

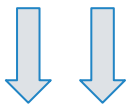
Disease Modelling with ABMs



By William Chettleburgh, Jared Bloch, Matei Gheorghiu, Cong Fu

Introduction & Questions

- ▷ Due to the spread of COVID-19, it has become increasingly important to determine methods of modelling the spread of disease



- ▷ Informed public policy decisions can be made.

SIR Model: A compartmental model using a system of differential equations to determine the changes in the number of susceptible, infected, and recovered individuals over time.

Limitations:

- ▷ Assume the population is large enough to treat all interactions as continuous rather than discrete
- ▷ Assume rates are proportional to current population sizes (when in reality, proportion of recovering people is proportional to the number of infected people a few days/weeks ago)

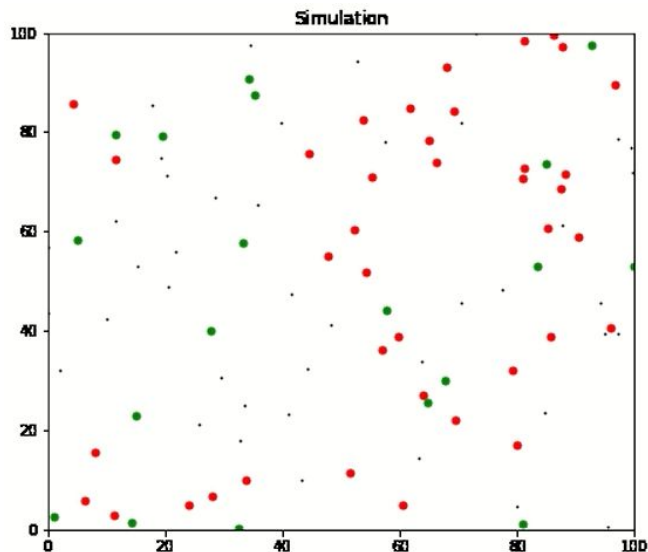
▷ Questions:

- How do the number of people who are susceptible, infected, and recovered change over time?

- How do the values of the parameters and the assumptions made affect the course of the disease?

- How does the model change if we allow agents to re-catch the disease or agents have a chance of dying?
- ~~How does the model compare to the SIR model?~~

Packages Used



Example visualization using Matplotlib

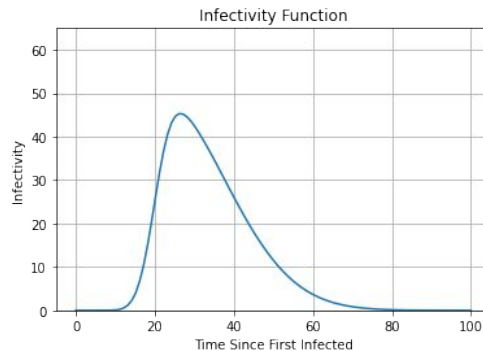
Package and Tool:

- ▷ Matplotlib : *Used for making scatter and line plots (as well as GridSpec for customizing the subplots)*
- ▷ Numpy: *Used for storing locations and calculating distances*
- ▷ IPython.display: *Used for creating the animation*
- ▷ Sympy: *Used for symbolic mathematics (for writing the different mathematical functions used in the model)*
- ▷ Scipy: *Provides functions used in the formula for a skewed normal distribution and for the generation of truncated normal distributions*

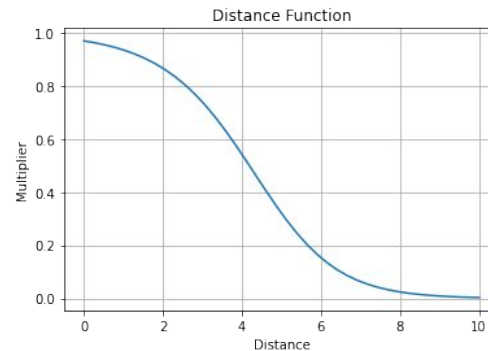
Methodology

- ▷ Use agents to represent individual people who are either susceptible, infected, or recovered
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- ▷ Each agent has an “exposure level” which determines how likely they are to catch the disease - this increases when they are near infected agents
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- ▷ To calculate how much the exposure increases, the following functions are used:

$\Delta\text{Exposure} =$

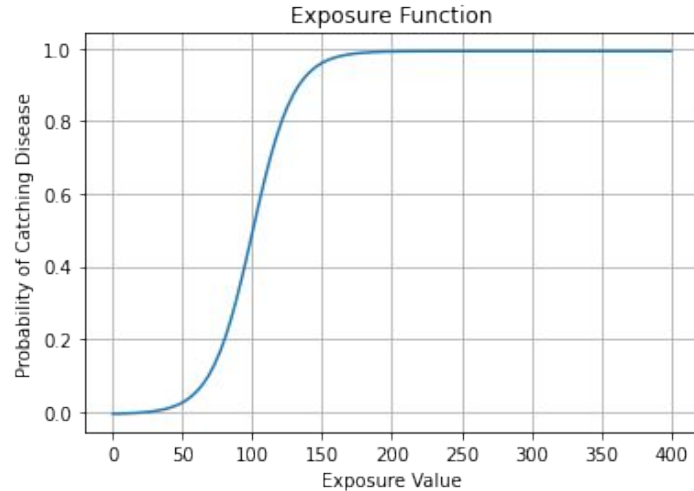


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Methodology

- ▷ To determine the probability of catching the disease, we use the exposure function show below:

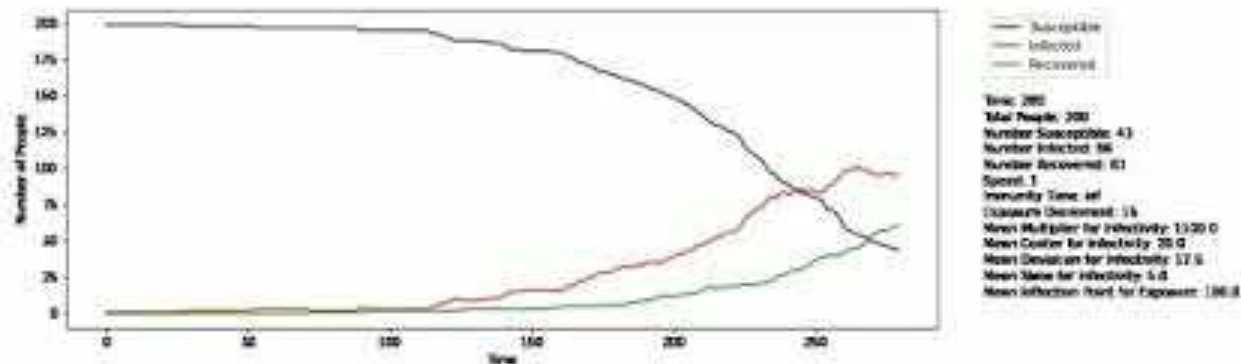
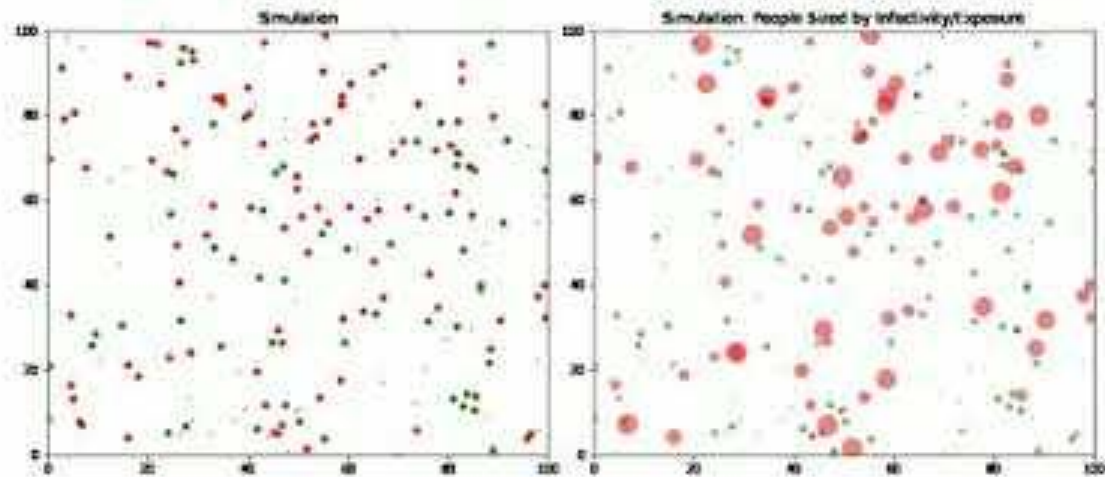


Note that the middle of the curve (the exposure at which probability is 50%) is called the inflection point.

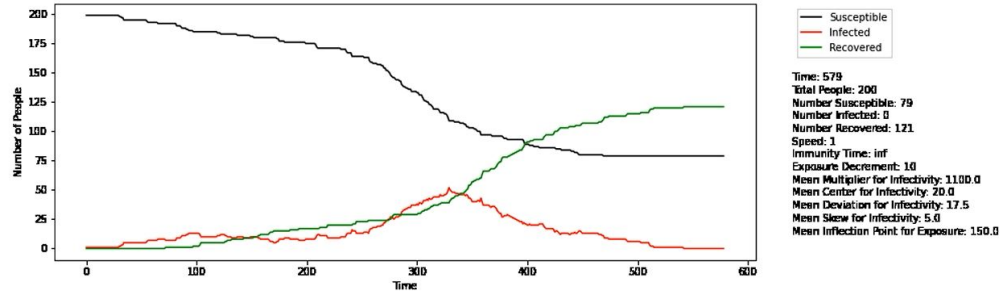
- ▷ The agents move around randomly on a grid (the edges wrap around)

- ▷ Once the infectivity of an agent falls below 1, they are considered recovered

- ▷ To represent an agent's immune system (and to prevent infrequent exposure from causing infection), the exposure level of each agent is decremented each unit time

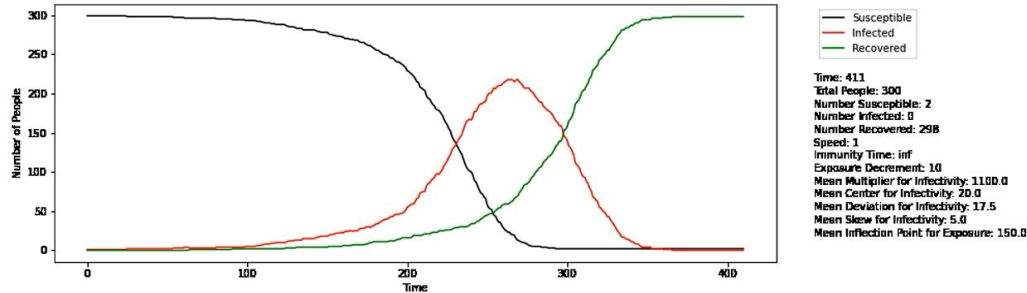


Effect of Number of People



↑↑ 200 People ↑↑

↓↓ 300 People ↓↓



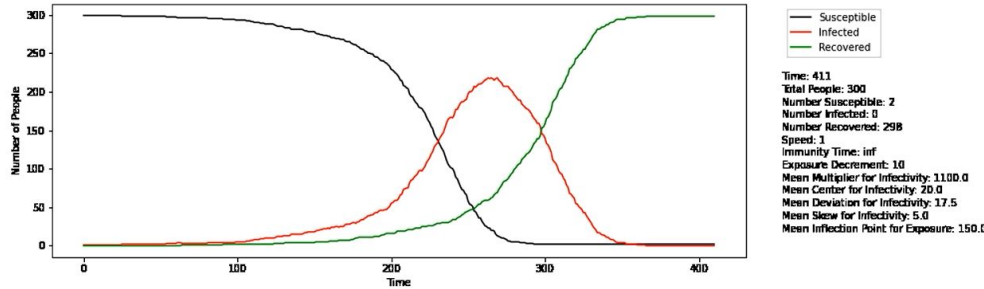
- ▶ Smaller population led to a larger percent of people who never got infected (39.5% for 200 people and .67% for 300 people)

- ▶ With more people, the spread is quicker (200 people peaks at 320, while 300 people peaks at 280)

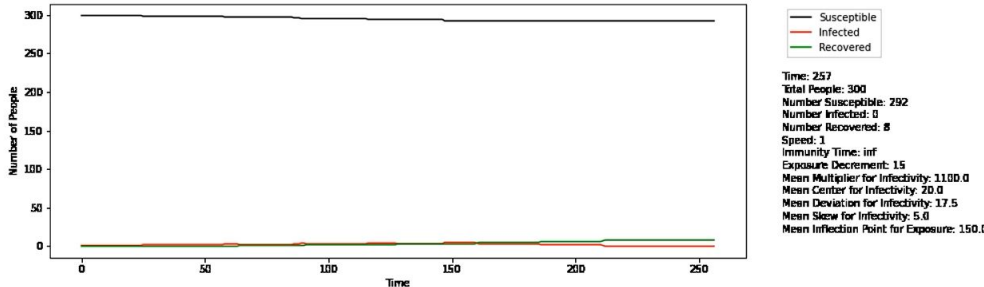
- ▶ More people allow for smoother curves

- ▶ Less people causes more noise in the data

Effect of Exposure Decrement



↑↑ 10 Decrement ↑↑ ↓↓ 15 Decrement ↓↓



- ▶ The disease quickly died out for the higher exposure decrement
- ▶ Typically, people get infected because they are exposed to more than one person
- ▶ Thus, with a higher exposure decrement, the disease has a harder time infecting enough people to start, and thus dies off
- ▶ This won't always be the case

Getting Reinfected

- ▷ The functions exhibit periodic behavior, with recovered lagging infected

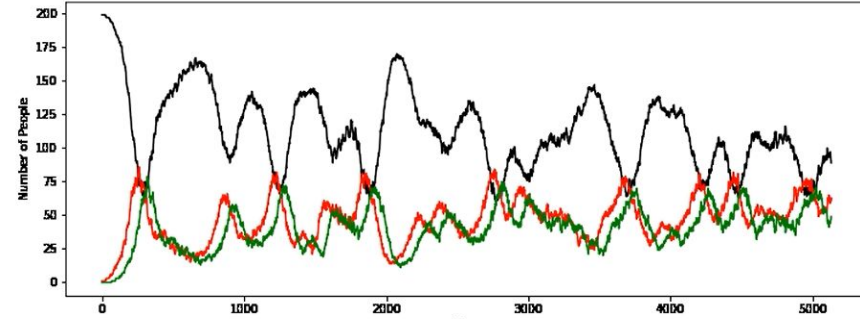
- ▷ For more people, the amplitudes were greater

- ▷ For less people, there are typically more susceptible agents than infected

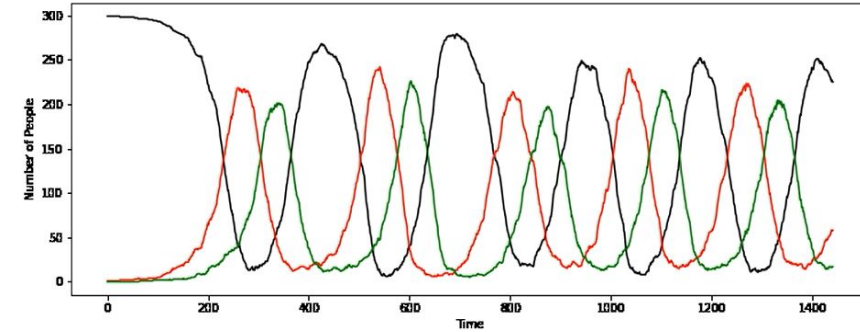
- ▷ For less people or higher decrement, the oscillations were less consistent

- ▷ For large exposure decrement, there were periods of equilibrium, small oscillation, and large oscillation

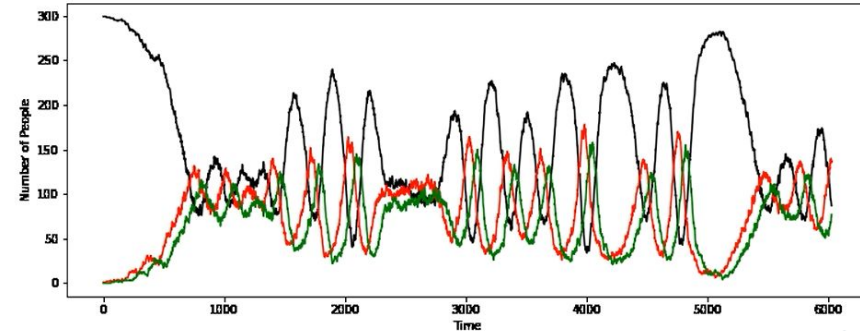
200 People
10 Decrement



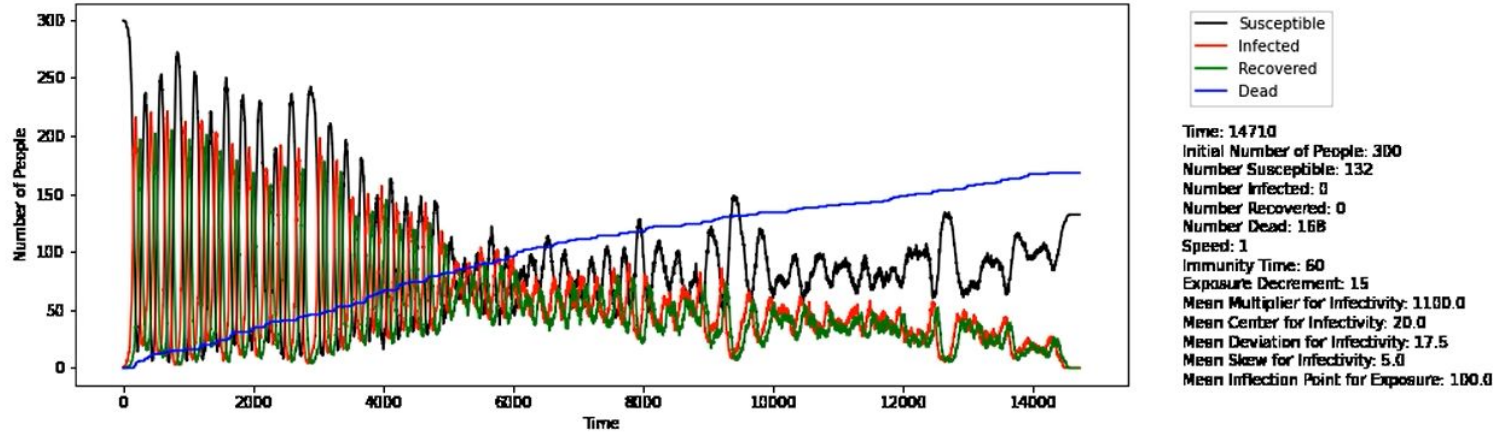
300 People
10 Decrement



300 People
15 Decrement

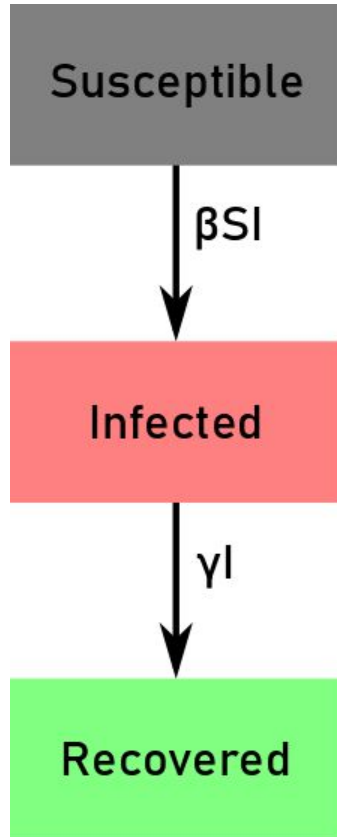
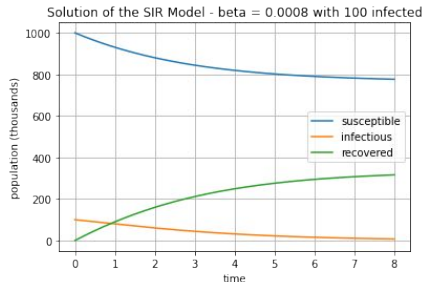
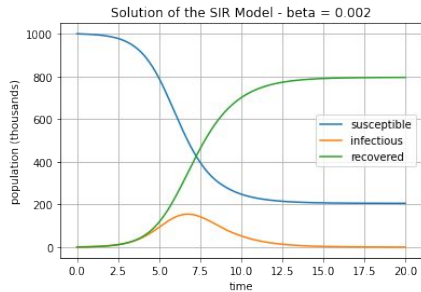
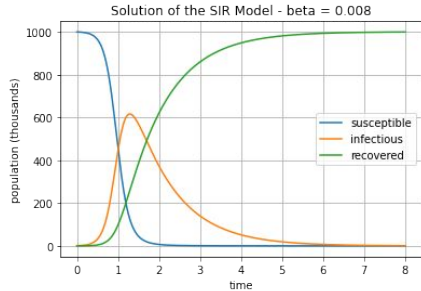


Model with Death



- ▽ Curves of each group decrease and dead increases
- ▽ Amplitude of oscillation decreases
- ▽ The death line is somewhat concave down (the rate of deaths slows as the population diminishes)
- ▽ The deaths tend to increase during peaks in the infected population
- ▽ Infected and recovered curves continue to approach 0, but the susceptible curve levels out (since as the number of people decreases, it becomes harder for the disease to spread)
- ▽ 44% of people survived

SIR - Original

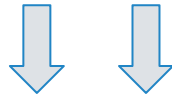


- ▷ The SIR model predicts several similar outcomes:
 - Everyone catching the disease
 - A subset of the population catching the disease
 - The disease dying off
- ▷ Unlike the ABM, the SIR model has skewed infected curves
- ▷ When the disease dies off, the SIR model predicts it will strictly decrease, while the ABM suggests it may remain constant for a while

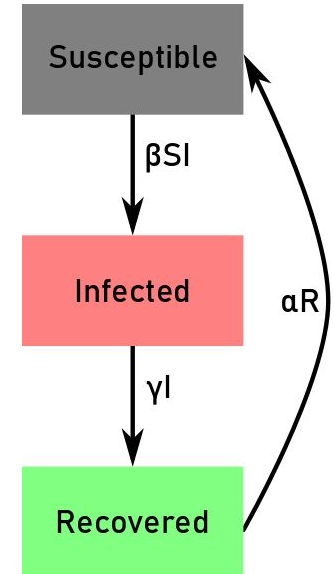
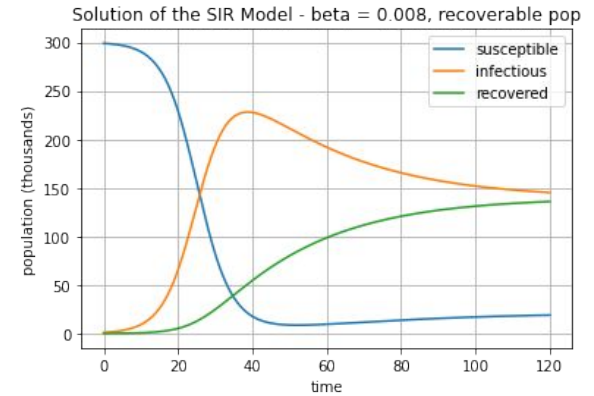
SIR Model - Reinfection

- ▷ Unlike the ABM model, the SIR model reaches an equilibrium without oscillation

- ▷ This can be explained by the fact that the SIR model uses the current populations to determine the rates, whereas in reality (and in the ABM), there are fixed delays (such as time it takes to recover),



Resulting in the rates depending on previous values of the populations



Summary

- ▷ How do the number of people who are susceptible, infected, and recovered change over time?
 - The infected population increases and decreases to form a single, symmetric peak, except in the case where the disease dies off
 - The susceptible population decreases logistically, while the recovered population increases logistically
- ▷ How do the values of the parameters and the assumptions made affect the course of the disease?
 - Increasing the number of people increases the peak and smooths the curves
 - Increasing exposure decrement does the opposite, possibly even preventing the disease from taking off
- ▷ How does the model change if we allow agents to re-catch the disease or agents to have a chance of dying?
 - Re-catching the disease causes oscillations to occur, where the oscillations are more predictable the more infectious the disease (and the more people)
 - Death causes the curves (and amplitudes) to decrease, although the susceptible curve will level out rather than approach 0
- ▷ How does the model compare to the SIR model?
 - Both models predict scenarios where the disease dies out, infects some of the population, or infects all of the population
 - The ABM predicts oscillations when people can recatch the disease, while the SIR predicts a stable equilibrium

Difficulties/Complications

- ▷ Computational efficiency: every pair of infected/uninfected agents had to be checked to see if they were within range, leading to quadratic time

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- Solved by running the model in the background and saving the frames, so that they could be viewed later

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- ▷ Difficulty tracking/defining exposure time when a person might be exposed to multiple infected agents

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- Solved by creating the exposure system described previously (which doesn't rely on tracking exposure time directly)

References

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