

A Monte-Carlo Epidemic Transmission Model

Hansen Xia

PHYS 25000 Computational Physics, University of Chicago

Background

- Monte Carlo Method:
- Repeated random sampling of a system for some macroscopically measurable quantity/observable
- Time evolution of the system depends only on current state (Miller 2024)
- Random Walk:
- A walk in a geometric space (e.g., 2D grid) where every step is independent from previous steps
- Random walks account for randomness of population movement (Sugaya et al. 2018)
- Epidemic dynamic is inherently random, so a general analytical solution does not make sense
- High relevance for public health and disease control measures

Methods

- Set up: 2D grid
- States: Infected, healthy, recovered, dead, vaccinated
- Age group statistically distributed among population
- Age group assigned infection risk factor
- Social distancing & Vaccination as weighting factors
- Loop through individuals, check distance (<5) for all susceptible individuals against infected ones
- Recovery: NOT dead AND recovery period reached
- Scale Invariance Assumed

Base setup parameters:

Grid: 100 * 100

Population: 1000

Step size: 1

Initial Infected: 10

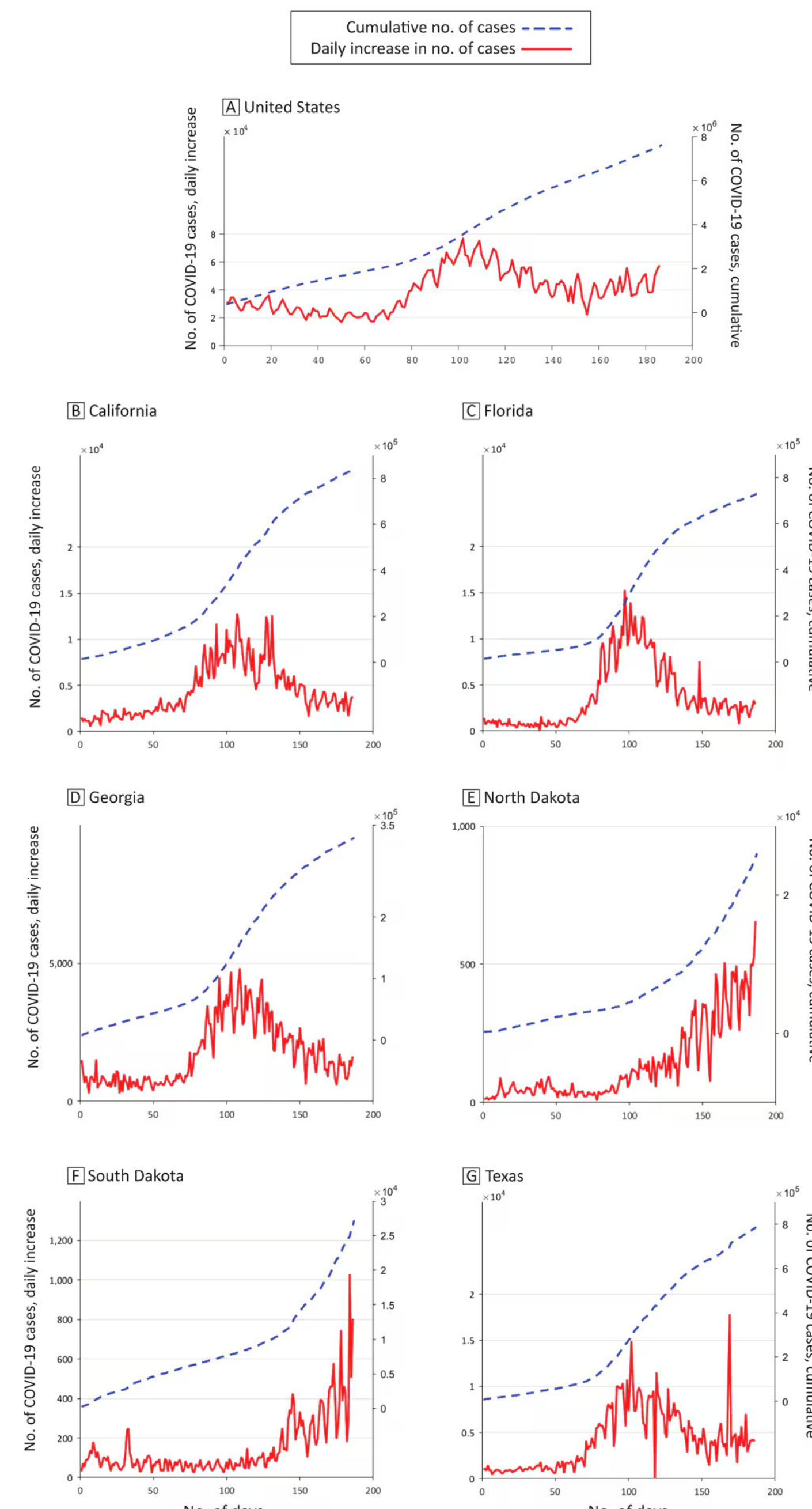
Recovery period: 14 (COVID)

Vaccine efficacy: 0.9

Time steps: 500

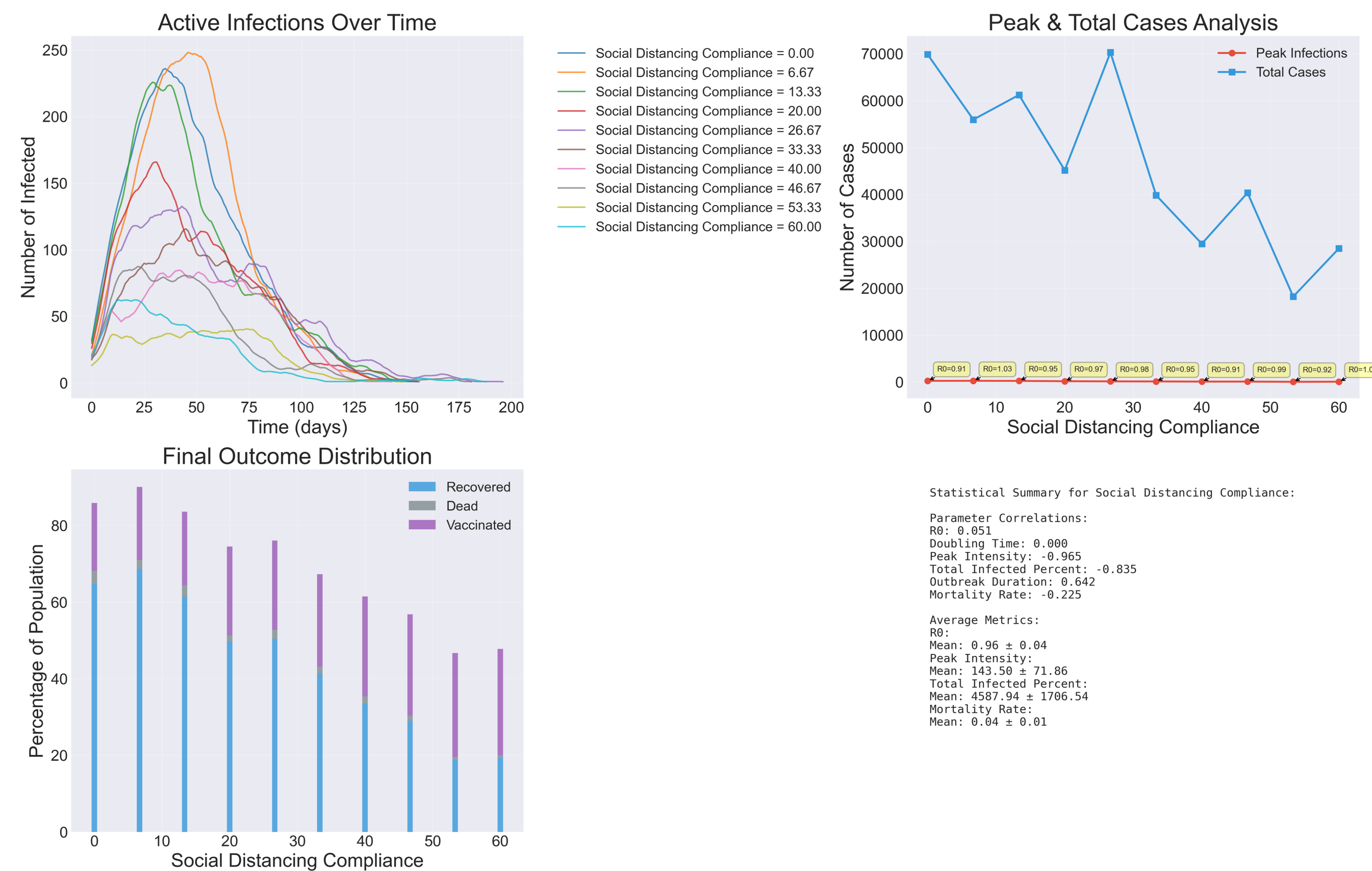
Objective

- Understand transmission dynamics from infection curves
- Varying key parameters (vaccination rate and social distancing) to test parameter sensitivity for infection curve
- Perform statistical evaluations for parameter sensitivity testing

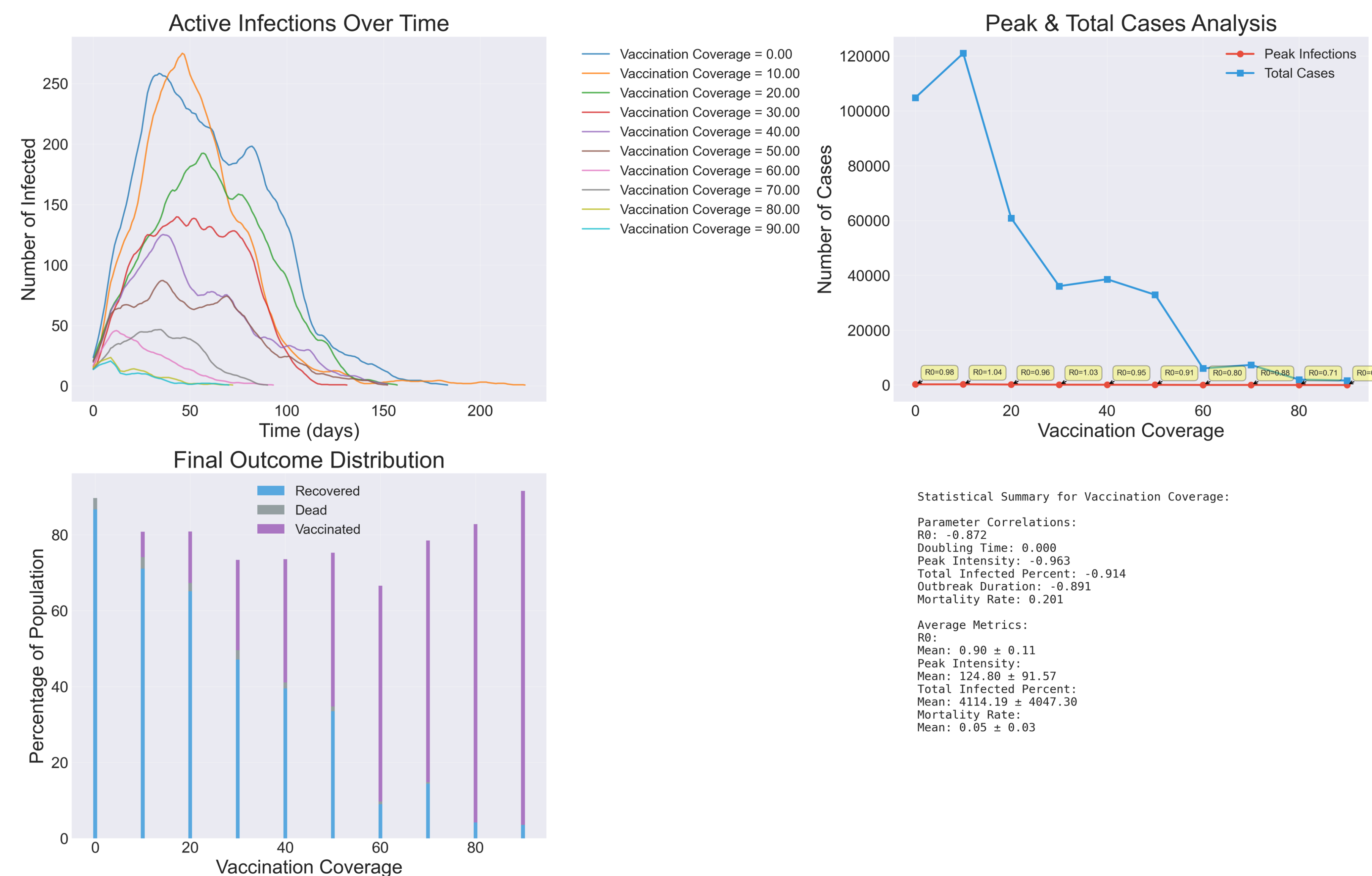


Results

Social Distancing Analysis



Vaccination Rate Analysis



Conclusion

- Effective vaccines (0.9 efficacy) decreases total infections substantially
- Social distancing has significant effect (less than vaccines)
- Further explorations:
- Parameter fitting (by fixing others)
- Larger scale to test scale invariance of observables (higher computing power needed)
- Time series analysis for longer time frames (macroscopic periodicity)
- Grid-wise regional infection time-evolution

Limitations

- does not account for non-local population flow & new variants & delayed transmission (airborne & contaminants)
- only useful for short term prediction; longer term may require time-series analysis
- assumes scale invariance (follows immediately by using random walks)
- only tracks ACTIVE infections

References

- Fang D, Guo L, Hughes MC, Tan J. Dynamic Patterns and Modeling of Early COVID-19 Transmission by Dynamic Mode Decomposition. *Prev Chronic Dis* 2023;20:2300089. DOI: <http://dx.doi.org/10.5888/pcd20.2300089>
- Miller, David, PHYS 250-Autumn2024-Lecture6.pdf, Department of Physics, UChicago, accessed Nov 2024
- Sugaya, S., Kenkre, V.M. Analysis of Transmission of Infection in Epidemics: Confined Random Walkers in Dimensions Higher Than One. *Bull Math Biol* 80, 3106–3126 (2018). <https://doi.org/10.1007/s11538-018-0507-2>