

Mervs: A Student Modeling Exercise on Morphology-Aware Oscillator Coupling

1. Project Summary

This is a study done on a project, where the objective is to examine the synchronization impacts that can occur due to morphology-aware neighbor rewiring on a computational model. The study makes a qualitative remark on understanding that existing rewiring prescriptions are not universal, that is, the rewiring prescription can lead to parameter-dependent differences in synchronization outcomes.

Similarly, several oscillator models implicitly assume that networking properties do not rely upon cell geometry or fluctuations of neighbor relationships. When reading several articles concerning reading segmentation clock and arrangement of cells, I proceeded to ask myself a question after developing a model based upon a simplistic computation: i.e., do changes in neighbor relationships have any impact upon achieving contrasting behavior when rewiring in comparison to null assumptions? For example, would this particular assumption never really be an important component of any model unless it is first made explicit? Even though it could have important effects upon changes in neighbor relationships?

2. The Question: Exploring an Assumption in Oscillator Models

This project stems from the motivation of designing an rigorous test for the following ubiquitous assumption of models:

- How the interactions between two cells in model oscillators work. I aimed at researching the possible effects of neighbor changes, which is usually neglected in models. The basic, underlying question of this work is:

“If neighbor relations change over time, does morphology-aware local rewiring generate distinct sync/defect characteristics compared with null rewiring hypotheses?”

To do so, I propose a basic computational model to disentangle the contribution of the rewiring rule.

3. Conceptual Basis from Literature

The following table maps how specific concepts from the field conceptually informed the design of this student-level toy model. This is not a comprehensive literature review; no parameters were fitted from these papers and no results were directly reproduced. Instead, these ideas served as the conceptual guidance for the model's structure.

Conceptual Guidance for Model Design

Idea from Literature	How It Was Used in This Toy Model
The segmentation clock as a system of coupled oscillators.	Justified the use of a Kuramoto-like framework, representing cells as coupled phase oscillators.
The common modeling practice of treating coupling strength (ϵ) and interaction delay (τ) as fixed or predefined parameters.	This motivated the exploration of a model feature—dynamic neighbor rewiring—that is usually implicit or ignored, rather than explicitly tested, in oscillator-based descriptions.
The principle that spatial geometry and dynamic neighbor exchange can influence cell signaling.	Justified the central experiment: comparing a morphology-aware local rewiring rule (<code>alt_local</code>) against geometry-agnostic nulls.

This conceptual basis guided the construction of the toy model.

4. Toy Model Overview

The above schema is, by construction, a simple model created solely with the intention of evaluating the relative effect of different neighbor re-wiring strategies in an artificial environment. It is intended to be utilized for the verification of presumptions rather than considered seriously as a model of real-world biology.

Cells as Oscillators

Each cell is modeled abstractly as a phase oscillator, meaning the state of the cell is given by the phase of the cell, which changes over time according to the intrinsic frequency of the cell as well as the frequency of the neighboring cells.

Neighbor Interactions

Oscillators do not interact with every other oscillator in the system. Instead, they only influence their immediate neighbors, as defined by a dynamic neighbor graph.

Key Parameters

- **Rewiring Rate (ρ):** This parameter controls the rate at which neighbor connections in the graph are updated over time. A value of $\rho=0$ corresponds to a static network.
- **Interaction Delay (τ):** A time delay applied to the interactions between neighboring oscillators. The influence of a neighbor's phase is based on its state at a time $\tau - \tau$ in the past.
- **Coupling Strength (ϵ):** A fixed parameter that determines the strength of influence neighbors have on each other's phase evolution.

The Three Compared Conditions

The core of the project involves comparing three distinct experimental conditions, or "arms":

- `null_fixed`: A baseline condition where the neighbor graph is static and no rewiring occurs ($\rho=0$).

- `null_global`: A null model where neighbor edges are rewired randomly across the entire system. This represents a morphology-agnostic "well-mixed" assumption where new neighbors can be chosen from anywhere.
- `alt_local`: The alternative hypothesis, where neighbor rewiring is local and geometry-aware. This serves as a minimal proxy for morphology-dependent interactions, where cells can only form new connections with others in their immediate vicinity.

Comparing these conditions required a quantitative metric for synchronization error.

5. Measurement: A Proxy for Synchronization Error

The defect rate is the key metric used to evaluate this model's behavior. As a proxy for synchronization errors, it is model-specific: it counts the number of instances at which the phase difference between any two neighbors exceeds a certain threshold. The higher the defect rate, the worse the local synchronization.

This metric is computed over a "tail time window" at the end of each simulation run to ensure the measurement reflects the model's steady-state behavior; it excludes initial transient dynamics from analysis through this procedure. The "defect rate" is to be used as an internal metric for comparing conditions within a model and should not be over-interpreted as a direct measurable biological quantity.

6. Key Observations from Model Screening

The following figures demonstrate the sensitivity of the model regarding the rewiring assumption, considering a screening of various parameter values regarding the rewiring rate parameter, as well as the interaction delay parameter, τ .

On the Interpretation of Results: The following results show that our model responds to the structural assumptions that were made in comparison to our defined alternative hypothesis and our set of null hypotheses. They show modeling principles and should not be interpreted as biological causes for somitogenesis.

Figure 1 is a plot of the mean defect rate versus the neighbor rewiring rate (ρ) under the three model conditions. This graph illustrates the model dependence on the parameters, but it does not validate a particular mechanism.

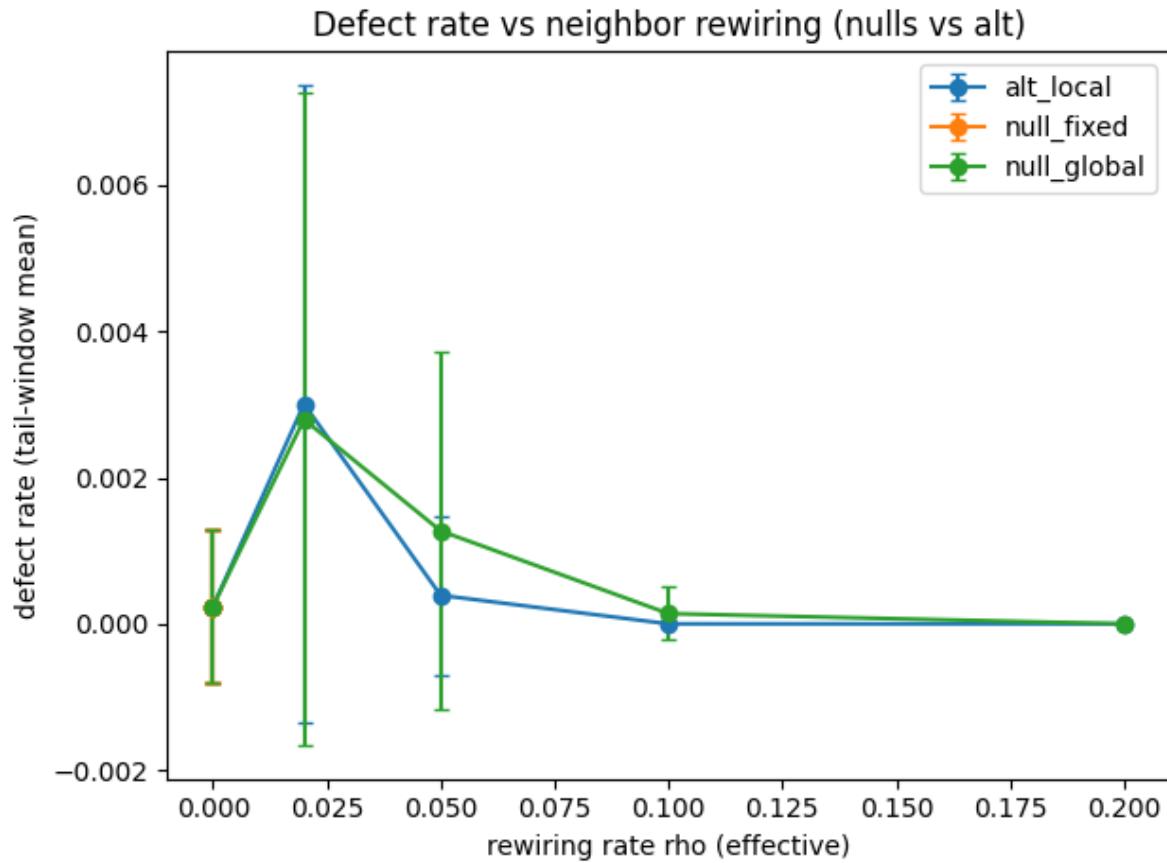


Figure 1: Comparison of defect rates across three neighbor rewiring conditions. The rewiring rate (ρ) controls how frequently neighbor connections change. "Defect rate" is a model-specific proxy for synchronization errors. The separation between the `alt_local` and `null_global` curves at certain ρ values indicates that the rewiring assumption can alter model outcomes. Error bars reflect the standard deviation across multiple simulation seeds.

To isolate the effect of the rewiring rule, we measure Δ_{defect} , defined as `defect(alt_local) - defect(null_global)`. Positive values indicate that the morphology-aware rule produced more synchronization defects than the global null, while negative values indicate it produced fewer. Figure 2 visualizes this difference as a heatmap across a region of the (τ, ρ) parameter space. This heatmap represents a single simulation seed and is shown as an example realization, not a general statistical conclusion.

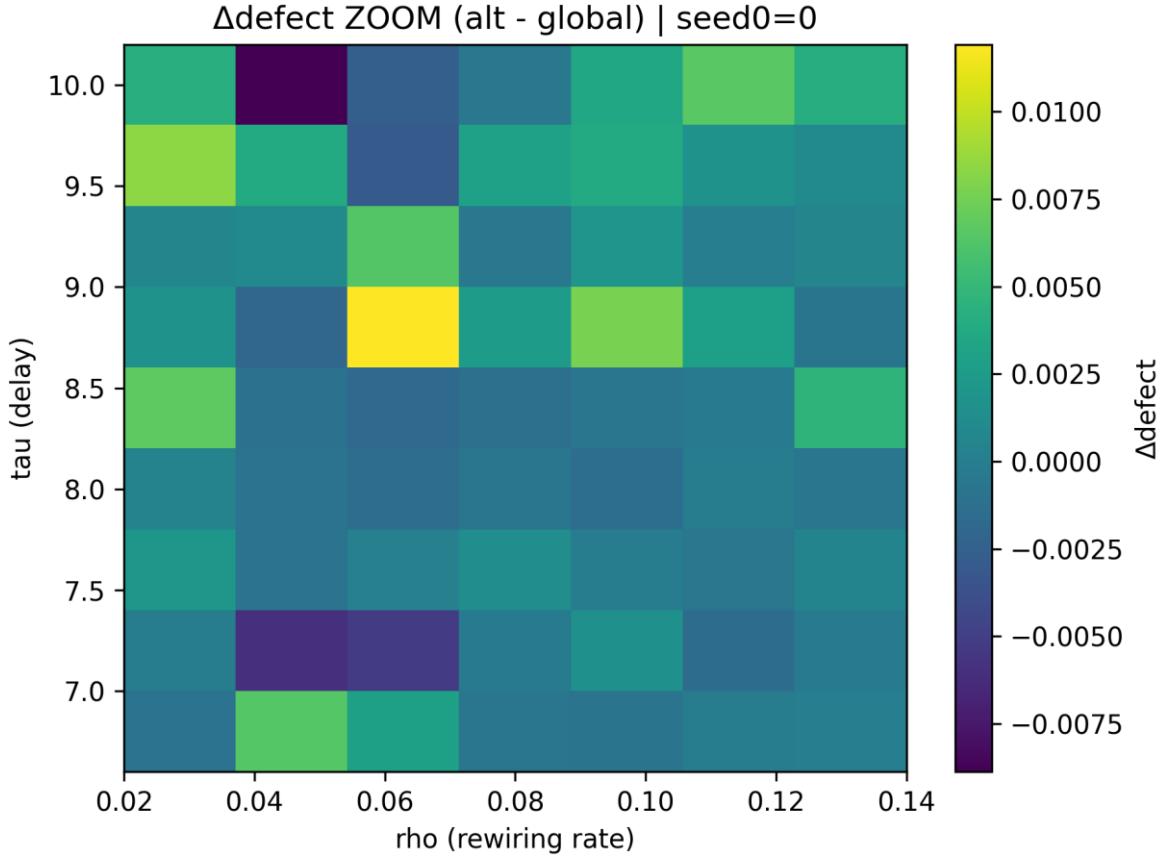


Figure 2: A heatmap of Δ_{defect} (the difference in defect rate between `alt_local` and `null_global` conditions) for an example simulation run (seed=0). Yellow regions indicate parameter combinations where `alt_local` produced more defects than `null_global`, while purple regions indicate where it produced fewer. This illustrates that the effect of the rewiring rule is localized to specific parameter regimes.

The key findings from this parameter screening are:

- **Parameter-dependent effect:** The performance difference between `alt_local` and `null_global` is confined to specific parameter regimes, particularly at low-to-intermediate rewiring rates (ρ) and is sensitive to delay (τ), as shown in Figures 1 and 2, respectively.
- **Observable separation:** For certain values of the rewiring rate (ρ), a clear separation in the mean defect rate emerges between the morphology-aware (`alt_local`) and global null (`null_global`) conditions.
- **High-rewiring convergence:** At high rewiring rates, the defect rates for all conditions tend towards zero in this experimental setup, suggesting that very rapid neighbor exchange can wash out the differences between rewiring rules.
- **Variability across runs:** The presence of error bars (Figure 1) and the single-seed nature of the heatmap (Figure 2) underscore that these are screening-level results subject to simulation variance.

These screening results highlight that model behavior can be sensitive to structural assumptions that are often treated as secondary, reinforcing the need to test such assumptions explicitly.

7. Acknowledged Limitations

This model's conclusions should be considered within the following limitations:

- This is a toy model using abstract phase oscillators, not a detailed simulation of molecular Notch-Delta kinetics.
- Key parameters like coupling strength (ϵ) and delay (τ) are scanned as inputs, not emergent properties of the system.
- The results show sensitivity to the initial random seed and further statistical analysis is required to confirm the stability of these patterns.
- No direct comparison to experimental data has been performed.

8. Key Learning Outcomes

The primary value of this project was in developing a more rigorous modeling mindset. The key takeaways were not about biology, but about the scientific process itself:

- Gained experience in translating a qualitative biological intuition (i.e., "cell geometry might matter") into a precise, falsifiable computational comparison.
- Developed a practical understanding of the critical importance of designing and testing against appropriate null models (`null_fixed` and `null_global`).
- Acquired a sensitivity analysis mindset, recognizing that model behaviors are often conditional on specific parameter regimes.
- Learned to clearly articulate the scope and limitations of a modeling exercise, distinguishing between demonstrating a principle and claiming a discovery.

9. Potential Next Steps

This exercise suggests several avenues for future work:

- Incorporate more mechanistic detail, allowing parameters like coupling strength (ϵ) or delay (τ) to become emergent properties based on local cell states.
- Move from an abstract graph to a more realistic tissue geometry, potentially using vertex model frameworks.
- Conduct a more extensive analysis with a larger number of seeds to ensure statistical stability and quantify the variance of the observed effects.
- Explore potential links to experimental observables that could, in the future, inform parameter ranges or validate model behaviors.

10. References

The following papers provided conceptual guidance for the model's design.

- Herrgen, L. et al. (2010). Timer-like mechanism of Notch signaling in the segmentation clock. *Nature*.
- Morelli, L. G. et al. (2009). Delayed coupling theory of vertebrate segmentation. *HFSP Journal*.
- Oates, A. C., Morelli, L. G., & Ares, S. (2012). Patterning embryos with oscillations: tales from the segmentation clock. *Development*.
- Kuramoto, Y. (1984). *Chemical Oscillations, Waves, and Turbulence*. Springer-Verlag.