



# Mobility-Based SIR Model: Comparative Analysis of COVID-19 and Influenza



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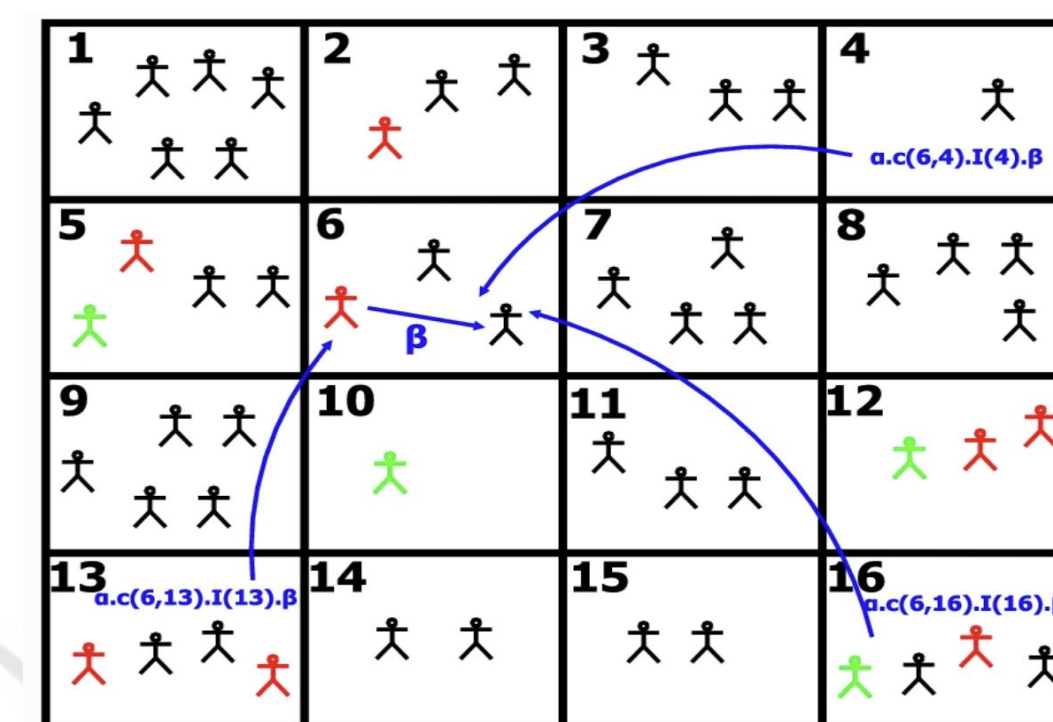
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## Introduction

- Our project aimed to create a mobility based SIR model to understand the impact of social connectivity and quarantining on disease spread.
- Helping to understand transmission of such diseases can help to be prepared for future pandemics or diseases.
- SIR and SIRD models are a common way of modeling disease spread by simply separating overall populations into groups.
- Basic SIR models typically assume a well mixed population and tend to lack accuracy in real-world scenarios.
- To model a more realistic spread of diseases in a population, different parameters were altered. These factors included mobility and connectivity between different groups within a population, mortality, and birth rates.
- Changing these parameters can provide a better understanding of certain diseases within a population and the impact of quarantining, especially in more socially connected locations over others.

## Proposed Methods

- Modify basic SIR model to include mobility parameter so that the population is split as shown in **Fig 1**.



**Fig. 1:** Visual representation of how the model includes social connectivity between locations

- Use model from Goel et. al (2021) as guide to our SIR implementation. Specifically following the mean-field equations for the dynamics of the pandemic (**Fig 2**).

$$\frac{dS_i(t)}{dt} = -\frac{\beta S_i(t) I_i(t)}{N_i(t)} - \frac{\alpha S_i(t) \sum_j c_{ij} \frac{I_j(t)}{N_j(t)} \beta}{N_i(t) + \sum_j c_{ij}}$$

$$\frac{dI_i(t)}{dt} = \frac{\beta S_i(t) I_i(t)}{N_i(t)} + \frac{\alpha S_i(t) \sum_j c_{ij} \frac{I_j(t)}{N_j(t)} \beta}{N_i(t) + \sum_j c_{ij}} - \frac{\mu I_i(t)}{N_i(t)}$$

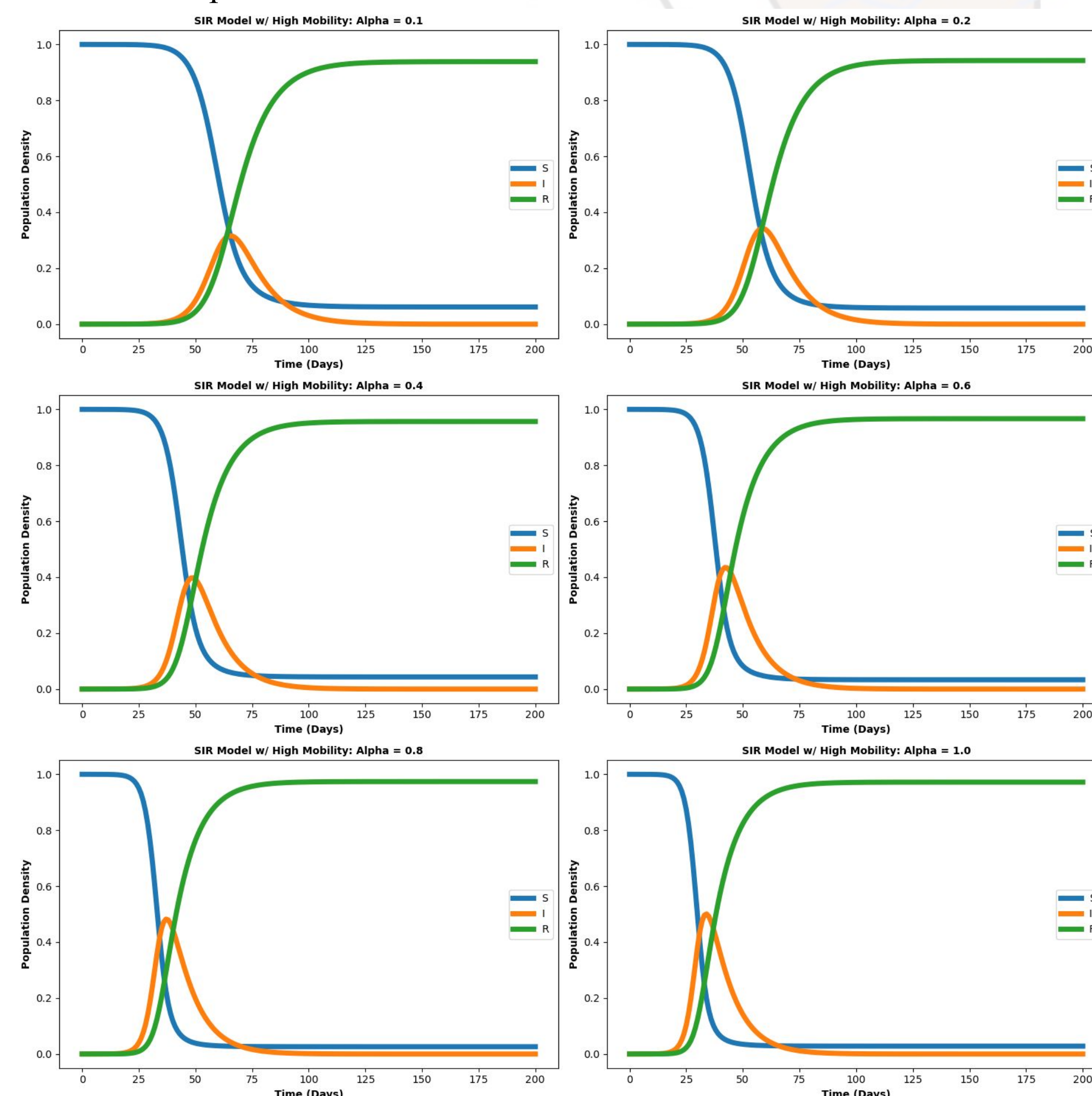
$$\frac{dR_i(t)}{dt} = \frac{\mu I_i(t)}{N_i(t)}$$

**Fig. 2:** Equations describing the SIR dynamics including social and outside connectivities

- Utilize object-oriented programming to implement mobility and connectivity between different regions of the grid.
- Simulate various mobility parameter values, dynamic mobility, and infection originating at various locations in the population: random, highly connected, lowly connected.
  - Initiating a pandemic randomly involves selecting a seed infection location arbitrarily.
  - Simulating a pandemic in a highly-connected location means the seed location is selected strategically to be a location which is strongly connected to other locations, implying highest mobility of individuals.
  - Simulating a pandemic in a lowly-connected location involves strategically selecting a seed location which is weakly connected to other locations, implying least mobility of individuals.
- Incorporate death rate of various infectious diseases into the model-SIRD and implement similar plots with varying parameters as those in the SIR model.
- Visualize the impact of both social and outside connectivity on infection rates, specifically on identifying when the maximum number of infections is reached.

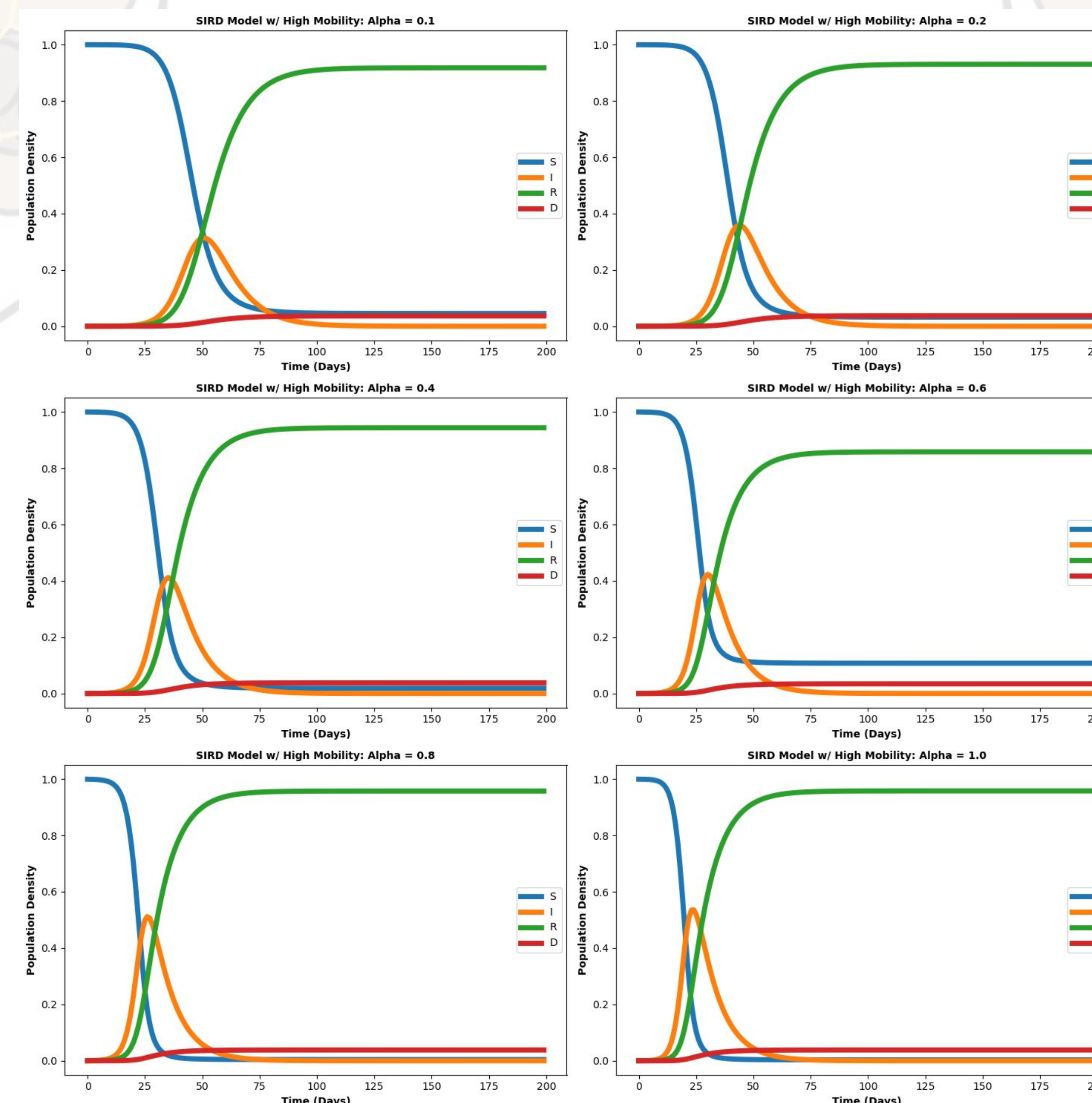
## Results

- All of these results show the value of quarantining and limiting in-person connections in terms of minimizing the peak number of infections
- The plots in **Fig 3** highlight how as alpha increases, the maximum number of infections increases and is reached in a shorter amount of time. Hence, alpha, or social connectivity within a locations plays an important role in disease spread.



**Fig. 3:** SIR plots over varying alpha (social connectivity) values

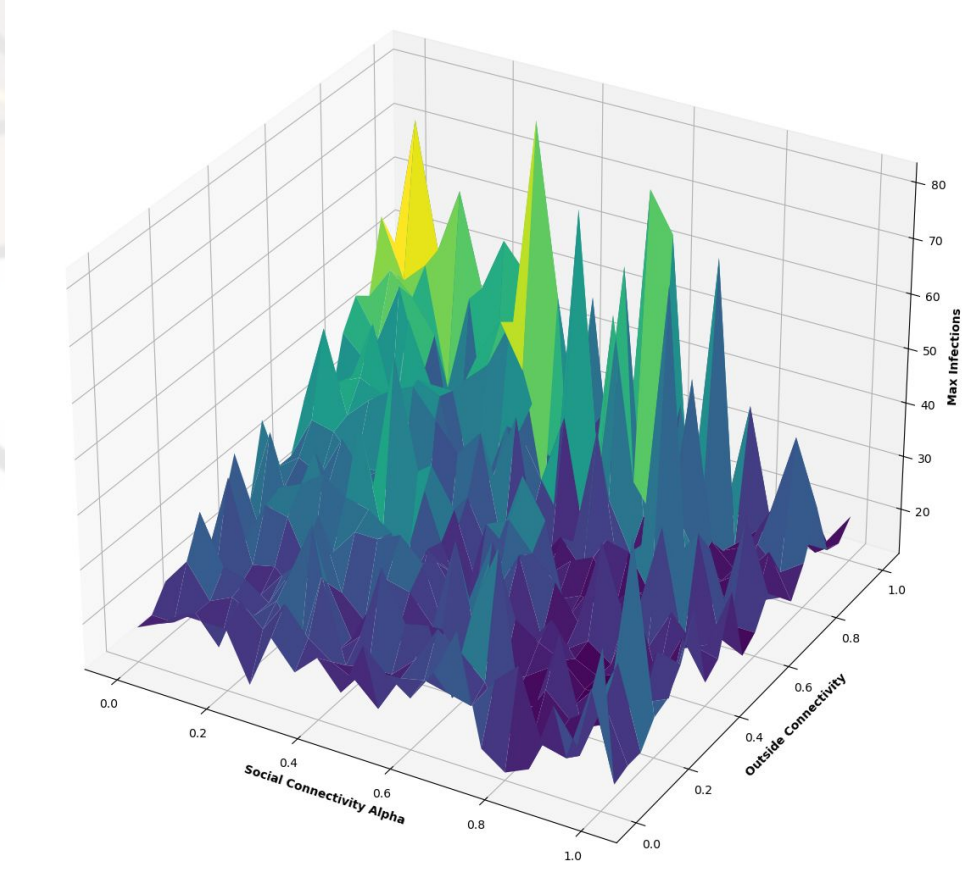
- Fig 4** includes a disease-related death rate, in this case to COVID-19, to create a SIRD model.
- The plots show similar results to the model without a death rate in terms of minimizing the peak number of infections.



**Fig. 4:** SIRD plots over varying alpha (social connectivity) values

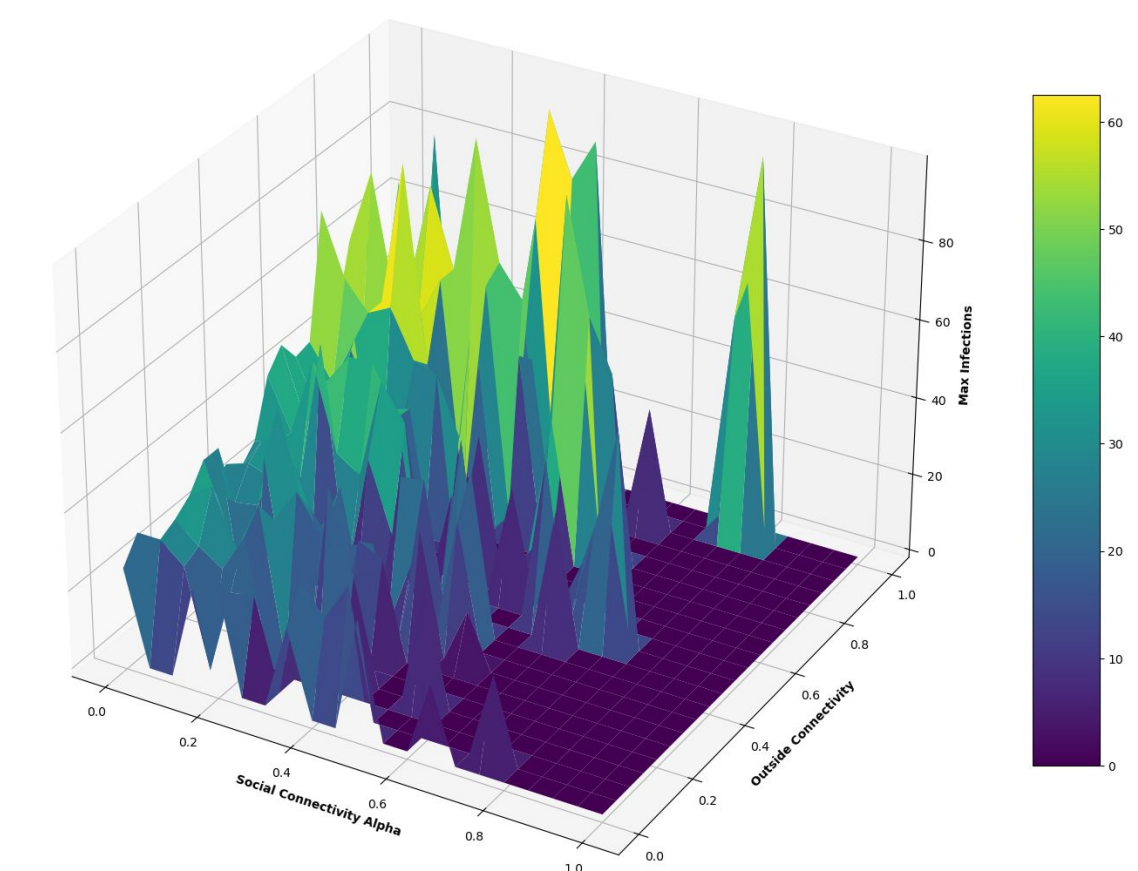
- Looking at the interaction between alpha and outside connectivity, it is evident that the number of days until maximum infection can be significantly delayed when reducing social connection while quarantining entire locations
- The models (**Fig 5** and **Fig 6**) were based on the birth rate (0.009), COVID death rate (0.004), and the general death rate (0.014) for Estonia.

Combining Alpha and Outside Connectivity



**Fig. 5:** A 3-D representation of days until maximum infections with varying alpha and outside connectivity based on the SIR model

Combining Alpha and Outside Connectivity



**Fig. 6:** A 3-D representation of days until maximum infections with varying alpha and outside connectivity based on the SIRD model

## Discussion and Future Steps

- Mobility restriction and quarantine do have a significant impact on infection spread.
- Based on the results we obtained, we observed that as alpha increases, the infections reach the peak in a shorter period of time. We also observed that infections grew at a higher pace when the seed location for the infection was chosen to be a highly connected locations.
- Future steps would include a more in depth analysis to understand the impact of different recovery, death, and infection rates on a connected population.