When Epidemics Meet: Understanding Spatiotemporal Interactions of Two Pathogens on Metapopulation Networks via Reaction-Diffusion Dynamics
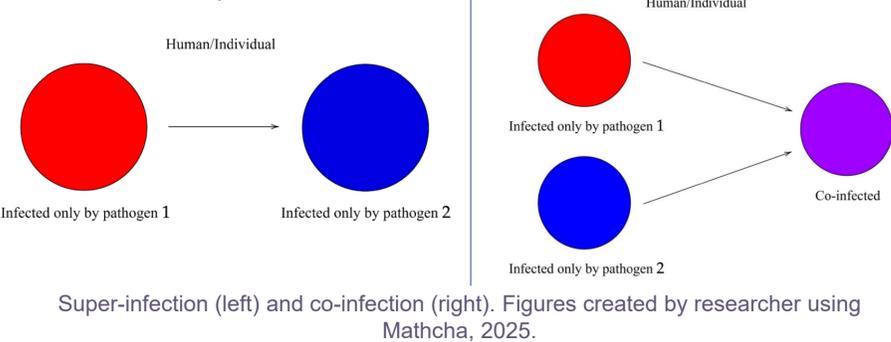
Introduction

The field of **epidemic modeling** allows us to forecast infectious disease outbreaks and case counts, and inform policy decisions, including public health emergencies, lockdowns, and mask mandates.

> Epidemics involve interacting pathogens with coupled dynamics, which have not been thoroughly investigated. The goal of this research is to capture these multi-pathogen interactions with more accurate models.

We focus on the following phenomena:

- **Super-infection:** One pathogen replaces another pathogen in a host
- **Co-infection:** A host can be infected with both pathogens simultaneously

Human/Individual

Infected only by pathogen 1 → Infected only by pathogen 2

Human/Individual

Infected only by pathogen 1
Infected only by pathogen 2 → Co-infected

Super-infection (left) and co-infection (right). Figures created by researcher using Mathcha, 2025.

Reaction-Diffusion Systems

- Reaction-diffusion systems were originally used to understand biological morphogenesis (animal pigmentations, vegetation patterns, limb formation, etc.).
- The formation of these spatial structures, called **Turing patterns** [2], result from small perturbations to a uniform state that grow into instabilities.
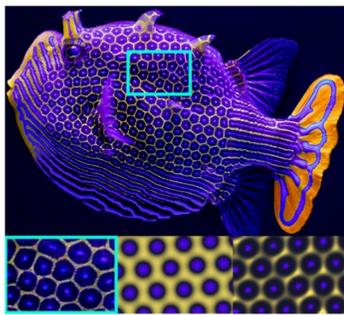
Turing pattern in boxfish pigmentation [1]. Alessio, B. M., & Gupta, A. (2023). Diffusiophoresis-enhanced Turing patterns. *Science Advances*, 9(45). https://doi.org/10.1126/sciadv.adj2457

Reaction-diffusion system in networks

$$\frac{du_i}{dt} = f(u_i, v_i) + D_u \sum_{j=1}^{n} L_{ij} u_j,$$

$$\frac{dv_i}{dt} = g(u_i, v_i) + D_v \sum_{j=1}^{n} L_{ij} v_j.$$

- u_i and v_i: concentration of morphogens in node i.
- $L_{ij} := A_{ij} - \delta_{ij} k_i$, where k_i is node i's degree, A_{ij} is an entry of the graph's adjacency matrix. Moreover, δ_{ij} is 1 if $i = j$ and 0 otherwise.
- The entries L_{ij} form the negative of the graph Laplacian.

## Multiplex Bi-Virus Reaction-Diffusion (MBRD) Framework

We introduce a novel framework, the **Multiplex Bi-Virus Reaction-Diffusion** (MBRD) framework, which establishes two-pathogen reaction-diffusion epidemic models in networked settings. By modeling **on multiplex metapopulation networks**, we capture **spatiotemporal** characteristics of infection spread and account for varying levels of population movement:

- The **MBRD-SI** model incorporates super-infection, and the **MBRD-CI** model incorporates co-infection.
- Reaction terms capture infection severity within geographic communities, while diffusion terms describe spread of infections between regions.
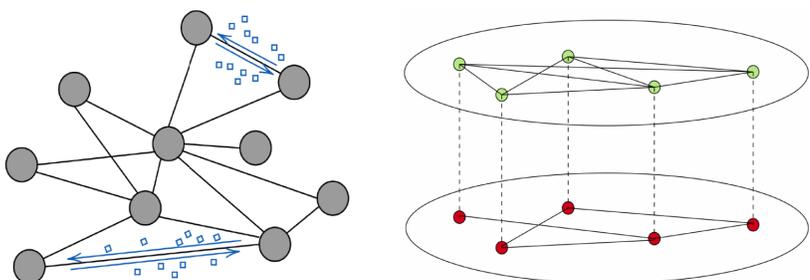
Single-layer metapopulation network (left) and multiplex network (right). Nodes are geographic communities and edges represent migration. Figures created by researcher using Mathcha, 2025.

Pattern Formation
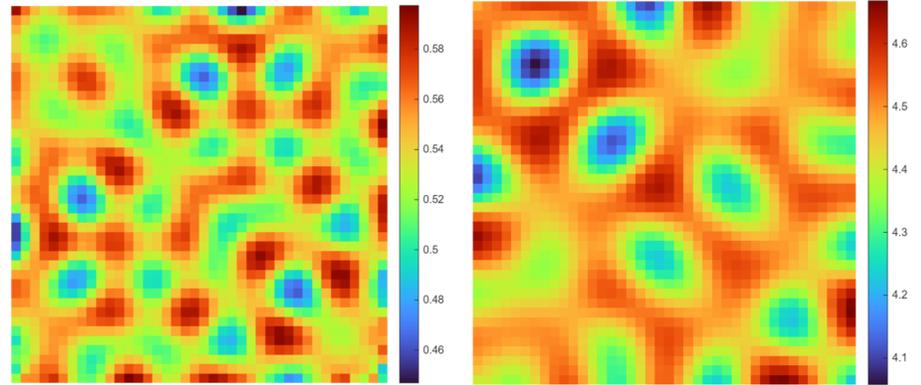
Turing pattern with MBRD-SI (super-infection model) on LA12-LA12-LA12 network (left) and Turing pattern with MBRD-CI (co-infection model) on LA12-LA12-LA4 network (right). Figures created by researcher using MATLAB, 2025 [3].

Parameter Analysis

- **Bi-pathogen interactions.** Dominance of one pathogen can inhibit pattern formation, and intermediate co-infection values can induce pattern growth.
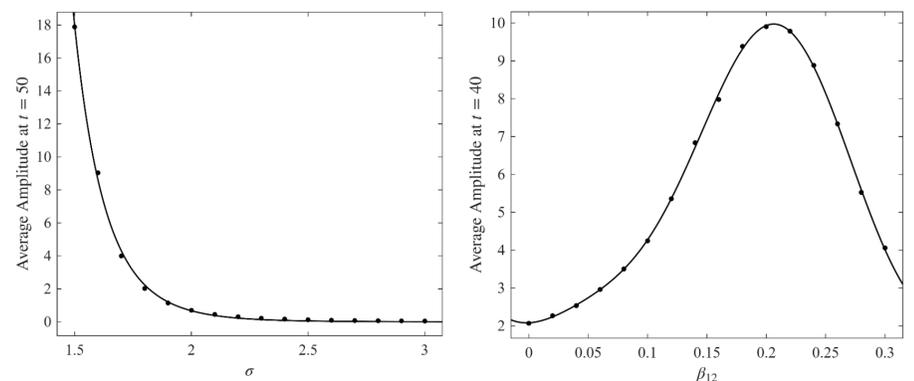
Average amplitude for varying σ (super-infection rates) (left) and average amplitude for varying β_{12} (co-transmission rate) (right). Figures created by researcher using MATLAB, 2025 [4].

- **Population movement.** Variations in population movement between susceptible, pathogen 1-infected, and pathogen 2-infected groups can inhibit pattern formation. Greater levels of population movement overall can increase the size of community clusters with high infection severity, harming a greater number of regions.
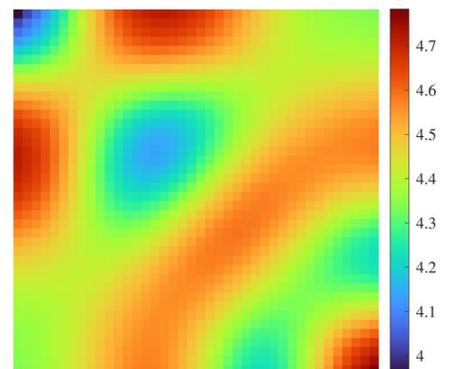
Large clusters generated with LA24-LA24-LA24 network (right). Figure created by researcher using MATLAB, 2025.

Future Work

We can account for factors such as vaccinations, age-structuring, and cross-immunity; extend the present model to a system with three, or in general n-pathogens; or capture varying movement levels or one-directional migration with weighted or directed networks. We can also adapt MBRD to analyze other contagion processes, including

- **Information Propagation:** Spread of conflicting or related rumors in a network of societies.
- **Malware Propagation:** Analyzing computer virus and anti-virus dynamics, or pairs of viruses that support one another's survival by infecting the same host computer (e.g., Vobfus and Beebone).
- **Election Forecasting:** Modeling spatial dynamics of voting intentions in states and regions to predict election outcomes and explain spread of political ideologies throughout countries.

References

[1] Alessio, B. M., & Gupta, A. (2023). Diffusiophoresis-enhanced Turing patterns. *Science Advances*, 9(45). https://doi.org/10.1126/sciadv.adj2457

[2] Turing, A. (1990). The chemical basis of morphogenesis. *Bulletin of Mathematical Biology*, *52*(1-2), 153-197. https://doi.org/10.1016/s0092-8240(05)80008-4

[3] Yu, A., & Schaposnik, L. P. (2025). Spatial super-infection and co-infection dynamics in networks. *arXiv preprint arXiv:2508.15740*

[4] Yu, A., & Schaposnik, L. P. (2025). Dynamics of Infection Spread and Hotspot Growth in Bi-Pathogen Networks. *arXiv preprint arXiv:2509.03374*