Numerical Analysis of Discrete-time Networked Competitive Bivirus SIS Models

Authors: **Yifan Xu**, Sebin J. Gracy, Cesar A. Uribe

Presenter: **Yifan Xu** • Rice University

Motivation

- **Goal**: understanding virus spread using mathematical modeling and computational simulations.

Image from: https://www.freepik.com/premium-vector/epidemiology-pandemic-outbreak-research-concept_8169994.htm

Problem Statement

- **Goal**: understanding virus spread using mathematical modeling and computational simulations.

- Traditional focus on single-virus models
  - We focus on **competitive bivirus** processes in a population.

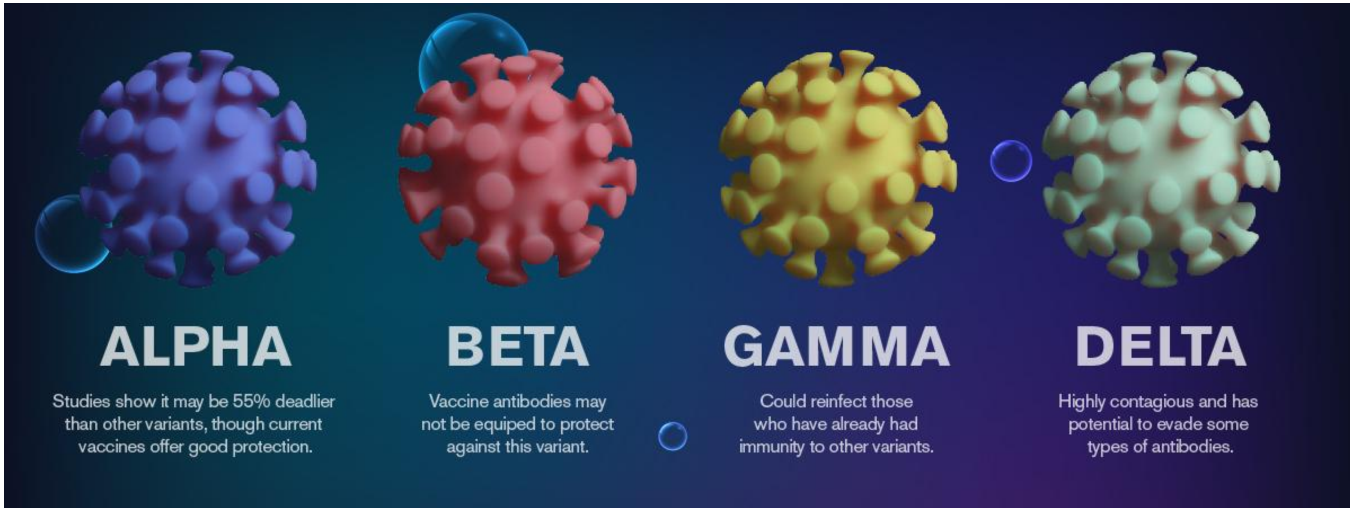
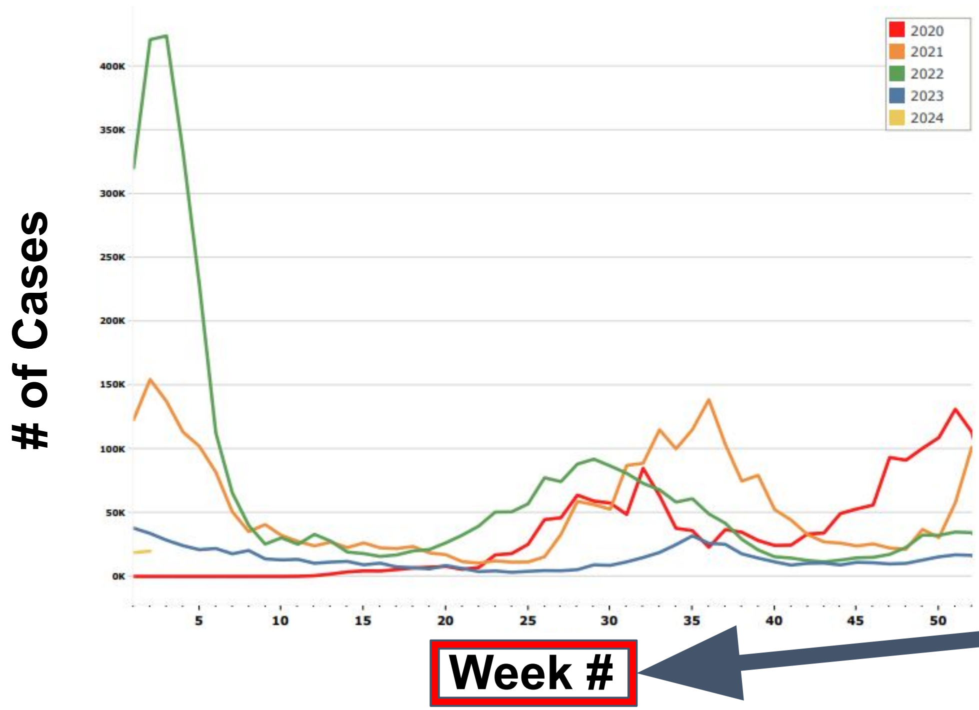


Image from: https://news.asu.edu/20210812-sars-cov-2-theme-and-variations

Problem Statement

- Traditional focus on continuous-time models
  - We highlight the **discrete-time** approach used to match real-world virus data collection.

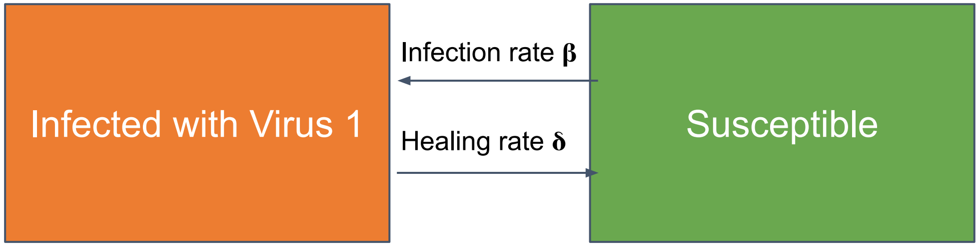


One data point per week

Image from: https://www.dshs.texas.gov/sites/default/files/IDCU/disease/COVID-19/2024/2024Wk02Jan18.pdf

SIS Framework - Individual Setting

- How will people behave when they recover?
- We adopt the susceptible-infected-susceptible model: Individuals become susceptible again after recovery.
- Infection and healing rates are properties measured from the virus itself.



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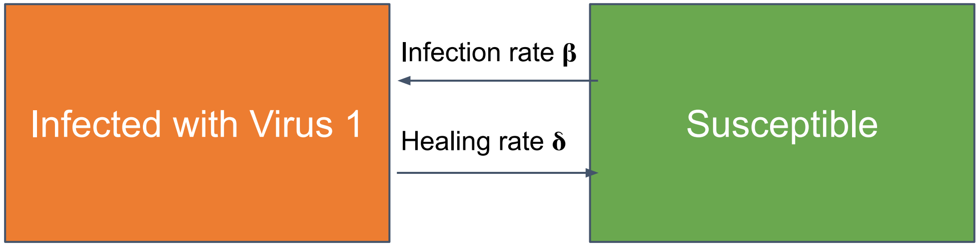
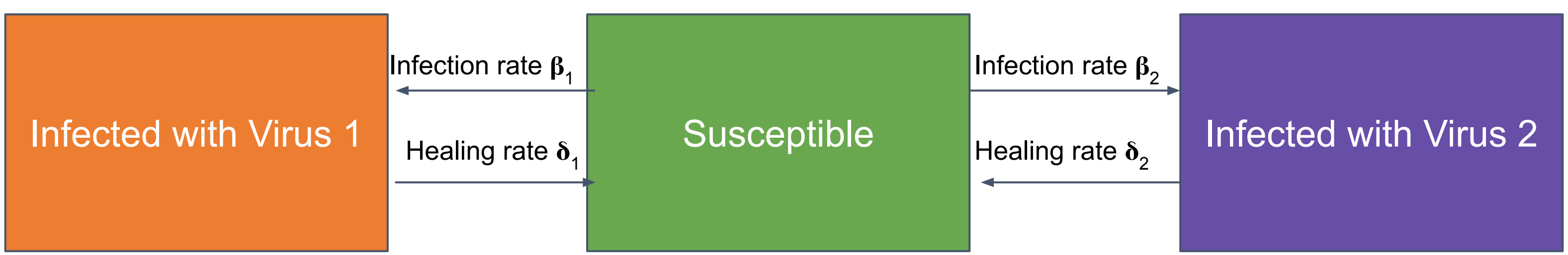


BUT…

SIS Framework - Individual Setting

- What if there are two (competitive) viruses involved?
- An individual can only be infected with **up to one** virus.
  - e.g., dengue virus VS zika virus
- Infection and healing rates **specific to virus**



SIS Framework - Network Setting

- **Node** represent the **group of people in cities**

- **Edges** represent **Strength of connectivity** between nodes

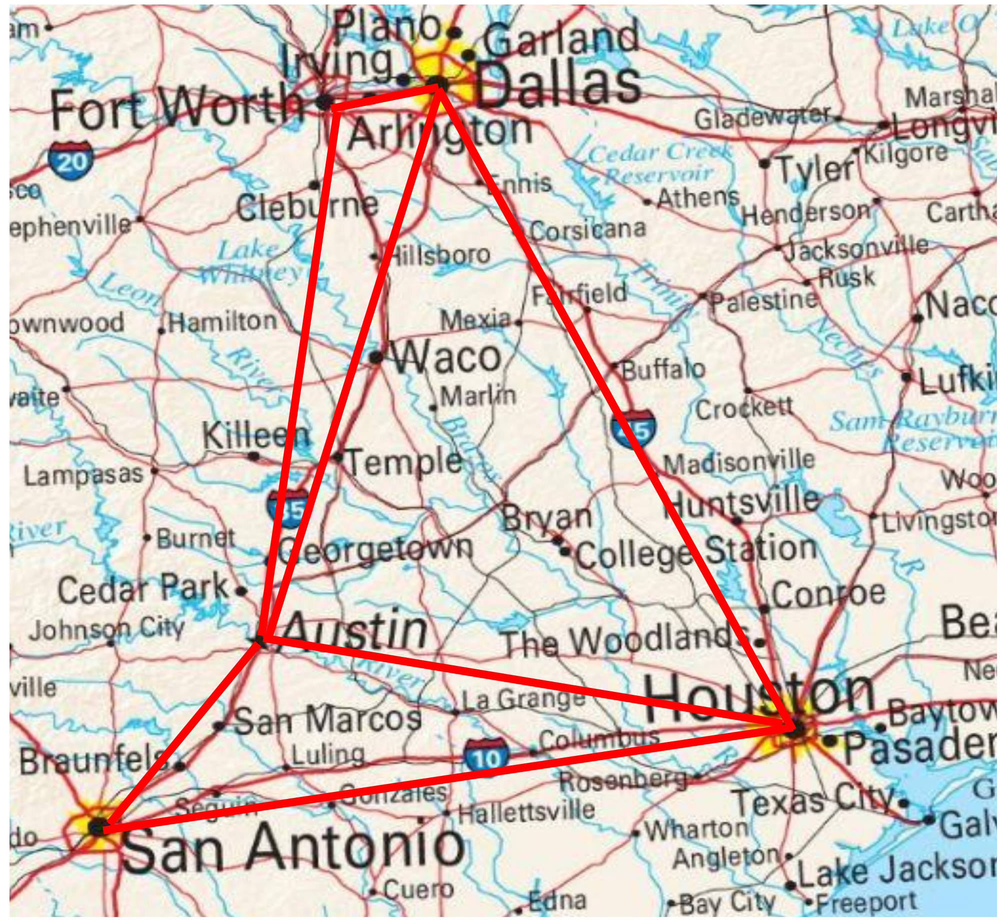
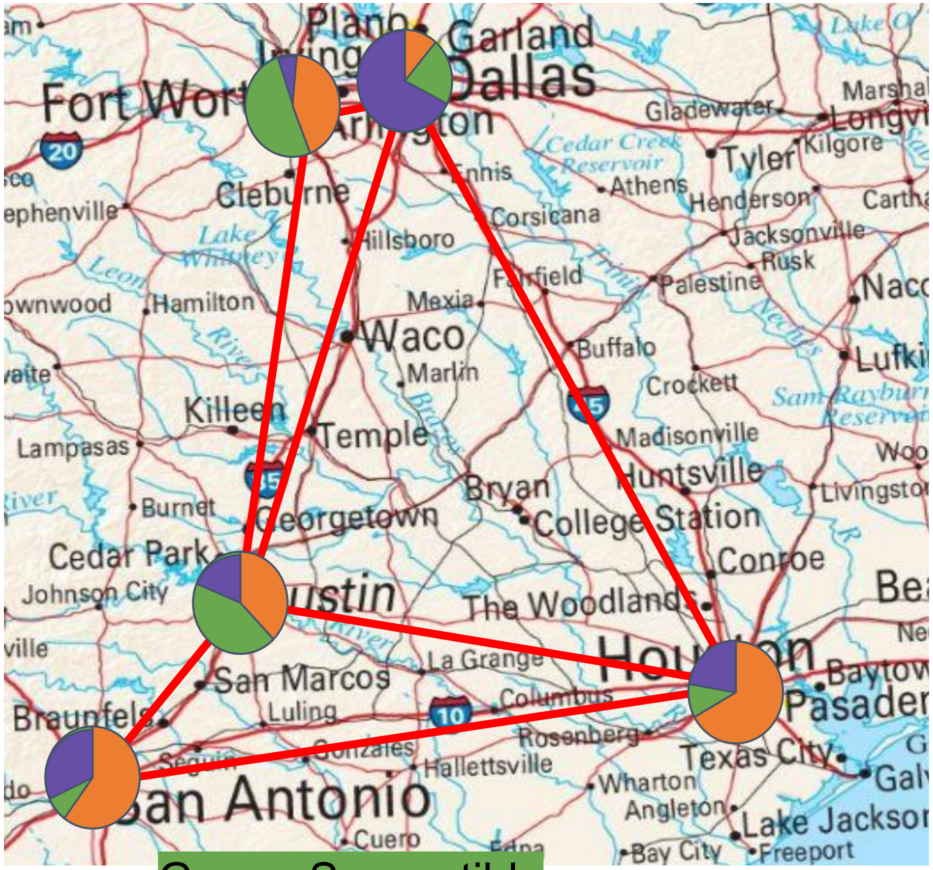


Image from: https://ontheworldmap.com/usa/state/texas/texas-highway-map.html

SIS Framework - Network Setting

- For each node (population), a **portion** is susceptible, the rest are infected

- Each portion of infected population will try to **'infect' its neighbors** in with **their respective virus** the next time-step!



Green: Susceptible
Orange: Infected with virus 1
Purple: Infected with virus 2

Image from: https://ontheworldmap.com/usa/state/texas/texas-highway-map.html

SIS Framework - Network Setting

Model Setup

The Single Virus case

- $\beta_{i,}\ \delta_i$ denote the infection and healing rates of node i, respectively
- The model captures $\boldsymbol{x}_i[t] \in [0, 1]$, the portion of the population that's infected at node i, at time t.

$$\underbrace{x_i[t+1]}_{\substack{\text{Infection}\\ \text{level at}\\ \text{time } t+1}} = \overbrace{x_i[t]}^{\substack{\text{Infection}\\ \text{level at}\\ \text{time } t}} + \underbrace{h}_{\substack{\text{Sampling}\\ \text{parameter}}}\left(\underbrace{(1 - x_i[t])}_{\substack{\text{\% of Susceptible}\\ \text{at time } t}} \left(\sum_{j=1}^{n} \underbrace{\beta_i}_{\substack{\text{Infection}\\ \text{Rate}}} \overbrace{a_{ij}}^{\substack{\text{Edge weight}\\ \text{between}\\ \text{node } i \text{ and } j}}\right) - \underbrace{\delta_i}_{\substack{\text{Recovery}\\ \text{Rate}}} \right) \underbrace{x_i[t]}_{\substack{\text{Infection}\\ \text{level at}\\ \text{time } t}}$$

The Competitive **Bi**virus case

- In the Bivirus case, we consider the portion infected with virus 1, 2 denoted $x_i^1[t]$, $x_i^2[t]$, respectively. β_i^1, δ_i^1, β_i^2, δ_i^2 defined similarly.

$$\begin{cases} x_i^1[t+1] = x_i^1[t] + h\left((1 - x_i^1[t] - x_i^2[t])(\sum_{j=1}^{n} \beta_i^1 a_{ij}) - \delta_i^1 \right) x_i^1[t] \\ x_i^2[t+1] = x_i^2[t] + h\left((1 - x_i^1[t] - x_i^2[t])(\sum_{j=1}^{n} \beta_i^2 a_{ij}) - \delta_i^2 \right) x_i^2[t] \end{cases}$$

Infection Rate of virus *1*

Infection level of virus *k* at time *t + 1*

Infection level of virus *k* at time *t*

Sampling parameter

% of Susceptible at time *t*

Edge weight between node *i* and *j*

Recovery Rate of virus *k*

Infection Rate of virus *2*

What happens “in the end”? (t $\rightarrow \infty$)

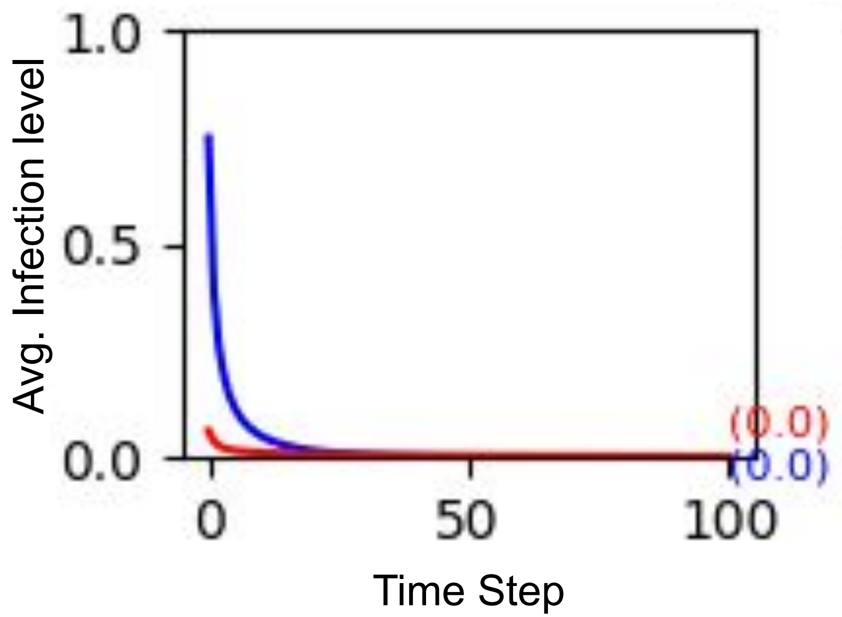
Image from: https://www.pngegg.com/en/search?q=question+mark

Theoretical Outcomes

- Three possible outcomes (equilibria):
  - Disease Free Equilibrium: $\rho(I - hD^k + hB^k) \leq 1$ for both viruses

spectral radius: largest absolute value among its eigenvalues

"Both viruses die"



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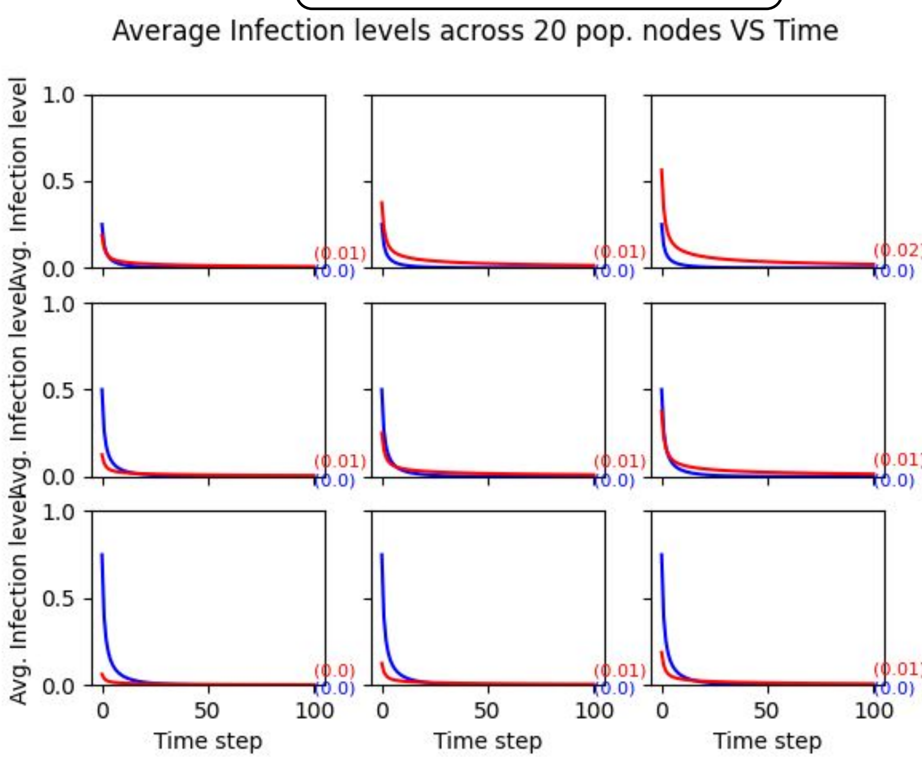
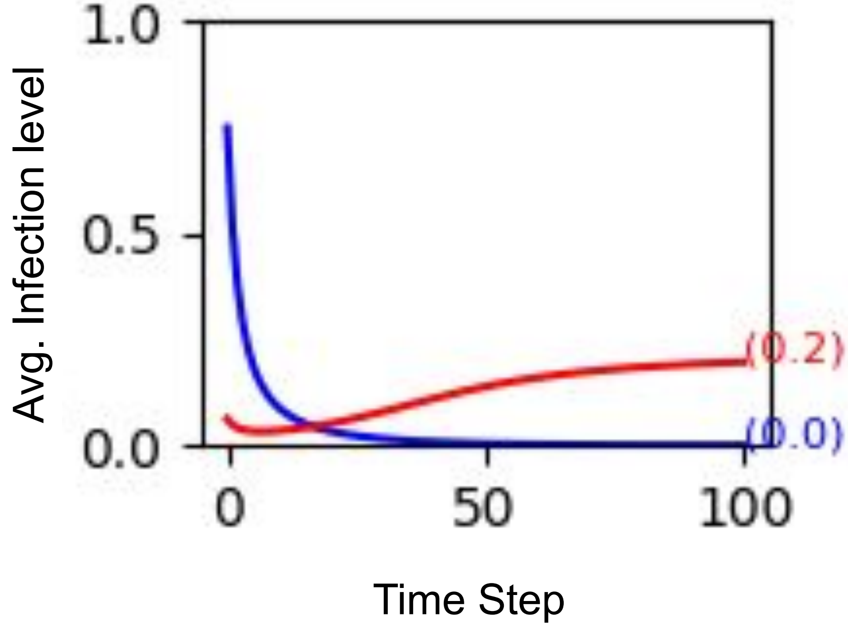


Theoretical Outcomes

- Three possible outcomes (equilibria):
  - Endemic Equilibrium: $\rho(I - hD^k + hB^k) > 1$ for dominant virus, $\rho(I - hD^k + hB^k) \leq 1$ for diminishing virus

"One virus survives, the other one dies."



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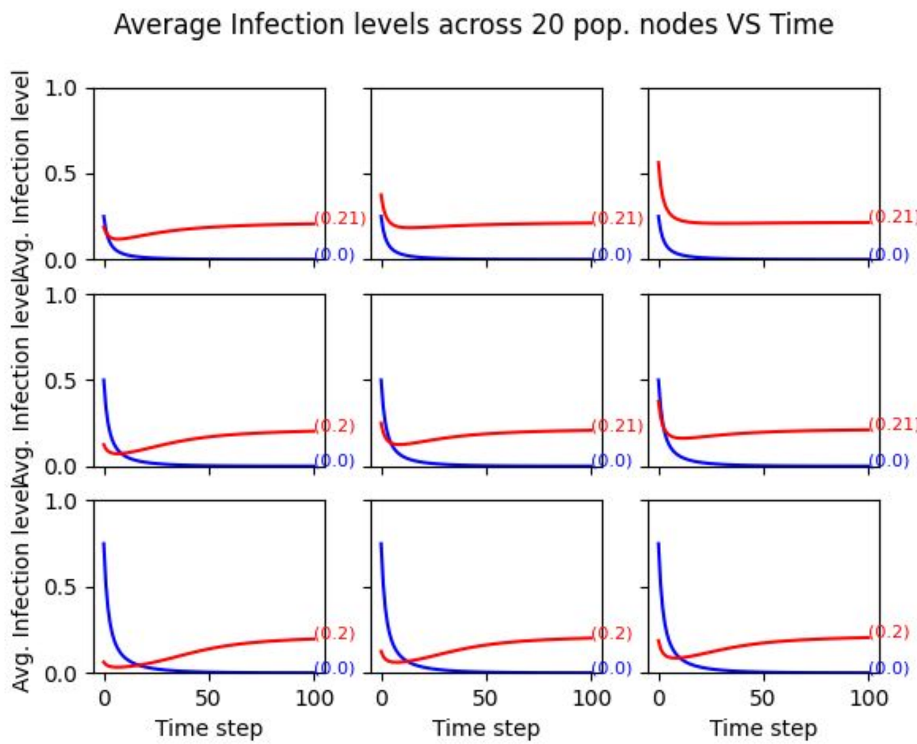
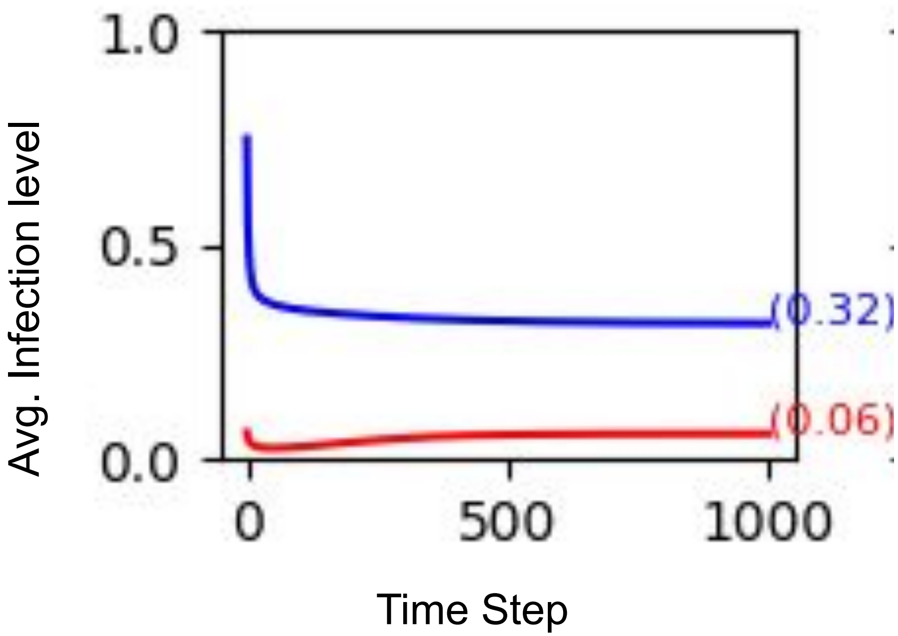


"One virus survives, the other one dies."

Theoretical Outcomes

- Three possible outcomes (equilibria):
    - Coexistence Equilibrium: $\rho(I - hD^k + hB^k) > 1$ for both viruses

"Both viruses survive"



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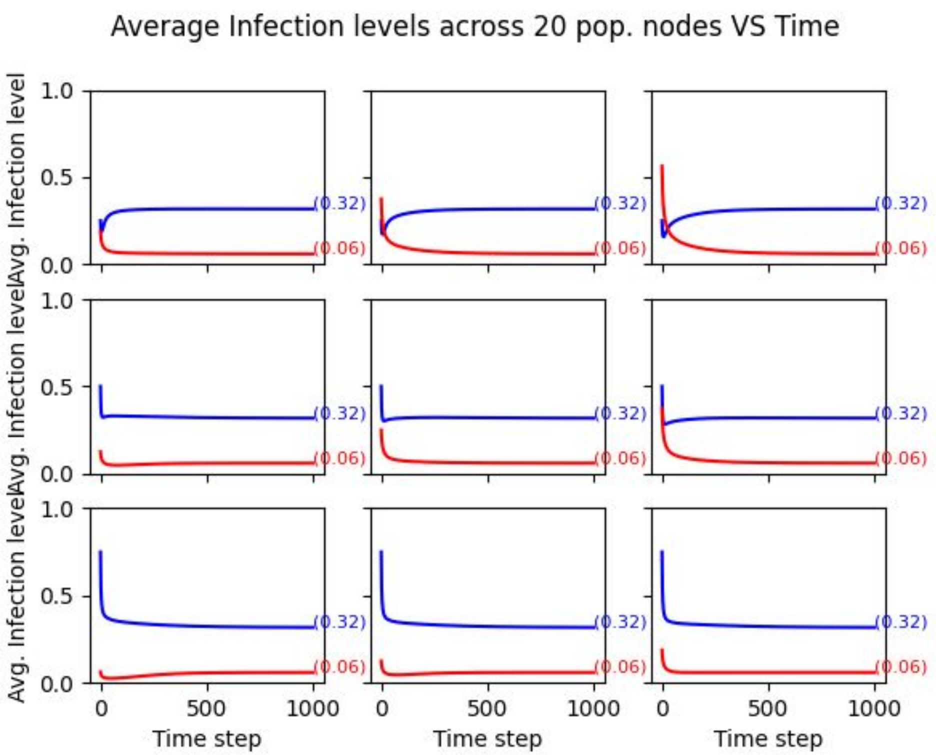

Real-world Simulations

Real-world Network Simulations

- Two real-world datasets were used

1. The Massachusetts County Travel Graph
2. The New York City Taxi Graph

Massachusetts County Travel Graph(Demo)

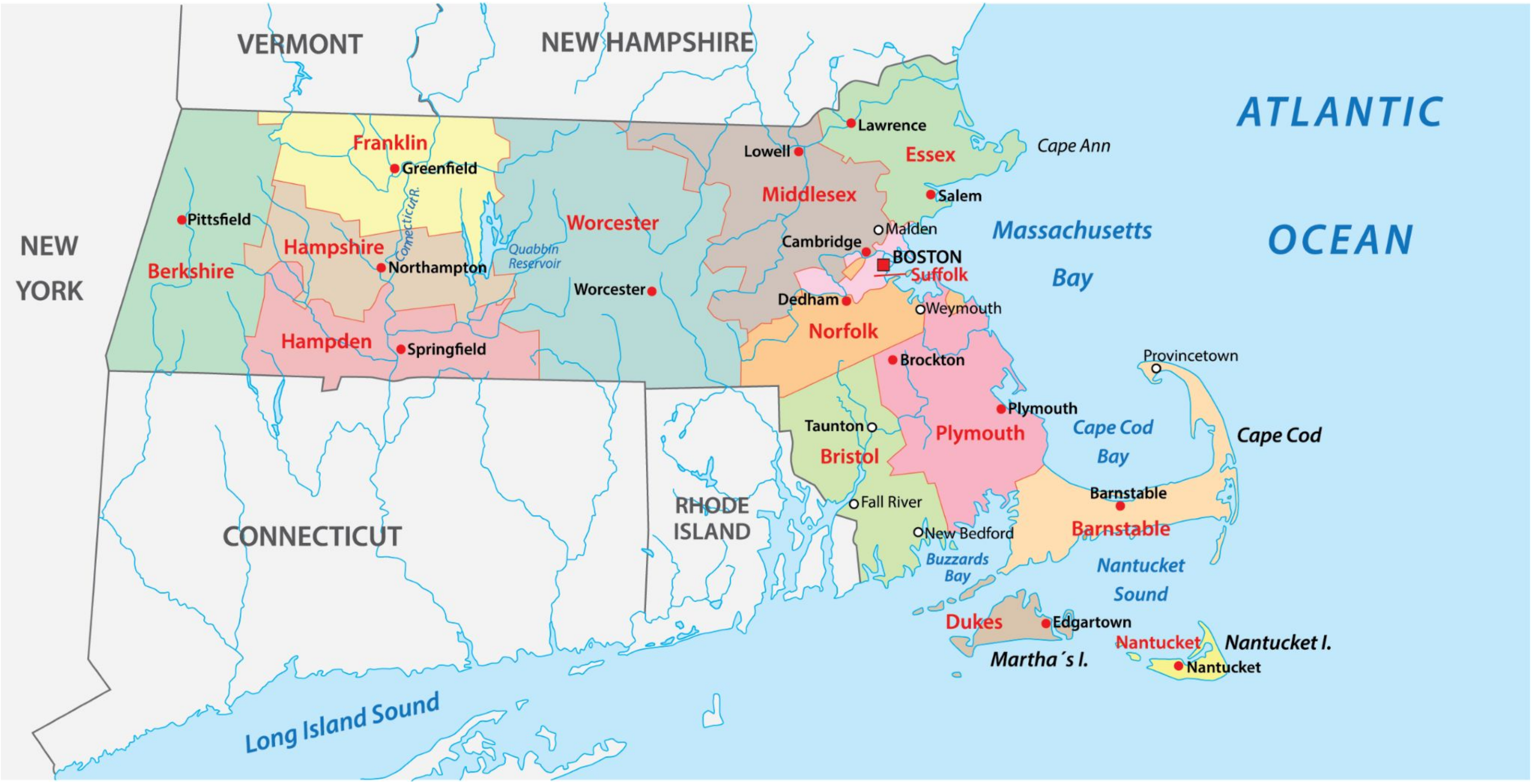

Image from: https://www.reddit.com/r/massachusetts/comments/171vp2h/if_the_massachusetts_counties_were_to_be_changed/

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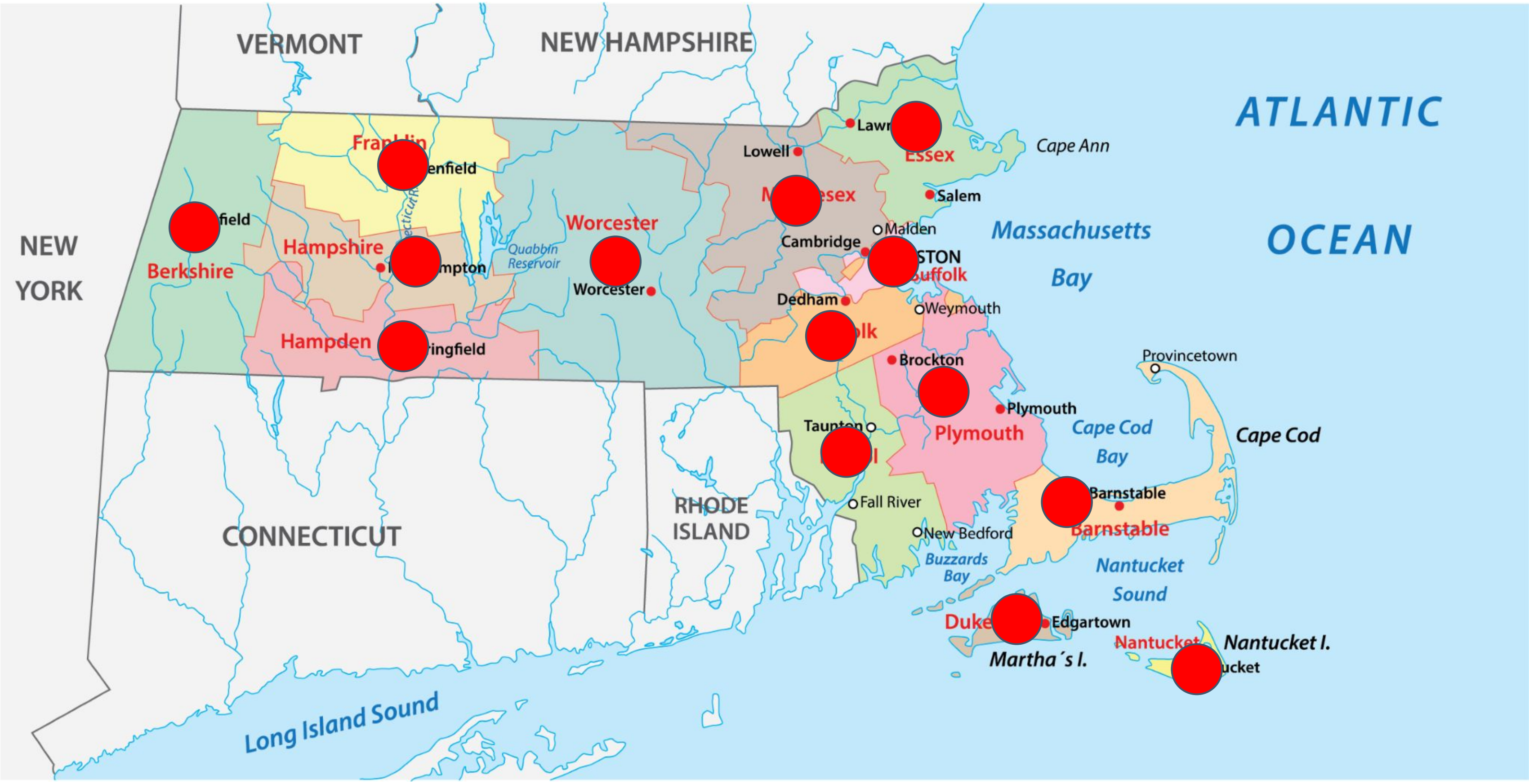

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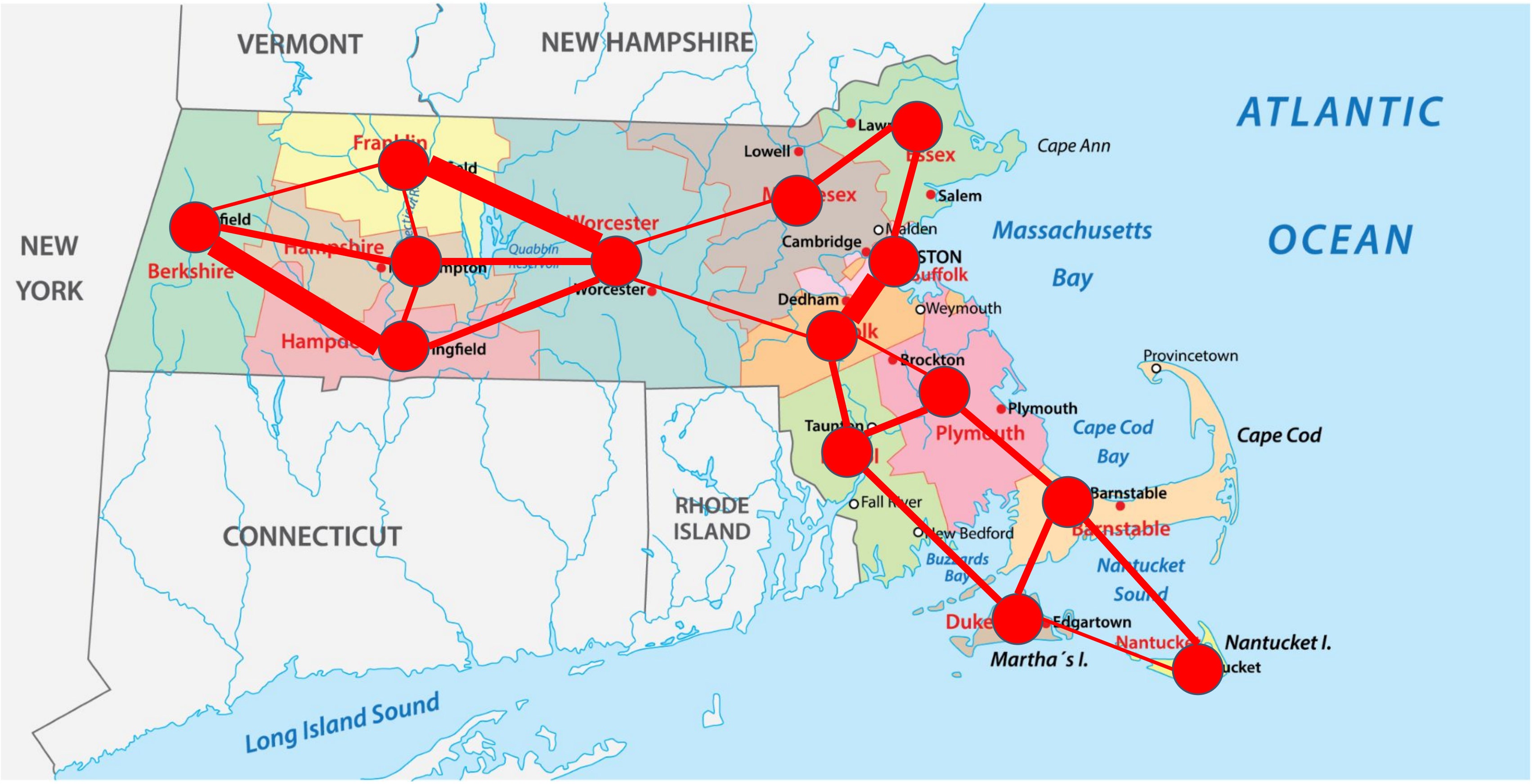

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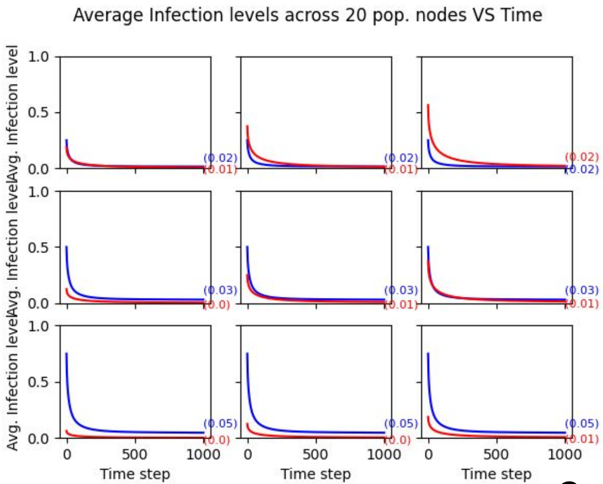
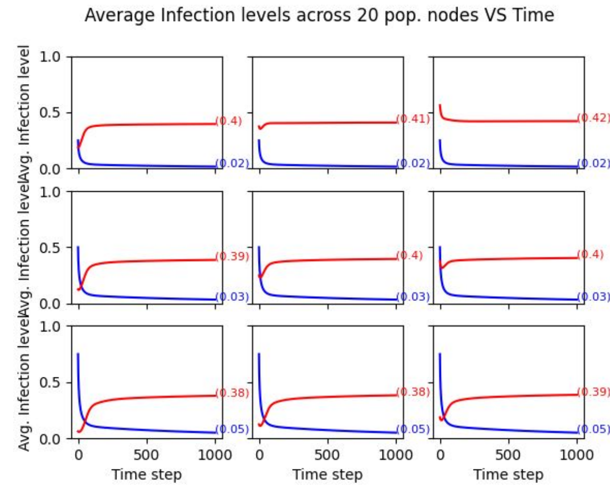
Massachusetts County Travel Graph

Disease-free Equilibrium



Endemic Equilibrium



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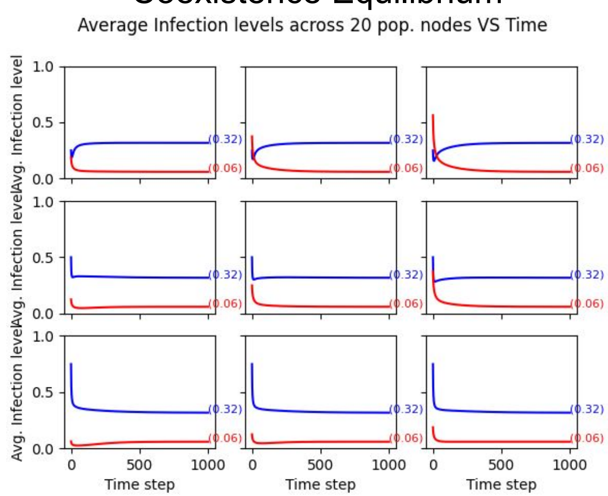

The New York City Taxi Graph(Partial)

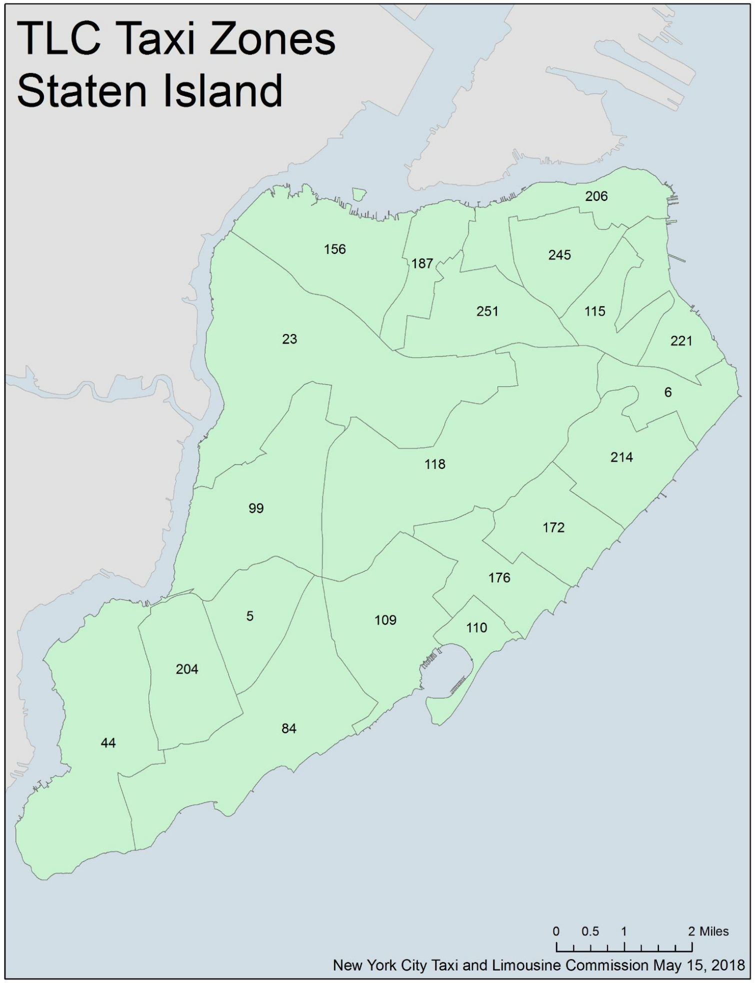

Image from: https://www.nyc.gov/site/tlc/about/tlc-trip-record-data.page

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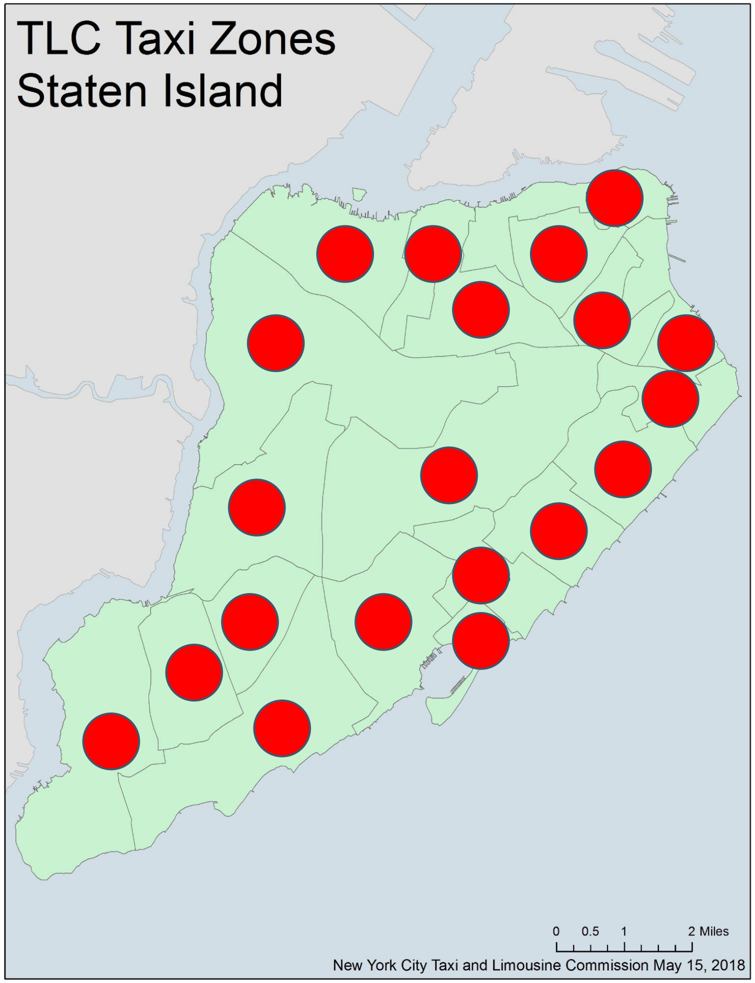

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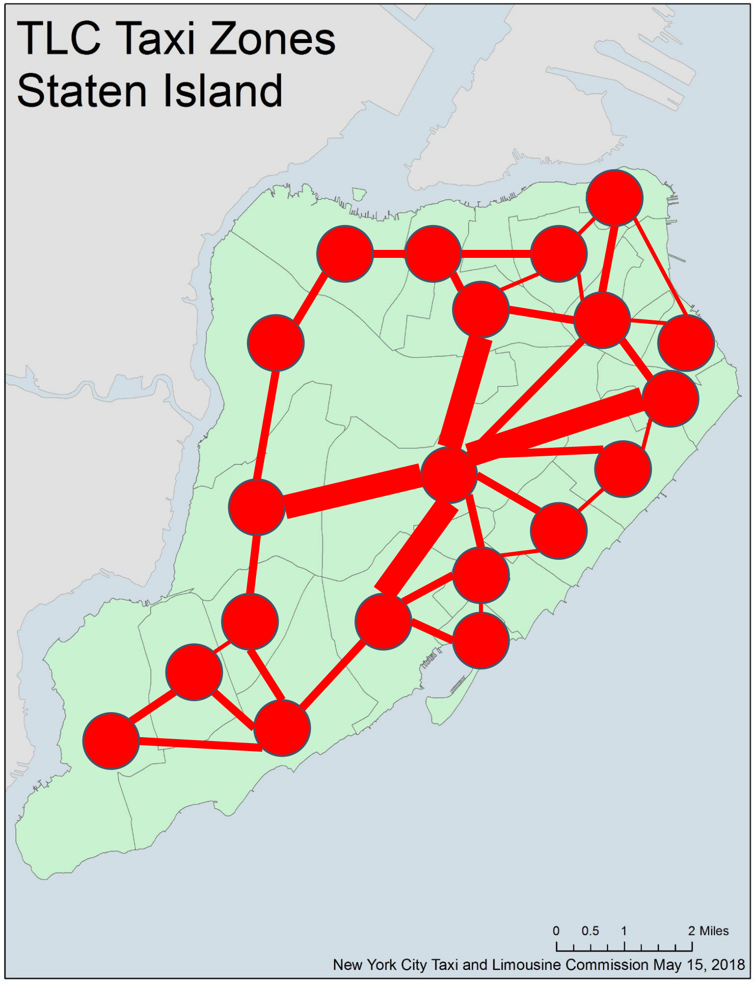

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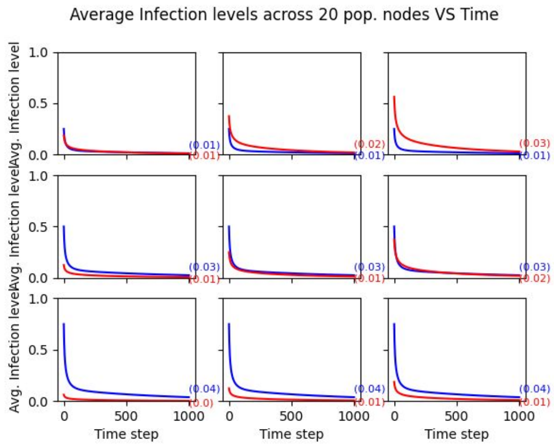

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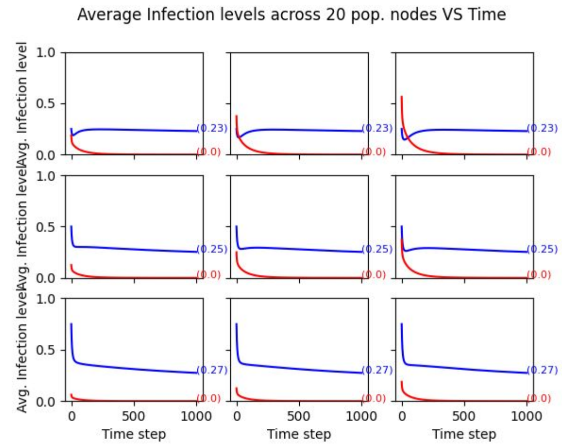

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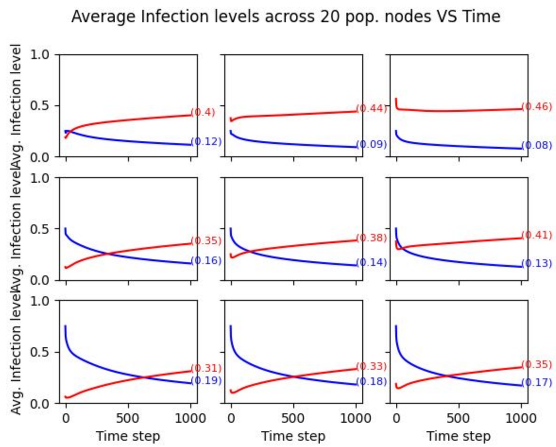

Conclusion & Future Work

- We verified the theoretical predictions regarding the various outcomes, under their respective conditions.

In the future, we can…

- Incorporate time-varying network dynamics for even **more realistic** predictions.

- Performing numerical simulations on larger, more complex datasets can yield **more convincing** results.

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