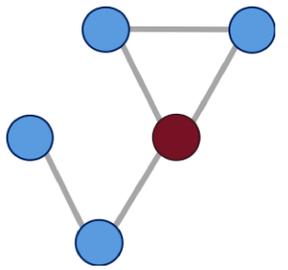




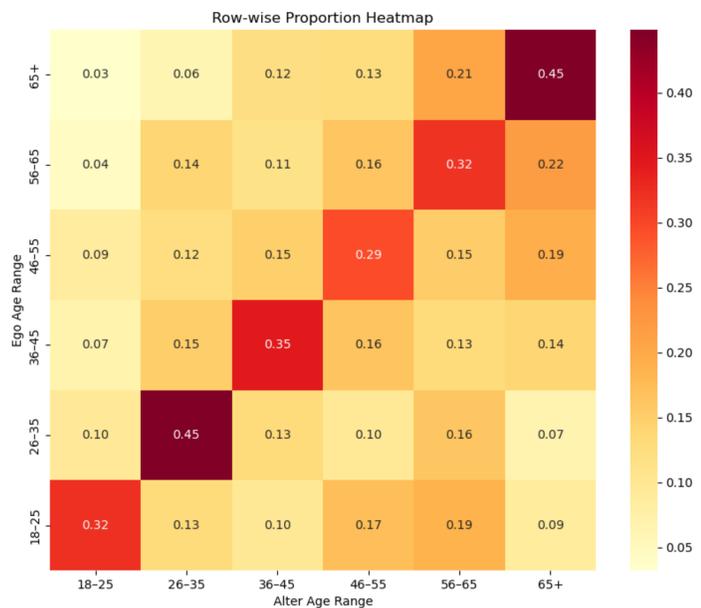
Modeling the spread of vaccination behavior and infection on survey-derived networks



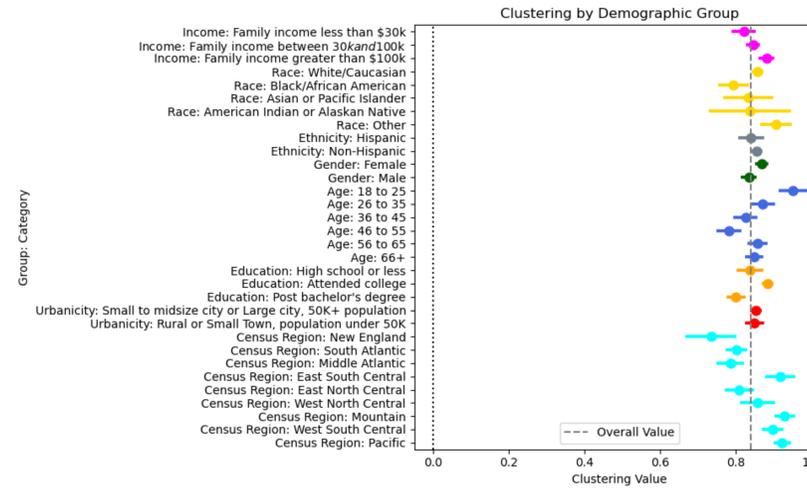
GEORGETOWN UNIVERSITY

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Assortativity



Clustering



Add caption for assortativity and clustering

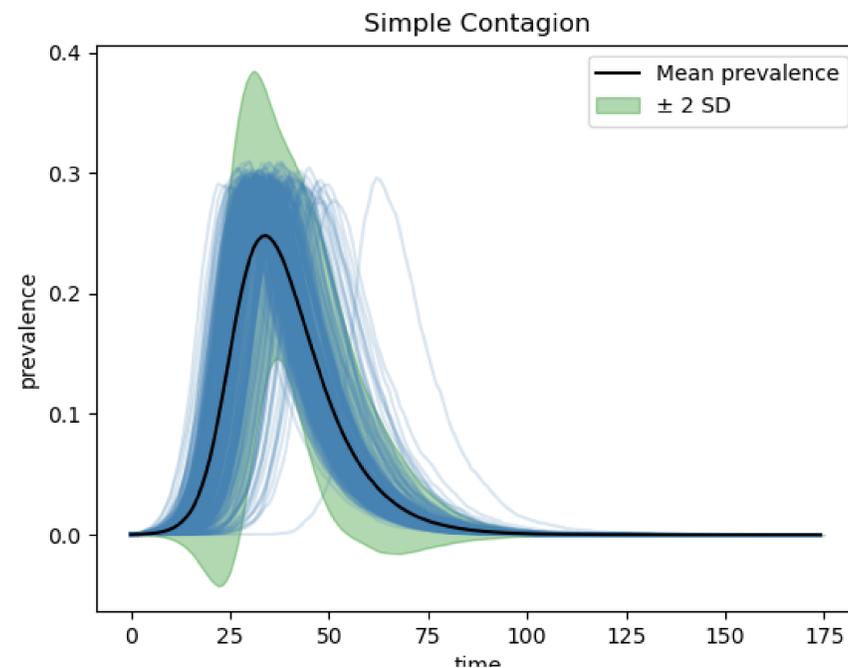
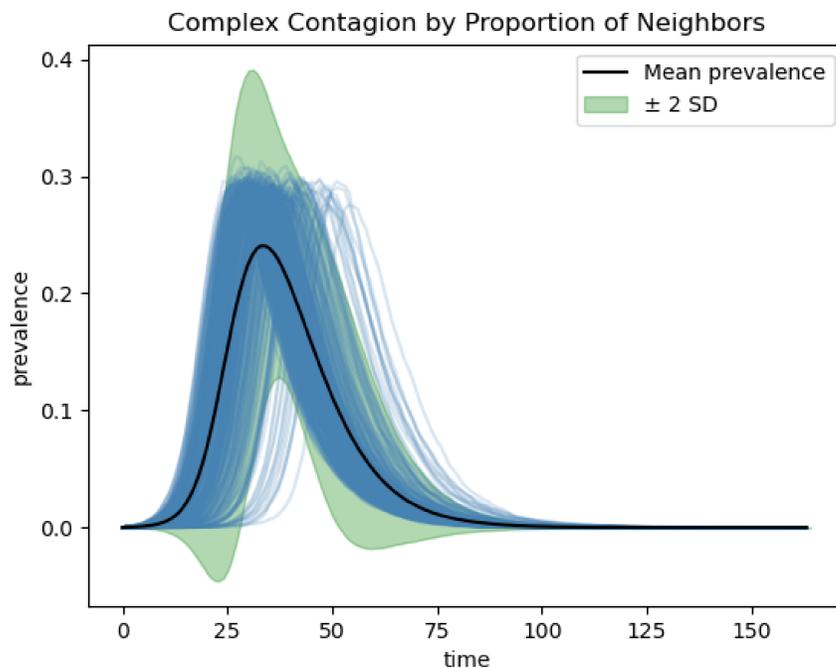
MOTIVATION

- **Dual Contagion:** Pathogens spread through physical proximity, while behaviors (like vaccination) spread through social influence via technology and face-to-face interaction.
- **Network Influence:** Network structure—specifically **clustering** and **assortativity**—dictates the speed and magnitude of both disease and social contagion.
- **The U.S. Gap:** While studies like POLYMOD exist for Europe, there is limited data on higher-order network metrics (beyond simple degree) for the large, heterogeneous U.S. population.
- **Epidemiological Risk:** Understanding susceptible depletion in clusters and demographic-based mixing is critical for tailoring public health policies.

DATA

- RAND American Life Panel (February 2022) survey of 2,145 U.S. participants.
- Ego-Network Construction:
 - **Nodes:** 2,089 eligible "egos" and up to 15 "alters" (contacts) per person.
 - **Edges:** Differentiated by contact type (Social vs. Face-to-Face) and frequency.
 - **Demographics:** Includes age, gender, race, urbanicity, and vaccination habits (Always, Sometimes, Never).
 - **Higher-Order Metrics:** Calculation of local/global clustering and assortativity by age, gender, and vaccination status.

Simulated Prevalence



Add caption for simulation models

APPROACH

- **Network Modeling:** Use **Exponential Random Graph Models (ERGMs)** to simulate full social and spatial networks based on survey-derived ego patterns.
- **Social Contagion Model:** Test four behavioral mechanisms for vaccination uptake:
 - Simple Contagion:** Pathogen-like spread via single-contact influence.
 - Complex Contagion:** Threshold-based uptake (requires multiple vaccinated contacts).
 - Historical Habit:** Persistence of previous years' behavior.
- **Disease Model:** Integrate a standard **SIR (Susceptible-Infected-Recovered)** model on the spatial network.
 - **Transmissibility (β):** 0.05 to 0.5 to reflect varying respiratory pathogens.
 - **Recovery (γ):** 5–7 days (standard influenza parameters).

TAKEAWAYS

- **Identify High-Risk Groups:** Generalize which demographic groups are at greater risk of infection based on their unique network structures (e.g., high clustering vs. high degree).
- **Social vs. Spatial Drivers:** Determine if infection clusters are a result of physical contact patterns or "behavioral clusters" (unvaccinated social groups).
- **Policy Implications:** Quantify how social contagion of vaccine hesitancy creates "pockets" of susceptibility that can lead to larger outbreaks.
- **Model Refinement:** Improve disease forecasting by decoupling information flow (social) from transmission events (physical).