

Predicting Epidemic Cascades Using Metapopulation Models

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Background

Metapopulation Models

Metapopulation models allow for simulating disease spread through geographic “patches” connected by a mobility network, with spread within each patch simulated using an ODE-based model. PatchSim is a metapopulation model developed by Dr. Venkatramanan and his colleagues [1].

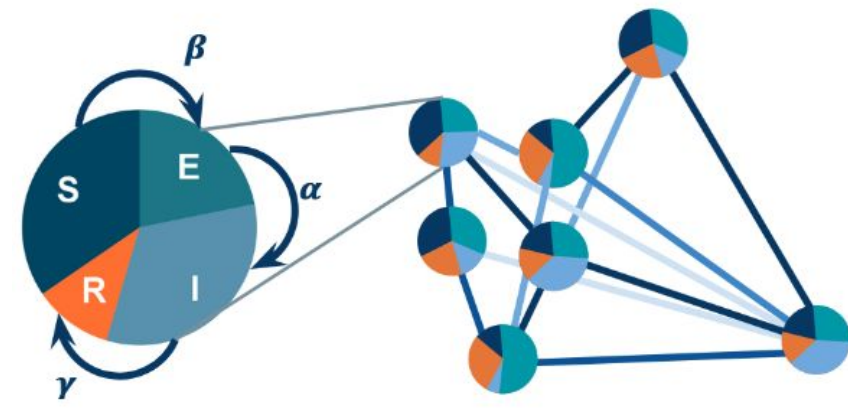


Figure #1

Cascades

Understanding temporal relationships in the orders in which infections arrive in certain locations allows us to make predictions about how disease will spread. Cascades are subsequences in the overall sequence of infections that are likely to occur given the initial conditions of an epidemic.

Goal

Use mobility networks for the United States along with SEIR metapopulation model PatchSim to determine how different disease conditions such as seed locations and spatial resolution affect where cascades appear in the US.

Methods

Generating the Mobility Network

- State and county-scale mobility networks were created using the Multiscale Dynamic Human Mobility Flow Dataset in the U.S. during the COVID-19 Epidemic [2]
 - Data was collected using mobile phone location data
- Mobilities were calculated using the pop flow for each pair of locations i, j divided by the total pop flow originating from i

Running the Simulation

- For each state, a simulation was run with cases seeded in that state
 - For the county-scale simulations, cases were seeded in the state’s most populous county
 - Seed cases were 10% of the seed location’s population
- All simulations used the same network (2020 safngraph) and the same disease parameters ($\beta=0.2487$, $\alpha=0.1667$, $\gamma=0.1$)

Analyzing Cascades

- For each simulation, determined the order in which each location surpassed a specific infection threshold (0.5% of the location’s population)
- Compared each pair of orderings using the Kendall rank correlation coefficient (τ)
- Using the orderings, found probability that i is infected before j and vice versa
- Using order probabilities, generated likely cascades
 - Likelihood of a cascade is the product of each pair in the sequence’s probability distribution of appearing in its order in the sequence
 - Generated using a recursive method to find all subsequences above a likelihood threshold (0.7 for state-level, 0.98 for county-level)

Rank Correlation Between Sims

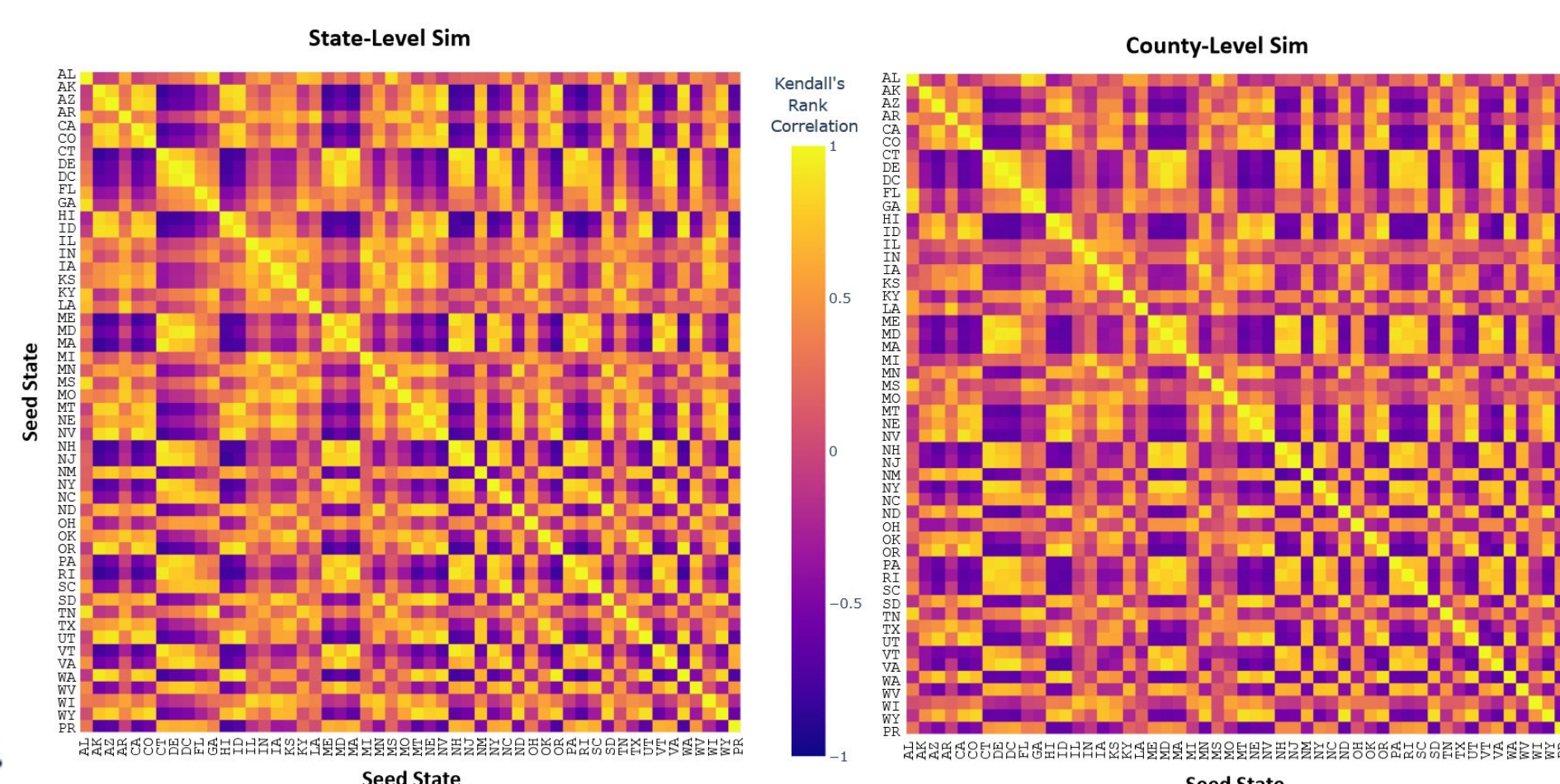


Figure #2

Results

Rank Correlations

- Patterns of rank correlations were almost identical between the state and county-level simulations
- When plotted against the distance between seed locations, τ generally decreases as distance increases
 - The plots are very similar between the 2 spatial resolutions
 - There are 2 less-dense right-shifted secondary curves visible

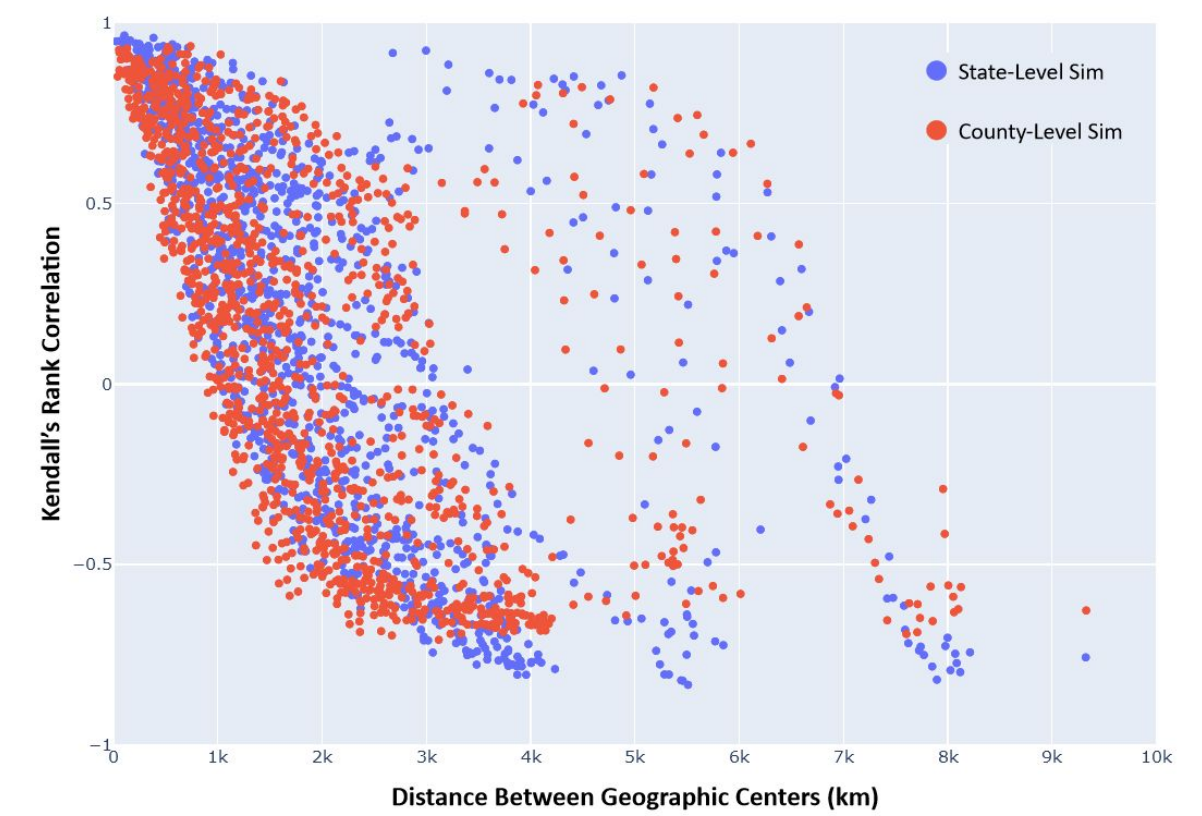


Figure #3

Order Probabilities

- When order preservation plotted against the distance between locations, there is little correlation distances and likelihood of order preservation
 - also shows 2 right-shifted secondary curves
 - Order preservation was measured as probability of the more probable order for each pair

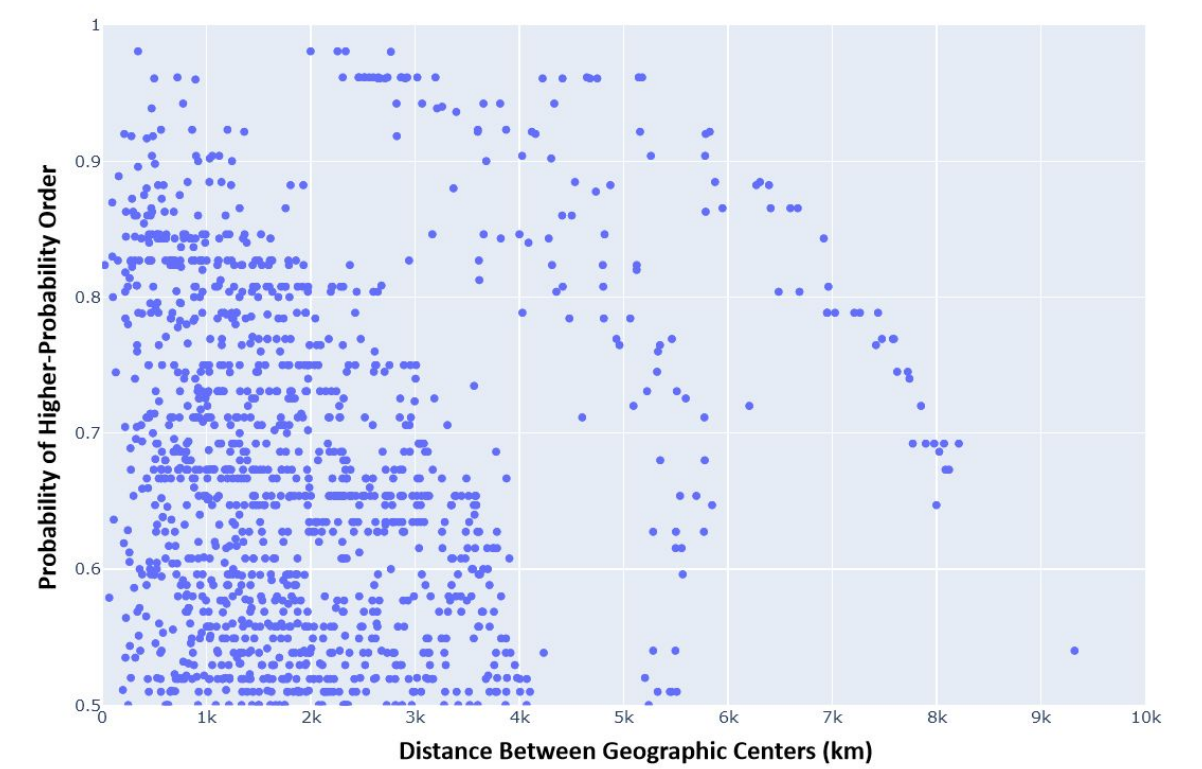


Figure #4

Likely Cascades

- Likely cascades vary significantly between the state and county level simulations
 - state level: most of the cascades were within the west US, and/or ended in Alaska or Hawaii
 - county level: cascades concentrated in clusters mostly within single states

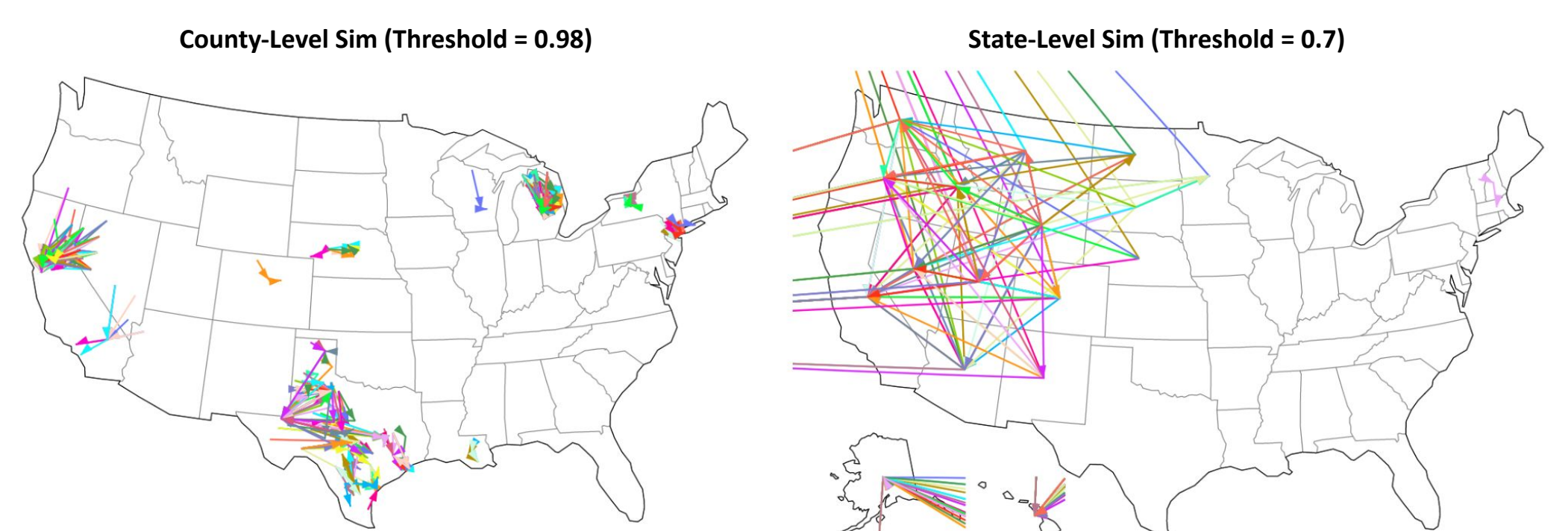


Figure #5

Future Directions

- Simulate using varying disease parameters and mobility network in addition to seed locations
- Use cascades to predict epidemic arrival times to locations given known infections
- Compare generated cascades to historical infection data
- Simulate using finer-resolution census tract-level network

References

- Venkatramanan S, Chen J, Fadikar A, Gupta S, Higdon D, Lewis B, Marathe M, Mortveit H, Vullikanti A. Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints. PLoS computational biology. 2019 Sep 16;15(9):e1007111.
- Kang, Y., Gao, S., Liang, Y. Li, M., Rao, J. and Kruse, J. Multiscale dynamic human mobility flow dataset in the U.S. during the COVID-19 epidemic. Scientific Data 7, 390 (2020).