by the diagonal average; late time by the slowest mode. However, when bulk properties are changed (5c), large- $t$  is also affected, whereas short- $t$  never is.

*Exhibit:* endpoint scatter plots and correlation–vs– $t$  curves.

- At the mid-time window, bulk spectrum and eigenvector geometry matter, hence where structure shows.

*Exhibit:* across-community variance vs  $t$  shows a dip; eigenvector shuffling compresses mid- $t$ .

- Rewiring with the same  $u$  yields  $|\Delta R_{\text{med}}(t)|$  rising with  $t$ ; redrawing  $u$  yields a mid- $t$  valley.

*Exhibit:* rewire panels under same- $u$  and different- $u$ , under both uniform and biomass perturbations.

## Appendix: tiny derivations

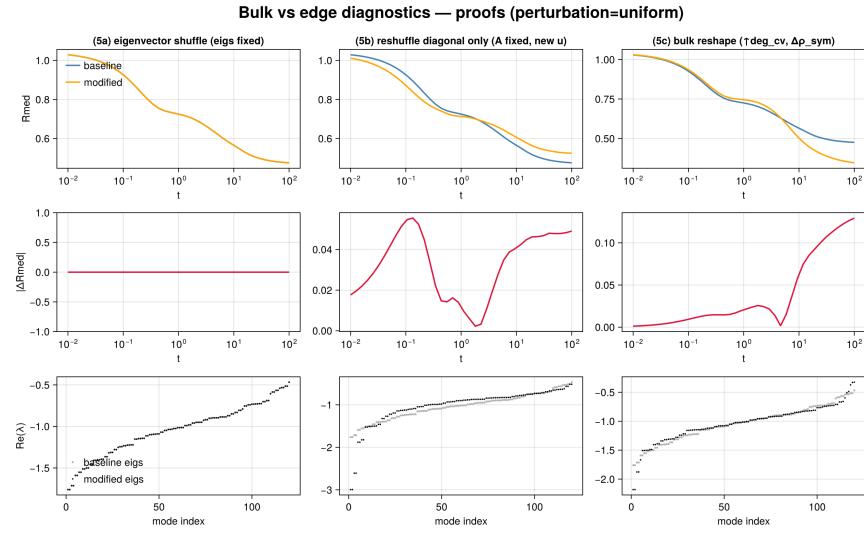
- Small- $t$  expansion. Using  $e^{tJ} = I + tJ + \mathcal{O}(t^2)$ ,

$$\Phi(t) = \text{tr}((I + tJ)C(I + tJ^\top)) + \mathcal{O}(t^2) = \Phi(0) + 2t \text{ tr}(JC) + \mathcal{O}(t^2).$$

Then  $\log \Phi(t) = \log \Phi(0) + 2t \text{ tr}(JC)/\Phi(0) + \mathcal{O}(t^2)$ , giving the predictor.

- Large- $t$  limit. With  $J = ZTZ^\top$  (real Schur),  $e^{tJ} = Ze^{tT}Z^\top$ . For large  $t$ , the block with largest real part dominates, decaying like  $e^{2t \max \Re \lambda}$ , hence the limit for  $R_{\text{med}}(t)$ .

## Extra plots



## Pair-wise rewiring experiments

### What we change and what we keep

We study how predictable the time-dependent median return rate  $R_{\text{med}}(t)$  is under controlled ‘rewiring’ of interaction matrices. The key idea is to preserve the multiset of pair interaction values while moving those values to different unordered pairs.

- Start from a source matrix  $A$  (ER-like non-trophic, trophic-ER with degree heterogeneity, or niche-structured).
- Build a target matrix, which:
  1. Collects all unordered pairs  $(i, j)$ ,  $i < j$  that are occupied in  $A$ .
  2. Stores their paired values  $(A_{ij}, A_{ji})$ .
  3. Places those same paired values on a new random set of unordered pairs.

This holds fixed the count of occupied pairs and the multiset of pair strengths (with directions), but destroys who is connected to whom.

- Additionally, instead of rewiring within the same topology class, we send the values to a purely random, no-structure ER-like non-trophic target with matched connectance and mean  $|A|$ .
- We compare  $R_{\text{med}}(t)$  for the source vs target along axes that matter for predictability:
  - Degree heterogeneity ( $\text{deg\_cv}$ )
  - Abundance heterogeneity ( $u\_cv$ )
  - Alignment between  $u$  and row-load of  $|A|$  (our fast alignment control; here we use negative alignment so that abundant species tend to have weaker outgoing load)
  - Magnitude correlations (symmetry-like magnitude correlation in  $A$ )

We compute either the mean absolute difference  $\langle |\Delta R_{\text{med}}(t)| \rangle$  or the fit  $R^2$  to the identity line across many random replicates.

### Same- $u$ vs Different- $u$ protocols

- **Same- $u$ :** We use the same abundance vector  $u$  for the source and the target. This isolates the effect of who is connected to whom given fixed species weights.
- **Different- $u$ :** Redraw  $u$  for the target (or reshuffle indices). This injects an additional source of variation that dominates small- $t$  behavior and often produces the characteristic mid- $t$  “valley” (compression), because small- $t$  depends mostly on the diagonal/weights, while large- $t$  is pinned by the spectral edge, leaving an intermediate regime where structural details average out.

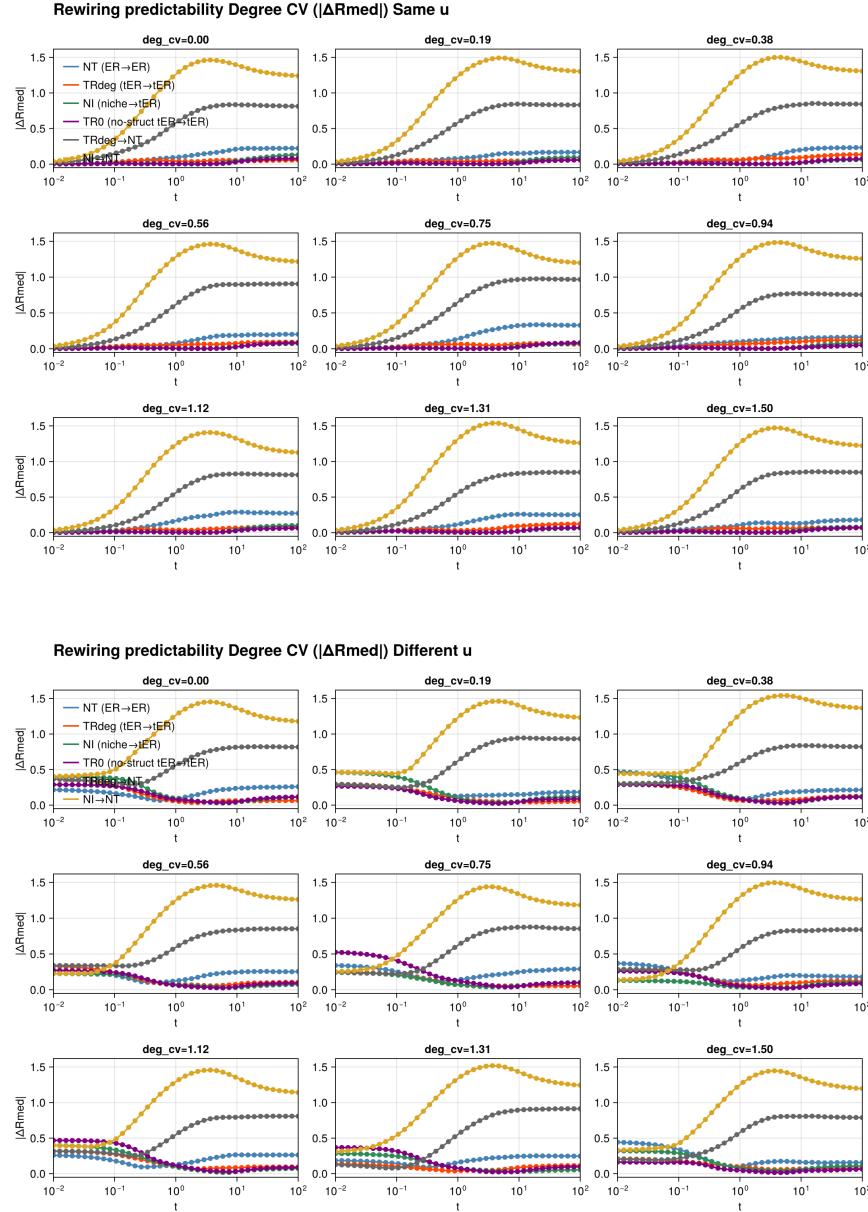
### Design of sweeps and lines

We run  $3 \times 3$  grids over each axis with 50 replicates per panel. Lines shown:

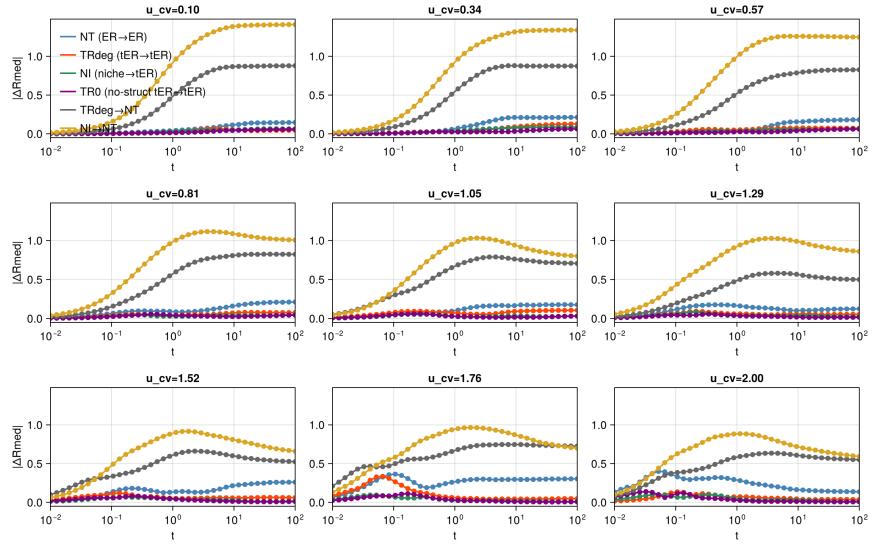
- NT (ER→ER): non-trophic ER rewired to non-trophic ER
- TRdeg (tER→tER): trophic ER with lognormal degree heterogeneity, rewired within class
- NI (niche→tER): niche-structured source mapped to trophic ER target
- TR0 (no-struct tER→tER): within trophic class but with uniform degrees (no structure)
- TRdeg→NT and NI→NT: send pair values onto the ‘pure random NT’ target (to-purerand control)

## Figures

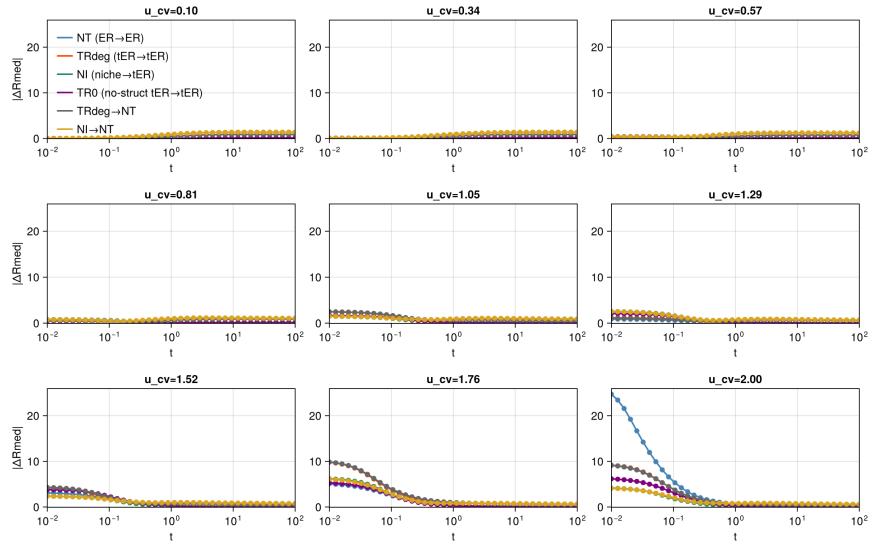
There are two cases per variable of study, one keeping the same  $u$ 's and one using redrawn  $u$ 's.



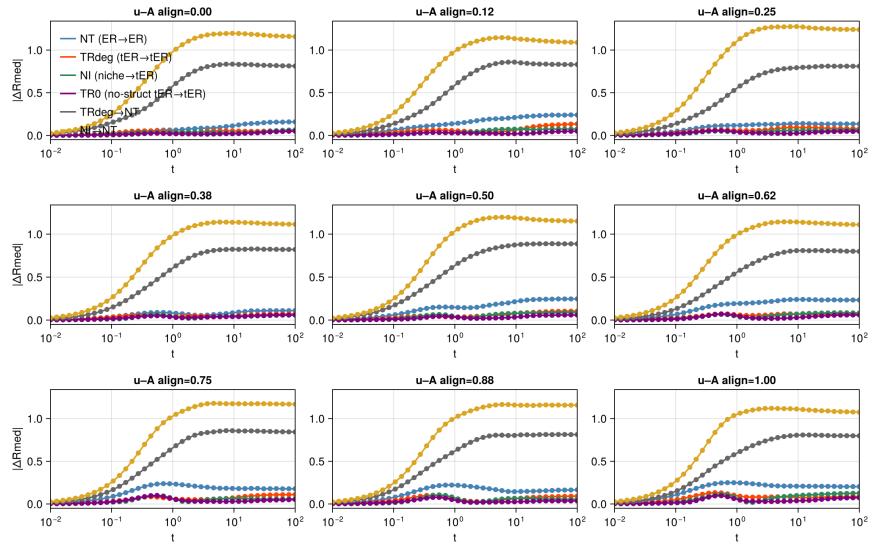
**Rewiring predictability  $u$  CV ( $|\Delta R_{\text{med}}|$ ) Same  $u$**



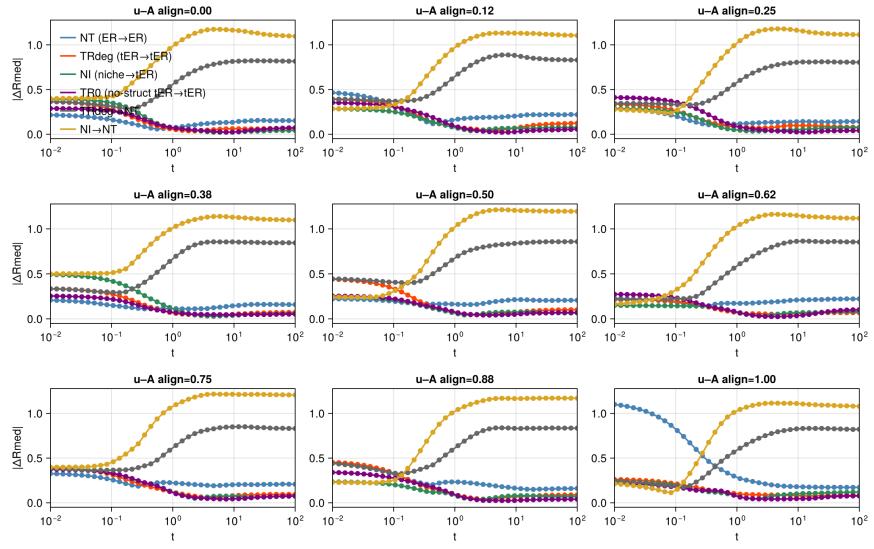
**Rewiring predictability  $u$  CV ( $|\Delta R_{\text{med}}|$ ) Different  $u$**



### Rewiring predictability u-A corr ( $|\Delta R_{\text{med}}|$ ) Negative Corr Same $u$



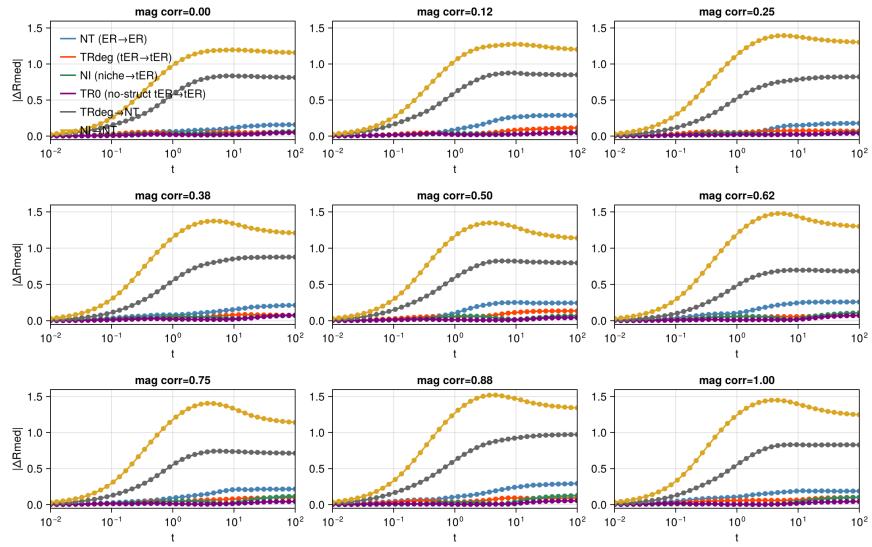
### Rewiring predictability u-A corr ( $|\Delta R_{\text{med}}|$ ) Different $u$



### Note on the alignment control

I use a simple greedy-random mix to align  $u$  with the outgoing row-load of  $|A|$ . With negative alignment, large  $u_i$  tend to be assigned to smaller out-degree values.

**Rewiring predictability mag corr ( $|\Delta R_{\text{med}}|$ ) Same u**



**Rewiring predictability mag corr ( $|\Delta R_{\text{med}}|$ ) Different u**

