

# Simulating Human Behavior in Classic Epidemic Progression

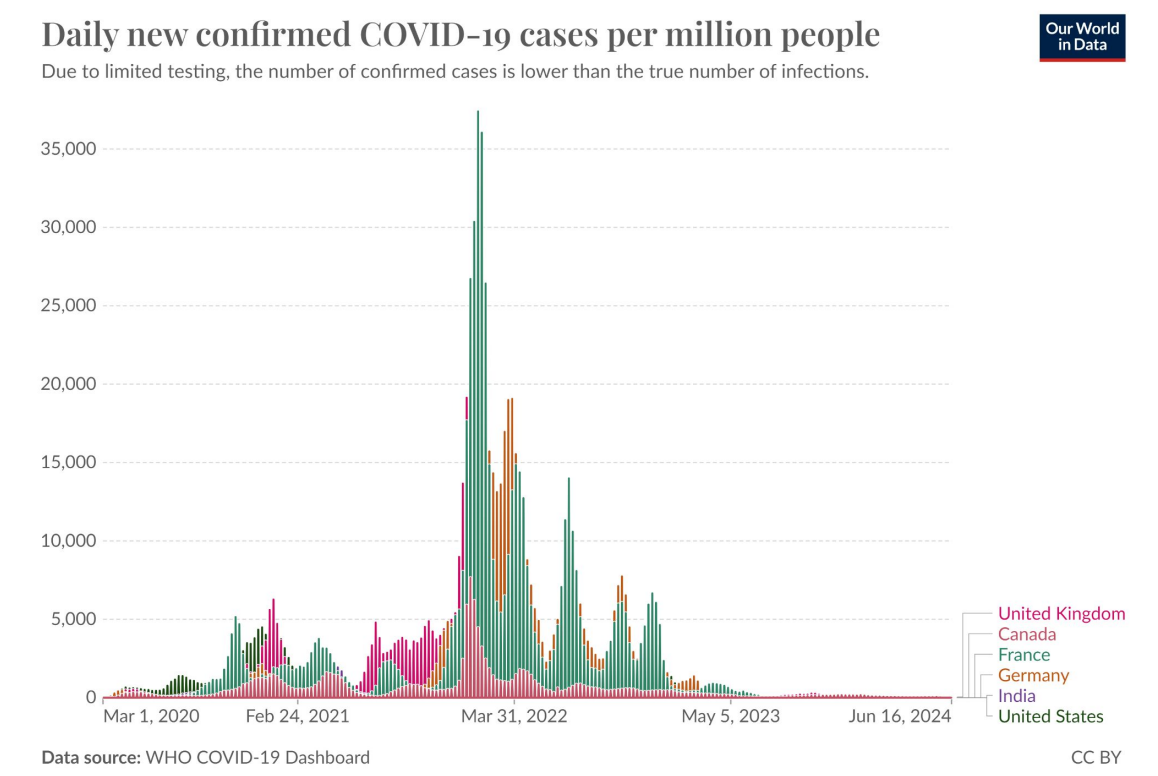
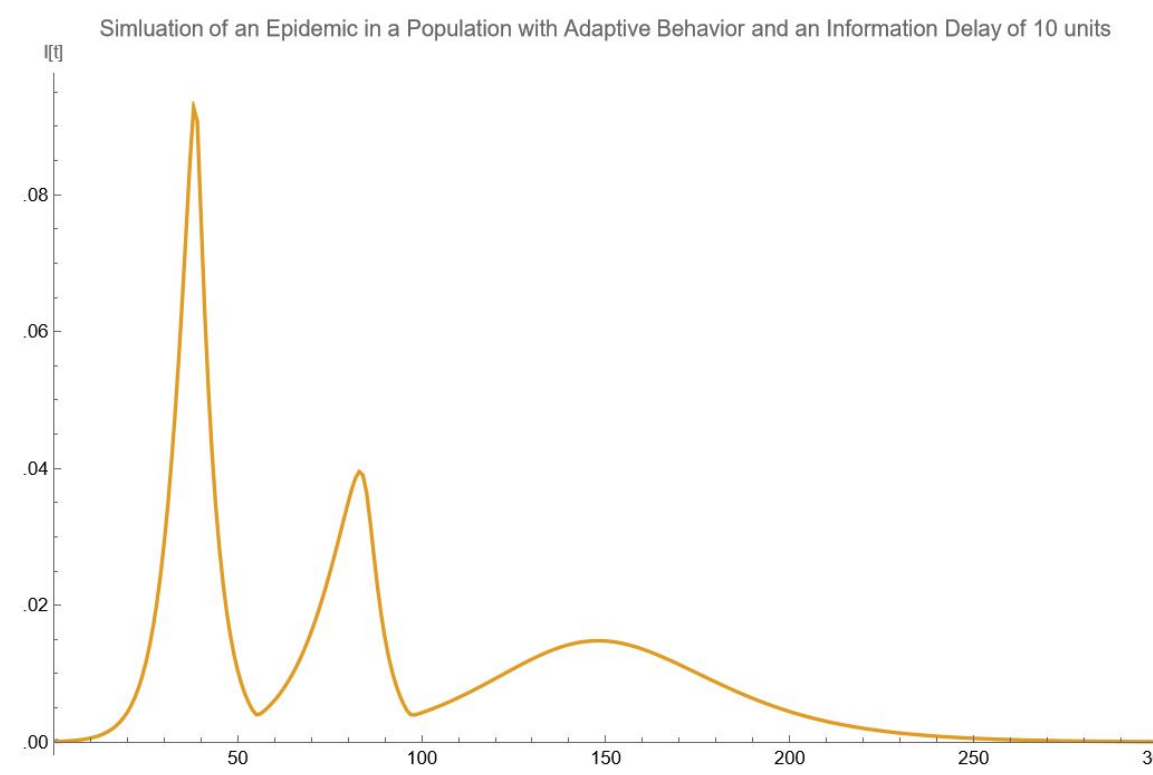
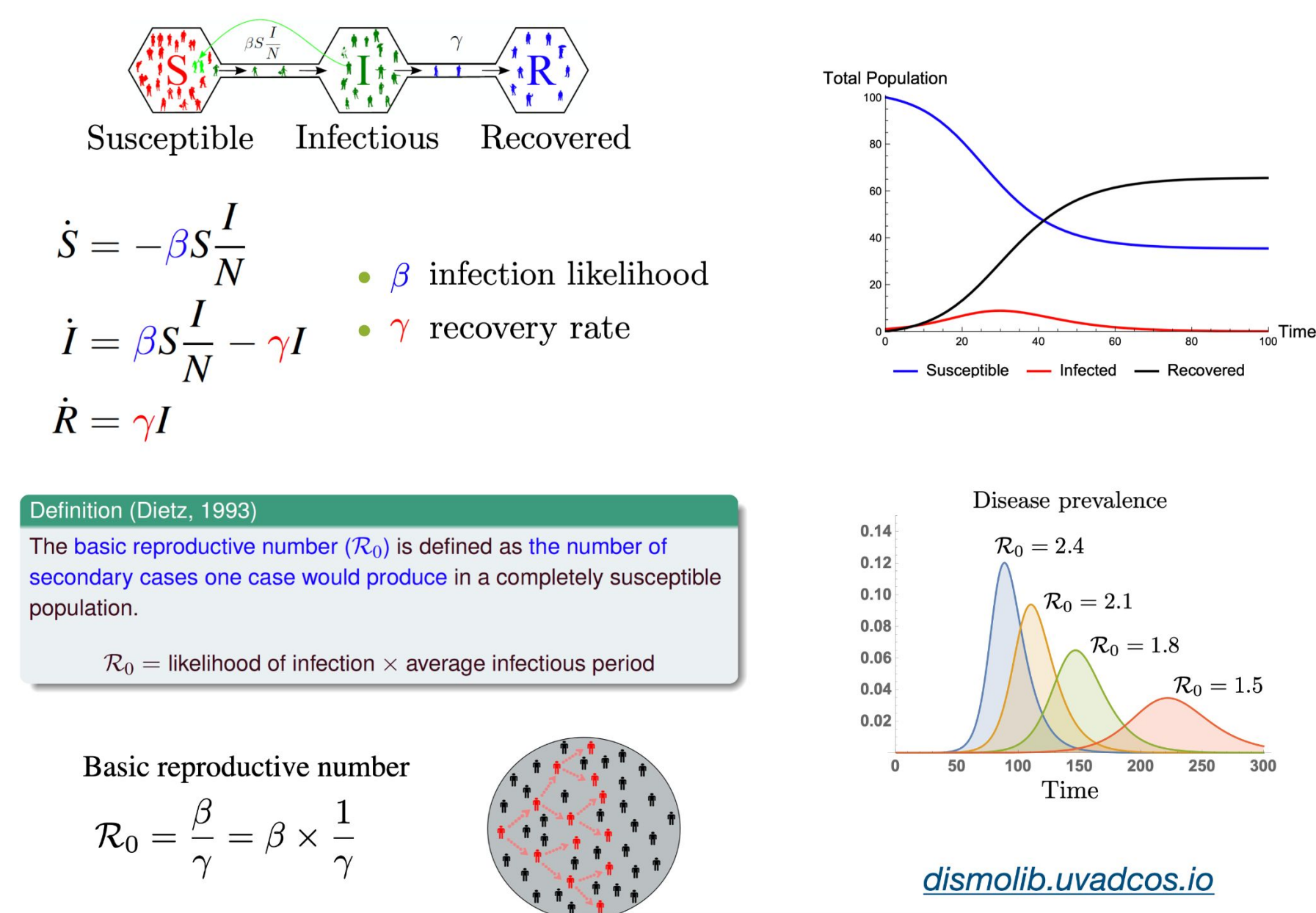
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## Introduction

The SIR model, developed by Kermack and McKendrick in 1927, is a fundamental epidemiological tool that divides a population into three compartments depending on individuals' health state: Susceptible (S), individuals at risk of infection; Infectious (I), individuals currently infected and capable of spreading the disease; and Recovered (R), individuals who have recovered and gained immunity. The model uses the transmission rate ( $\beta$ ) and the recovery rate ( $\gamma$ ) to describe how individuals move between these compartments, aiding in the prediction and management of disease outbreaks.

A key concept in this model is the basic reproductive number,  $R_0$ , which measures the average number of secondary infections from one infected individual in a fully susceptible population. If  $R_0$  is above 1, the disease can spread; if below 1, it will likely die out.  $R_0$  depends on the infectious period, transmission mode, and contact rate. However,  $R_0$  is not an accurate measure of the reproductive rate over time, as it ignores changes in individual behavior as the disease progresses through a population. Therefore,  $R_0$  is most effective in describing the disease's potential spread in its early stages.

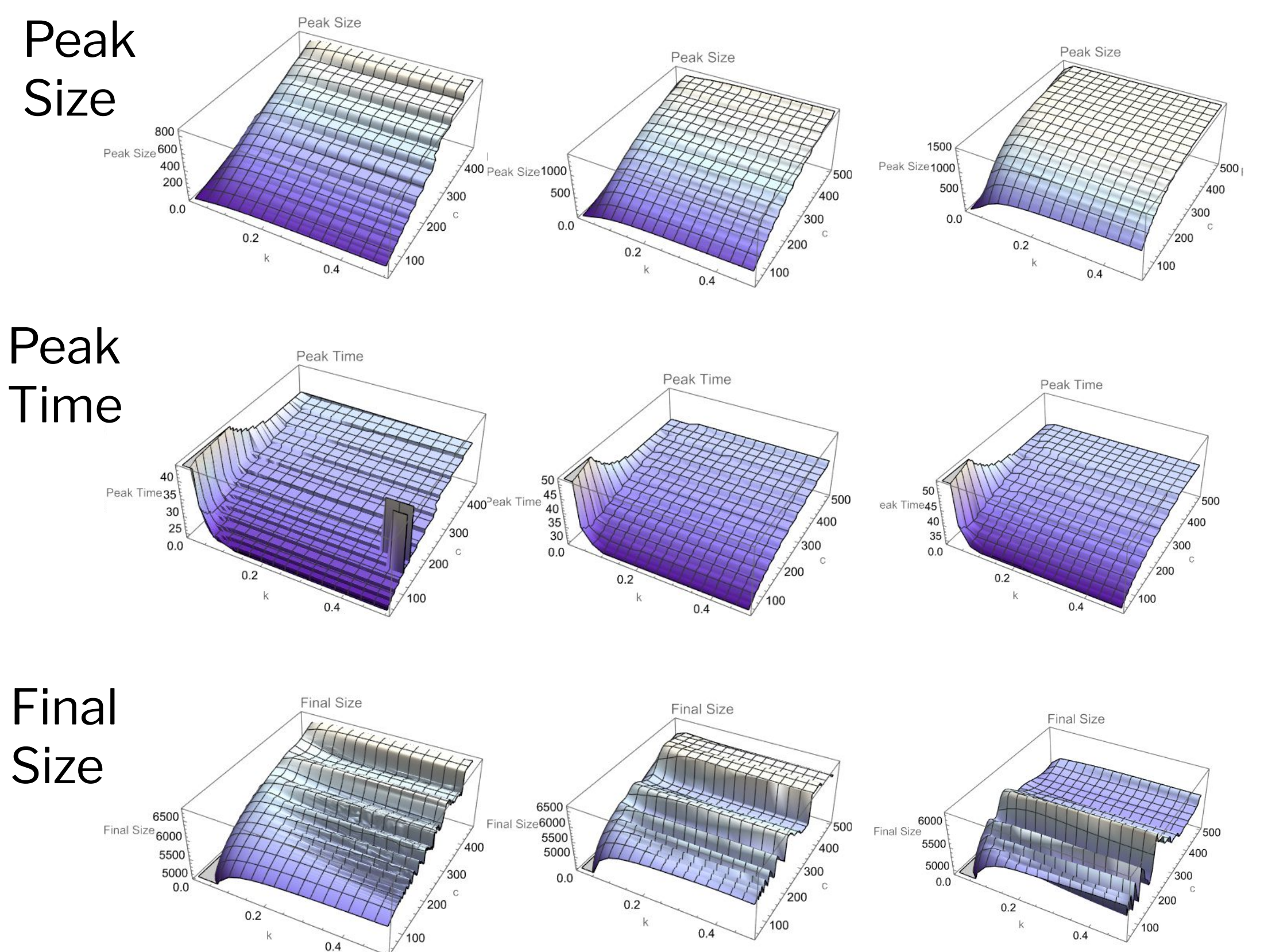
### Kermack-McKendrick Model (SIR model)



## Results

These graphs provide insights into why different countries or populations may experience similar epidemic developments despite having vastly different media, public policies, and attitudes. This phenomenon is illustrated by observing how varying combinations of response stringency ( $k$ ) and trigger threshold ( $c$ ) values can lead to equivalent peak sizes, peak times, and final epidemic sizes. Additionally, across different time delays (or information delays), similar epidemic development can be observed, resulting in comparable peak sizes, peak times, and final sizes. This can better help explain why different populations, with different policies, attitudes, and media, experience similar epidemic dynamics.

### Time Delay 5 | Time Delay 10 | Time Delay 15



## Methods

To simulate adaptive behavior in this mathematical model, a logistic sigmoid function was used as a scalar that varied based on the number of infectious individuals. The effect of behavioral responses characterized by the response stringency ( $k$ ) and trigger threshold ( $c$ ) on peak size, peak time, and the final size of the epidemic. To enhance realism, a time delay was introduced by subtracting a constant delay in  $i[t]$  to simulate an information delay, where the population is aware of the infected count at time  $t - \text{delay}$ . The effects were studied using specific time delays of 5, 10, and 15 units. Variations of  $k$  and  $c$  were plotted against peak size, peak time, and final epidemic size to observe the impacts.

## Future Work

Train a machine learning model using the data collected in this research which attempts to use the graph of the oscillating epidemic and attempts to predict the behavioral function

### References

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