International Journal of Mathematical Education in Science and Technology

Elizabeth G. Arnold, Elizabeth A. Burroughs, Owen Burroughs, Mary Alice Carlson

CLASSROOM NOTE

Using physical simulations to motivate the use of differential equations in an SIR model

Elizabeth G. Arnold[a], Elizabeth A. Burroughs[b], Owen Burroughs[b] and Mary Alice Carlson[b]

[a]Colorado State University, Fort Collins, CO, USA; [b]Montana State University, Bozeman, MT, USA

ARTICLE HISTORY
Compiled July 24, 2023

ABSTRACT
The SIR model is a differential-equations based model of the spread of an infectious disease that compartmentalises individuals in a population into one of three states: those who are susceptible to a disease (S), those who are infected and can transmit the disease to others (I), and those who have recovered from the disease and are now immune (R). The simplicity of the SIR model masks some of the complex biological processes that underlie the spread of a disease. This classroom note describes how to initiate teaching the SIR model with two concrete physical simulations to provide students first-hand experience with some of the nuanced behaviour of how an infectious disease spreads through a closed population. One simulation physically models disease spread by the exchange of fluids, using pH to simulate infection. A second simulation incorporates randomness through the use of a probability game to keep track of the state of each individual at each time step. Both simulations invite students to ask questions about what factors influence disease spread. The concrete experience from the physical simulations enables students to make connections to the abstract mathematical representation of the SIR model and discuss the sources of stochasticity present in the spread of an infectious disease.

KEYWORDS
Disease spread; Physical simulations; Epidemiological mathematical models; Cognitive development

1. Introduction

Mathematical modelling has long been emphasised as a component of undergraduate mathematics education, with an emphasis in K–12 classrooms emerging over the last decade and a half. Since 1980, the *Consortium for Mathematics and its Applications* (COMAP) has provided various modelling resources for teachers and students, including classroom modelling activities, opportunities for students to participate in modelling competitions, and publications with commentaries and articles about mathematical modelling. The Mathematical Association of America updated the *CUPM Guide to Majors in the Mathematical Sciences*, highlighting mathematical modelling as an essential element of undergraduate mathematics major coursework (CUPM, 2015). Within the kindergarten through grade 12 (K–12) setting in the U.S., the *Common*

CONTACT E. G. Arnold. Email: liz.arnold@colostate.edu

Core State Standards for Mathematics (NGA, 2010) identified 'model with mathematics' as one of the eight standards for mathematical practice that teachers should seek to develop in their K–12 students. More recently, COMAP and the Society for Industrial and Applied Mathematics released the *Guidelines for Assessment and Instruction in Mathematical Modeling Education* (GAIMME, 2016) report, which paints a picture of modelling in Pre-K–12 through undergraduate mathematics curricula. Overall, the message is clear: throughout their mathematical education, it is important for students to engage with mathematical modelling as a process of creating mathematical representations to understand and make decisions about the world.

Differential equations often provide a natural way to represent phenomena and behaviours occurring in the world and thus have a valuable role in mathematical modelling, and recent media coverage has highlighted the importance of epidemiological mathematical models in understanding disease spread. The COVID-19 pandemic has drawn worldwide attention to ways the dynamics of a population might change under different conditions (e.g., ways to 'flatten the curve'). One such epidemiological model of an infectious disease is the differential equation SIR model, which compartmentalises individuals into one of three states: those who are susceptible to a disease, those who are infected and can transmit the disease to others, and those who have recovered from the disease and are now immune (Figure 1).

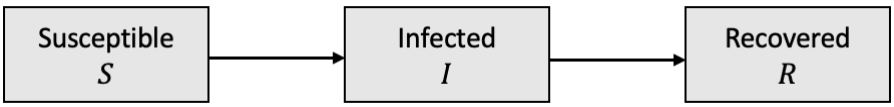

Figure 1. Movement between the three states of an SIR model.

The SIR model can be stated as a system of three ordinary differential equations (1) to represent the change in the number of individuals who are susceptible (S), infected (I), and recovered (R) at any time, t. Here, the parameters α and β are constant and represent the transmission rate and the recovery rate of the disease, respectively. Popular for its simplicity, the SIR model can be found in many course textbooks for ordinary differential equations (e.g., Bryan, 2021; Polking et al., 2005). Yet, the simplicity of the SIR model masks some of the complex biological processes that underlie the spread of an infectious disease, and students learning to model should be conscious of the assumptions they are making in using an SIR model.

$$\begin{aligned} \frac{dS}{dt} &= -\alpha SI, \\ \frac{dI}{dt} &= \alpha SI - \beta I, \\ \frac{dR}{dt} &= \beta I. \end{aligned} \tag{1}$$

Infection is a phenomenon that occurs on an individual level but is predicted by an SIR model at the population level. On an individual level, three major factors determine whether an individual will be infected with a pathogen: the infectious dose, the route of exposure, and the individual's (host's) susceptibility. The dose of infectious material that an individual receives is directly related to individual infection; doses

above the *infectious dose* for a given pathogen are likely to cause infection. Pathogens all have a unique infectious dose that represents the number of infectious particles (e.g., bacterial cells) required to cause infection. For some pathogens, this dose can be relatively high (for the bacterium *Staphylococcus aureus* it is usually greater than 10^3 bacteria) while for others it can be much lower (for bacteria in the genus *Shigella* it can be as low as 10^1 bacteria) (Vidlak & Kielian, 2016; Zaidi & Estrada-García, 2014). The dose of infectious material also usually impacts the severity of infection. Furthermore, the infectious dose (and, consequently, the likelihood and severity of infection) usually depends on the *route of exposure* to the pathogen. For example, the infectious dose of Influenza A is several orders of magnitude higher when exposed through an individual's nasal passages than when exposed directly through inhalation (Yezli & Otter, 2011). The final major factor that determines the likelihood of infection is the host's ability to prevent the infection, known as *host susceptibility*. This term encompasses a wide range of factors—such as the host's genetics, immune function, and microbiome—all of which influence whether an exposure to a pathogen will result in an infection. For example, in individuals with healthy gut microbiomes, infection with the bacterium *Clostridioides difficile* (*C. difficile*) is incredibly unlikely. In individuals with disrupted gut microbiomes (such as those who have recently received a large dose of antibiotics), *C. difficile* infection becomes possible (Czepiel et al., 2019).

The SIR model simplifies infectious disease modelling by limiting its scope to three variables and compartmentalising all members of a population into these variables (Tolles & Luong, 2020). While this strategy captures the general characteristics of disease spread well, the act of compartmentalization requires a modeller to disregard the stochastic and nuanced nature of disease transmission (Tatsukawa et al., 2022). In addition to the individual level factors that are determined by an individual's biology, diseases in a population are affected by behavioural factors, and the nature of interactions between the susceptible and infected persons all influence the probability of disease transmission in a manner that is stochastic and individual-specific (Belser et al., 2010). A more sophisticated model would account for these factors by incorporating different compartments and parameter values (e.g., it could include different compartments for individuals based on their predisposition for infection). This complexity, however, is often neglected when first introducing the SIR model in a mathematical modelling context.

The purpose of this classroom note is to describe two physical simulations that can be used in the classroom to motivate the use of differential equations in an SIR model by providing students with concrete experiences that are related to the biological and stochastic factors that influence disease spread. Though the resulting model proceeds much as it is described elsewhere, through these physical simulations students can simulate the biological parameters of dosage and the human-behaviour-influenced stochastics involved in susceptibility. The first simulation involves the use of simple laboratory materials (cups, pipettes, vinegar, baking soda, and phenol red or pH strips) and the spread of an infectious disease is physically modelled by the exchange of fluids, using pH to simulate infection. The second simulation incorporates randomness in its model of a spread of an infectious disease through the use of a probability game to keep track of the state of each individual (i.e., whether they are susceptible, infected, or recovered) at each time step. Both simulations invite students to ask questions about what factors influence disease spread, and together these simulations provide students an opportunity to develop conceptual understanding of the parameter values, α and β, in the SIR model.

2. Teaching Mathematical Modelling

Modellers exercise judgement in deciding what to include or exclude from a model, and a distinguishing feature of mathematical modelling, as opposed to solving applied mathematics problems, is that the modeller is responsible for making choices about what is important to include or exclude from a model. In order to make those choices, the modeller must have sufficient experience with (or empathy for those who experience) a situation in order to make wise judgements. In teaching mathematical modelling, then, the instructor is responsible for structuring the learning environment so that the students are making modelling decisions (Arnold et al., 2020). Because modelling problems are based on experience, the modelling process moves from a concrete phenomenon to an abstract representation of that phenomenon; likewise, the learning of mathematical modelling should begin with concrete experience before moving toward abstraction.

Educational theorists have long studied the development of human beings' thought processes, directly influencing what teachers understand about student learning in mathematics. Vygotsky (1896–1934), Piaget (1896–1980), and Bruner (1915–2016) are among some of the cognitive psychologists whose research has led to the notion that human cognitive development proceeds from concrete experiences to abstract knowledge (see Driscoll, 2014, for a comprehensive review). Rather than starting with the abstraction of a system of differential equations in an SIR model, we have found that starting with a concrete physical simulation that mimics the spread of a disease at the individual level provides students first-hand experience with some of the behaviour of how an infectious disease spreads through a closed population. For example, such a simulation highlights how the initial number of infected can impact the total number of individuals who became infected by the end of a simulation and how different interventions can mitigate the spread of a disease. Further, when we used these simulations, the concrete experience of physically simulating the spread of a disease evoked students' curiosities about their experience, and they began posing mathematical questions about the situation, some of which can be answered with an SIR model.

When students learn to reflect on situations in their everyday experiences and consider the mathematical questions those situations evoke, they are engaging in the modelling process and initiating the need for a mathematical model. For an instructor, it can be tempting to give students a dataset, write a system of ordinary differential equations that models the dataset, and then give students questions to answer about that model. However, when instructors start with a concrete experience rather than the abstract representation of that experience, students can experience the need for a model and initiate questions they want to answer with their models.

3. Examples of Two Physical Simulations to Model the Spread of an Infectious Disease

We have used the two activities described below to motivate the need for an SIR model and the use of differential equations. While versions of these simulations are found elsewhere (see, for example, COMAP, 2015, McPhee, n.d., or Nagatani, 2019), the particular versions described below were developed by the authors in order to focus on the aspects of disease spread as described in Section 2. The goal of these simulations is to elicit students' mathematical and biological curiosities about how an

infectious disease spreads and what aspects of the phenomenon are either attended to or simplified in the mathematical formulation of an SIR model.

3.1. Disease spread simulation using acid-base exchange

The acid-based disease spread simulation and discussion takes about 25 minutes and works well with 25 or more students, though we have had success with fewer students. We recommend running at least three rounds of this simulation, each for about 5 minutes. For each round, assign approximately 1 *patient zero* (that is, those who begin the round in an infectious state) for every 10 students. At the start of each round, students do not know whether they are infected or immune.

- Round 1: No intervention.
- Round 2: Choose one of the non-vaccine interventions.
- Round 3: Vaccine intervention.

Details for each round are described below, and in this section we also describe how to extend the simulation to carefully examine how changes in the simulation correspond to choices and parameters in an SIR model. We use this acid-base simulation to generate experience with the intersection of human behaviour and the characteristics of pathogens; although we do not use this simulation to collect data to compare to an SIR model, we do lead a discussion about students' interactions and observations and ask how those might relate to the parameters α and β of an SIR model.

Materials:

- Plastic water cups
- Pasteur pipettes (optional)
- 10% Acetic acid or vinegar
- Sodium bicarbonate (baking soda)
- 0.02% w/v Phenol red pH indicator solution (available at your university's chemistry stores or in the pool supplies aisle of home improvement stores) or pH strips

Safety Considerations:

- 10% acetic acid and (to a lesser extent) undiluted vinegar is a skin irritant. Take care when handling either. In the case of skin or eye exposure, wash with plenty of water and soap.
- Phenol red solution can be a skin irritant in high concentrations. The concentrations used here are not hazardous. Nonetheless, handle this solution with care, and gloves if practical. In the case of skin or eye exposure, wash with plenty of water and soap. Consult the Materials Safety Data Sheet (provided by the supplier of your Phenol red solution).

Figure 2. Materials needed and safety considerations for using the acid-base disease spread simulation.

Round 1. To prepare for the 'no intervention' round, determine how many students will be *patient zero*. For each student in the class, fill a clear, plastic cup about two-thirds full with water. For each patient zero's cup, secretly replace approximately 10% of the water in the cup with 10% acetic acid or 20% of the water with vinegar. Give each student a cup. (Note: we either number each cup, write down which number belongs to a patient zero, and then randomly pass the cups out to students, or we pass out 'patient zero cups' to specific members of the class and remember who they are.) Ask the students to circulate around the room and have short conversations (we've asked them to discuss either class-related topics, like 'what questions do you have about last night's homework?', or non-class related topics, like 'what did you have for breakfast?'). Each time two students speak to each other, have them transfer

about a pipette full of the solution in their cup into their partner's cup—they can also pour about a teaspoon's worth if you aren't using pipettes. The order in which they exchange solution in their cups does not matter. Have students spend about five minutes moving around the room, engaging in discussions with different students, and transferring their solution to their partner's cup (or enough time to ensure that most students have the chance to talk to at least one patient zero). Not all students will talk to every student in the class.

After approximately 5 minutes, ask students to go back to their seats and make predictions about whether they think they are 'infected' and about how many total people in the class will be 'infected.' Then, identify which students were patient zero and ask students to reconsider their predictions. Circulate among the students and drop a small amount of phenol red solution into each cup (or alternatively give them a pH strip to drop in their cup). If the solution turns yellow (or is acidic as measured by the pH strip's instructions), the person has been 'infected.' If the solution is pink or red (or the pH strip is not acidic as measured by the pH strip's instructions), the person is 'healthy' (Figure 3). (Note: we strongly recommend using phenol red, because the visual cues are readily apparent to a whole class by the colour of the solution; the pH strips provide the same information but in a less visually impactful way.)

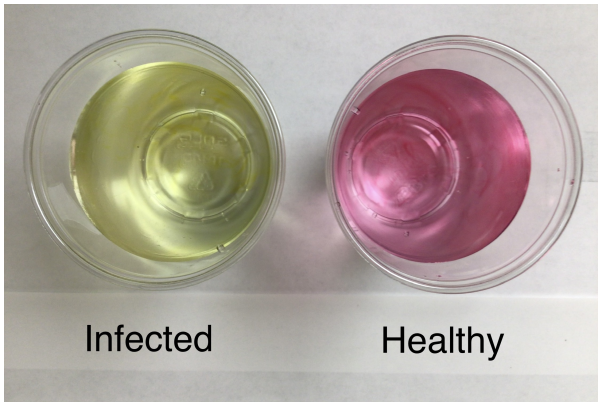

Figure 3. An example of a healthy and infected individual after exchanging water droplets with others, and testing with phenol red.

To demonstrate the effects of human behaviour on disease spread, run at least two more rounds of the simulation using one or more of the following adjustments. Adjustments that illustrate the effect of human behaviour on disease spread can focus on either non-vaccine or vaccine interventions.

Round 2. To prepare for the 'non-vaccine' intervention, prepare the cups as described above. Lead a discussion with the class about different non-vaccine interventions that can be used in this simulation of disease spread. The following ideas may emerge: 'social distancing' by limiting the amount of infectious material that gets transferred between students by asking everyone to only transfer a few droplets of solution into their partner's cup; 'social pods' by having students form several groups and only speak to individuals within their groups; 'limited interaction' by having students only speak to one or two other students; 'contact tracing and quarantine' by pausing the simulation partway through, revealing who the initial patient zero was, and having anyone who has spoken to that person stop talking to other individuals. As a class, choose one of these non-vaccine intervention methods and run the simulation for about 5 minutes, asking students to make similar predictions as they did in Round

1 at the end of this round. Circulate among the students and drop a small amount of phenol red solution into each cup (or alternatively give them a pH strip to drop in their cup) to identify who is 'infected.' Ask students what they noticed and what they wonder.

Round 3. For the 'vaccine intervention,' first prepare the cups as described above. Determine the number of students who will be 'vaccinated'; we have vaccinated anywhere from 40-60% of the class, but the instructor can vary this amount depending on what aspect of vaccination they are trying to demonstrate (e.g., herd immunity). For these students, secretly add 1–2 teaspoons (a healthy sprinkle) of sodium bicarbonate (baking soda) to their cups. Pass out cups to the students and run the simulation for about 5 minutes, as described in Round 1. At the end of the round, ask students to make their predictions and circulate the room, either dropping a small amount of phenol red solution or a pH strip into each cup. (One effect of this simulation is that 'vaccinated' individuals can transfer their 'vaccine' to others by transferring their solution. While this is not the case for most vaccines, some of the first live-attenuated vaccines could be transmitted from a recently vaccinated person to an unvaccinated person.[1])

Discussing the parameter values α and β. The acid-base disease simulation illustrates some of the biological complexity of disease spread by focusing on the interactions between individuals, sometimes called *agents*. In this simulation, several stochastic and agent-specific factors influence whether an infected individual will transmit their infection, such as the number of interactions the individual has and the amount of solution that the individual transfers between the cups (which, in practice, varies between individuals, modelling the stochastic nature of infectious doses). In this way, the acid-base simulation introduces an agent-based model where a series of simulated interactions between agents are used to determine or refine the parameters (α (transmission rate) and β (recovery rate)) of an SIR model (Susandi et al., 2021).

In this simulation, the transmission rate α is influenced by the number of contacts a person has for the duration of the simulation and the likelihood that a given interaction will result in an infection. Students can estimate the number of contacts they have and notice that the duration of the simulation will have an effect on this value. The likelihood that an interaction results in an infection is close to 1 in this simulation, because the transfer of an acidic solution will usually result in a solution that is also acidic, but if some individuals don't transfer much solution then the resulting solution may not be measured as acidic. And, in this simulation there is no recovery, because once a solution is acidic it will remain acidic, so the recovery rate β is 0.

3.2. Disease spread simulation using a probability game

The probability game simulation directly combines the randomness embedded within the game Rock-Paper-Scissors (RPS) with the three states of the SIR model. This simulation and corresponding discussions takes about 45 minutes and also works well with 25 or more students, though we've had success with fewer students. Each student will need a data sheet to keep track of their state (S, I, or R) at the end of each time step (Figure 4), and the instructor needs a way to compile a class dataset at the end

[1]The most famous of these is the oral polio vaccine which contains a poliovirus that does not cause disease but replicates and is shed in the same way as the wild-type poliovirus. It is a well-established phenomenon that immunity to polio is spread to members of a community who are not vaccinated as they become infected by the vaccine strain (Altamirano et al., 2018; Okayasu et al., 2011). This means that vaccination using the oral polio vaccine can benefit communities beyond just the individuals who are vaccinated.

of the simulation (we've used a shared spreadsheet).

Disease Spread Simulation
Rock-Paper-Scissors (RPS)

Time Step	S, I, R State
0	S
1	
2	
3	
4	
5	
6	
7	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
19	
20	

Instructions:

- Keep track of your state at each time step: Susceptible (S), Infected (I), or Recovered (R)
- Once infected, you remain infected for 7 consecutive time steps, after which you are now recovered (and can't transmit the disease anymore).
- Circulate the room and play RPS with a partner when instructed.
- After you play RPS, reveal your state to your partner.
- Determine if your state has changed.
- Update your state on your data sheet.

Figure 4. Data sheet for the Rock-Paper-Scissor disease spread simulation.

To begin the probability game simulation, decide on the behaviour of the outbreak the class will simulate. Specifically, the instructor or the class will need to decide how long someone remains infectious and whether infection leads to immunity. For example, in the data sheet in Figure 4, notice that the class decided that someone remains infectious for 7 consecutive time steps and that once they have recovered from the disease, they are immune and can no longer transmit the disease to someone else. Before initiating the simulation, the instructor or the class will also establish rules for using RPS to simulate the spread of a disease, that is, establish how the outcome of an RPS round, including a tie, can be interpreted as encountering a disease and either becoming infected or remaining susceptible. We don't provide students a full set of instructions about how to interpret the results of RPS, and we've found that students tend to establish that an individual's state will remain the same unless they are susceptible and lose RPS to an infected person, or they are infected, but the duration of their infection ends during the round, leading them to be recovered.

Then, give each student a data sheet and secretly assign an infection state of susceptible or infected to each person in the class. We have done this by indicating 'S' or 'I' on Time Step 0 in the students' data sheet and letting students know that if they see an 'S' on Time Step 0, they do not have the disease but are susceptible and if they see an 'I' on Time Step 0, they do have the disease and can spread it to others. It works well to start the simulation with 10–20% of the class being infected and then

increasing this number in future simulations (if desired). Ask the class to move around the room for a short period of time (about 15–30 seconds). To encourage 'random' movement, we played music and asked participants to dance as they moved. When the music stops, instruct all students to turn to someone nearby and play RPS. After they have played RPS, students reveal their state (S, I, or R) to their partner and then update their state on their data sheet. Continue this process until students have completed about 20 time steps (i.e., enough time steps so that infected individuals can become recovered members of the population). Figure 5 shows a sample data sheet for one student for a few time steps; the student's initial state was susceptible and they encountered and lost RPS to an infected person in Time Step 3, making them infectious in Time Steps 4 and 5.

Time Step	S, I, R State
0	S
1	S
2	S
3	I
4	I
5	I

Figure 5. A sample data sheet after five time steps.

Conclude the activity by compiling the students' individual data into a class dataset and leading a class discussion. Invite students to ask questions or share their reflections about their experience with this simulation. By examining the class dataset, students can make connections between their individual concrete experience during the simulation and the decisions they will make in creating a population-level model.

Discussing the parameter values α and β. Through playing RPS and encouraging students to take 'random movements' between time steps, the probability game simulation directly incorporates two kinds of stochastic and agent-specific factors that influence the disease's transmission rate (α). The first corresponds to individual level factors that are determined by an individual's biology; there is an inherent probability an individual will get sick when they are exposed, as represented by the 1 in 3 chance that a susceptible individual loses a game of RPS if they encounter an infected individual in the simulation. The second corresponds to the individual's behavioural factors and the nature of their interactions with others; the students' 'random movements' between time steps affect the probability they will be exposed to members of the population who are infected (which, in practice, varies between individuals, modelling the stochastic nature of exposure to an infectious disease). Both of these stochastic events are embedded in the transmission rate (α) of an SIR model, but are not directly apparent to many students from its mathematical representation.

The RPS activity also directly incorporates a recovery rate (β), because the simulation keeps track of time steps during which individuals are infected before they move to the recovered state. Figure 4 displays an instance of this simulation with the assumption that an individual remains infectious for seven time steps, after which they 'recover' and can no longer transmit or receive the disease. Students decided to count the recovery *after* the seventh time step, so $\beta = \frac{1}{8}$.

4. What Comes Next?

In our classes, we performed both simulations in a single 75-minute class period, beginning with the acid-base simulation, which focuses on the importance of dosage and human interactions in disease spread. Then, we moved to the second simulation, which focuses on the probability of being exposed to a disease within a population and the probability of getting sick when coming in contact with someone infected with a disease. Collectively, these two simulations highlight concrete examples of individual level factors that impact the spread of a disease within a population, demonstrate the importance of counting the number of susceptible, infected, and recovered members of a population, and provide opportunities for students to develop conceptual understanding of the parameter values in an SIR model.

In the acid-base simulation, the visual phenomenon of the solution changing colour (or the pH strip indicating acidity level) provides students with a concrete experience of how the hypothetical pathogen spreads through the classroom population. In the probability game simulation, the phenomenon of infection is more abstract—the RPS game results in a state for each individual, and the collection of individual states results in the class dataset, from which population level effects can be visualised. We use the first simulation as a quick launch and spend more time on the second simulation, before moving towards a fully abstract representation of disease spread using either discrete or continuous SIR models.

A particularly powerful aspect of these classroom activities is that they provide students an opportunity to build empathy—the ability to understand and share the perspective of another. In each of these simulations, the infection (or not) of each student happens at the individual level, but the SIR model predicts infection at the population level. These activities engage students in asking questions about how interventions at the individual level or susceptibility of an individual are carried forward to a population level model. By giving each student an identity in the population being modelled, this activity has the potential to bring forward the human value of *care for community* (Arnold et al., 2020, p. 82).

What comes after these simulations can vary and is up to the instructor and the amount of time they have to spend. Some may follow these simulations by deriving the system of ordinary differential equations in an SIR model and determining specific values for the parameters α and β. Others may focus on a computational approach and ask students to perform a numerical simulation in their program of choice (e.g., R, Matlab, Excel, Python, Netlogo, etc.) to generate and graph data, thereby showing the SIR curves. Recently, after implementing these two simulations in our classes, we asked students to build an agent-based model in Netlogo[2] (https://ccl.northwestern.edu/netlogo/) to replicate the probability game simulation, but using a much larger population (see Figure 6 for a sample).

To create this Netlogo program, students chose to create 'sliders' so that the user can adjust how many people are initially susceptible and infected; they also included a slider to indicate how 'close' two people need to be in order to come in contact with each other. Within Netlogo, students programmed all individuals to move around the environment for 20 'days' and when a susceptible person came in contact with an infected person, students set a probability to determine whether the susceptible person

[2]Netlogo is a free multi-agent programmable modelling environment. The Netlogo website (https://ccl.northwestern.edu/netlogo/) offers many tutorials and other resources when learning how to use the program. We recommend the book, *Agent-based and individual-based modeling: A practical introduction* by Railsback and Grimm (2019) to help students and instructors get started with Netlogo.

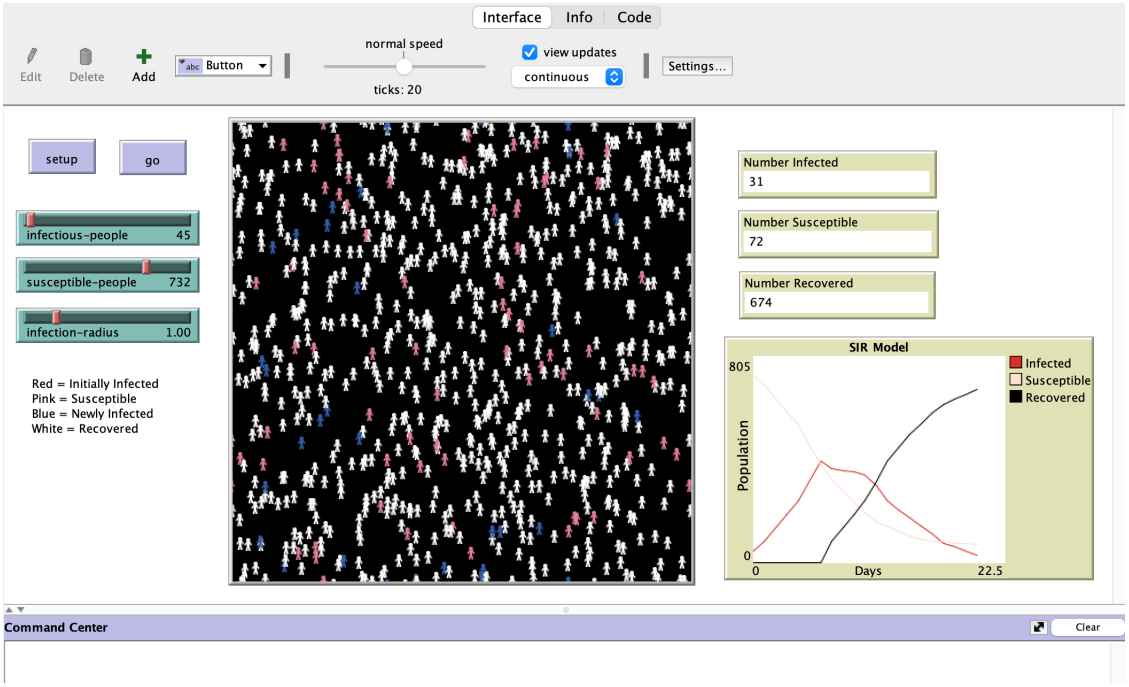

Figure 6. The interface of a sample Netlogo program to generate data for an SIR model based on the probability game simulation.

became infected from that contact. Students also programmed infected individuals to become recovered after a set amount of days. Within Netlogo, students kept track of each individual's state (S, I, or R) and created counters that output the total number of the population who were susceptible, infected, or recovered; this information was also displayed in a graph over time. (Netlogo also has a 'BehaviorSpace' where students can run the model many times, adjusting parameter values as needed and recording results of each model run, such as the total number of infected people, in a spreadsheet.) With their Netlogo model, students explored population-level effects by adjusting initial states for the number of individuals infected and susceptible; they generated numerical data and observed how the graphs of S, I, and R changed over time, depending on the initial states they used.

5. Student Engagement

In our experience, students found these simulation activities a fun and engaging way to learn about epidemiological modelling. They expressed appreciation for the ways the activity enabled them to see how mathematics can be used to understand an important topic that is relevant to their experiences. After participating in the simulations, students reflected on their experiences and began to ask mathematical questions that could be answered with an SIR model. For example, in the acid-base exchange simulation students have asked, 'how many of us became infected after coming in contact with [patient zero]?' and 'when will there no longer be individuals who are infected within our population?' In the RPS simulation, students have asked, 'How many people will get infected [at a particular time step]?', and they noticed when there is someone who is susceptible and manages to repeatedly win RPS; they then asked questions

about whether it's possible for everyone in the room to become infected and if so, at what time step will this occur. These questions demonstrate some of the ways that participating in these physical simulations gave our students experiences with moving between a phenomenon and a mathematical representation of that phenomenon.

As instructors, we found that the concrete experience from the physical simulations enabled students to make connections to the abstract mathematical representation of the SIR model and discuss the inherent stochasticity present in the spread of an infectious disease. Students also commented how these simulations introduced stochasticity and introduced them to a whole new side of modelling. We also appreciated our students' curiosities and the mathematical problems they posed after each simulation. Even more exciting was seeing our students exercise judgement in deciding what choices and assumptions to include or exclude from their models. Overall, these two physical simulations are an engaging way to get students up and moving in the class in a way that helps them learn about the nuanced nature of disease spread and the use of differential equations to model that spread.

Funding details

This work was partially supported by the National Science Foundation under Grant 1810992.

Disclosure statement

No potential conflict of interest was reported by the authors.

References

Altamirano, J., Sarnquist, C., Behl, R., García-García, L., Ferreyra-Reyes, L., Leary, S., & Maldonado, Y. (2018). OPV vaccination and shedding patterns in Mexican and US children. *Clinical Infectious Diseases: An Official Publication of the Infectious Diseases Society of America*, *67*(1), S85–S89. https://doi.org/10.1093/cid/ciy636.

Arnold, E. G., Burroughs, E. A., Carlson, M. A., Fulton, E. W., & Wickstrom, M. H. (2021). *Becoming a teacher of mathematical modeling, Grades 6-12.* National Council of Teachers of Mathematics.

Belser, J. A., Maines, T. R., Tumpey, T. M., & Katz, J. M. (2010). Influenza A virus transmission: Contributing factors and clinical implications. *Expert Reviews in Molecular Medicine*, *12*, e39. https://doi.org/10.1017/S1462399410001705.

Bryan, K. (2021). *Differential equations: A toolbox for modeling the world.* SIMIODE.

COMAP (2015). Mathematical modeling of disease outbreak. Retrieved from https://www.comap.com/membership/free-student-resources/item/mathematical-modeling-of-disease-outbreak-student.

CUPM (2015). *CUPM curriculum guide to majors in the mathematical sciences.* Mathematical Association of America.

Czepiel, J., Dróżdż, M., Pituch, H., Kuijper, E. J., Perucki, W., Mielimonka, A., Goldman, S., Wultańska, D., Garlicki, A., & Biesiada, G. (2019). Clostridium difficile infection: Review. *European Journal of Clinical Microbiology & Infectious Diseases*, *38*(7), 1211. https://doi.org/10.1007/S10096-019-03539-6.

Driscoll, M. P. (2014). *Psychology of learning for instruction.* Pearson Education Limited.

GAIMME (2016). *Guidelines for assessment & instruction in mathematical modeling education.* SIAM.

McPhee, L. (n.d.). Transmission of a communicable disease. Retrieved from https://www2.nau.edu/lrm22/lessons/disease/disease_lab.html.

Nagatani, T. (2019). Infection promotes species coexistence: Rock-paper-scissors game with epidemic on graphs. *Physica A*, *535*, 122531. https://doi.org/10.1016/j.physa.2019.122531.

National Governors Association Center for Best Practices & Council of Chief State School Officers (2010). *Common core state standards for mathematics*, Authors.

Okayasu, H., Sutter, R. W., Czerkinsky, C., & Ogra, P. L. (2011). Mucosal immunity and poliovirus vaccines: Impact on wild poliovirus infection and transmission. *Vaccine*, *29*(46), 8205–8214.

Polking, J., Boggess, A., & Arnold, D. (2005). *Differential equations*. Pearson.

Railsback, S. F. & Grimm, V. (2019). *Agent-based and individual-based modeling: A practical introduction*. Princeton University Press.

Susandi, A., Taufik, I., Aditiawati, P., & Viridi, S. (2021). The relation between agent-based model and susceptible-infected-recovered model for spread of disease. *AIP Conference Proceedings* 2320, 050032. https://doi.org/10.1063/5.0038221.

Tatsukawa, Y., Arefin, M. R., Utsumi, S., Kuga, K., & Tanimoto, J. (2022). Stochasticity of disease spreading derived from the microscopic simulation approach for various physical contact networks. *Applied Mathematics and Computation*, *431*, 127328. https://doi.org/10.1016/J.AMC.2022.127328.

Tolles, J., & Luong, T. (2020). Modeling epidemics with compartmental models. *Journal of the American Medical Association*, *323*(24), 2515–2516. https://doi.org/10.1001/JAMA.2020.8420.

Vidlak, D., & Kielian, T. (2016). Infectious dose dictates the host response during staphylococcus aureus orthopedic-implant biofilm infection. *Infection and Immunity*, *84*(7), 1957. https://doi.org/10.1128/IAI.00117-16.

Yezli, S., & Otter, J. A. (2011). Minimum infective dose of the major human respiratory and enteric viruses transmitted through food and the environment. *Food and Environmental Virology*, *3*(1), 1. https://doi.org/10.1007/S12560-011-9056-7.

Zaidi, M. B., & Estrada-García, T. (2014). Shigella: A highly virulent and elusive pathogen. *Current Tropical Medicine Reports*, *1*(2), 81. https://doi.org/10.1007/S40475-014-0019-6.