INTRODUCTION

The COVID-19 pandemic has made discussions about infectious disease commonplace. It became clear, as COVID-19 spread, that researchers do not always have sufficient data and often rely on models to predict different scenarios based on the possible characteristics of the virus (attack rate, waning immunity, virus surface stability, etc.) and behavior of society (physical distancing, wearing masks, cleaning frequency, etc.). Physical distancing and quarantine have increased the demand for teaching in virtual formats. Literature shows that, when done properly, virtual educational experiences can be as effective as traditional teaching, even in lab-based courses. Furthermore, virtual education may be improved by using modeling and simulations (1–4). In 2011, the American Association for the Advancement of Science Vision and Change document established educational foci to include using models and simulations (competency #3) and understanding complex systems (core concept #5) (5). Since then, model building has been shown to be an effective active learning technique in the science classroom (6). Additionally, developing and revising models helps students mature as scientists (7). Finding ways to implement effective online instruction and teach modeling complex systems can be daunting. The two activities described here provide enjoyable, unique online learning activities to teach college biology students about complex systems and modeling using the timely and fascinating topic of infectious diseases. Student participants were general biology majors in an online, upper-division topics course on pandemics being offered at a small teaching-focused private university. All surveys were submitted anonymously.

PROCEDURE

Activity 1: Evaluating existing models (simple implementation)

Since the beginning of the pandemic, numerous COVID-19 simulations have been published online, and an instructor may ask students to find their own simulations to evaluate. For this study, students were asked to investigate four simulations: (i) “Why outbreaks like coronavirus spread exponentially, and how to ‘flatten the curve’” from The Washington Post (8); (ii) “Outbreak” by Kevin Simler of Melting Asphalt (9); (iii) the “COVID-19 Outbreak Tool” from Harvard Medical School (10); and (iv) a custom StarLogo Nova (block-based coding platform) model created by Daniel Wendel of the Scheller Teacher Education Program at Massachusetts Institute of Technology (11). Table 1 characterizes the benefits and drawbacks of each model. See Appendix 1 for more detailed descriptions of the simulations.

The students, who had all previously taken a general microbiology course, used a discussion board to identify their favorite and least favorite models and provide rationale. In this version, the discussion took place early in the course, with the goal of introducing models and evaluating how they might be used (teaching, prediction, public outreach, etc.). Alternatively, late-course or upper-division courses may allow for more analytical prompts (e.g., “Evaluate the representation of transmission/host susceptibility/personal protective equipment [PPE]/etc. in this model,” or “What aspects of this model might be confusing or misleading to the general public?”). After posting, students debated their selections and rationale.

Activity 2: Coding custom models (more instructor preparation and expertise required)

In block-based coding, users organize computer logic and rules spatially and visually, allowing students to design and understand modeling of scientific phenomena without requiring previous coding education (Fig. 1) (12). StarLogo Nova has been used by researchers at MIT and in the...
### TABLE I

Benefits and drawbacks of four online simulations

<table>
<thead>
<tr>
<th>Model</th>
<th>Benefits</th>
<th>Drawbacks</th>
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<tbody>
<tr>
<td>Washington Post</td>
<td>Easy, clean, linear, and supported by well-written explanations</td>
<td>No flexibility with variables, limited in scope, no variation possible</td>
</tr>
<tr>
<td>Melting Asphalt</td>
<td>High degree of variable flexibility (up to 9 at once), rapid runs, good explanations for each variable</td>
<td>Stylized visuals, too many choices and variables</td>
</tr>
<tr>
<td>Harvard Medical School covid19sim</td>
<td>Based on real and current data, focused analysis on public health policies</td>
<td>Poor flexibility, limited interactivity, no animations (graphs only)</td>
</tr>
<tr>
<td>StarLogo Nova</td>
<td>Open source, freedom to manipulate simulation beyond initial variables, searchable database</td>
<td>Confusing interface, limited flexibility (without code manipulation), pixelated visuals</td>
</tr>
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Biograph High School biology curriculum to teach Next Generation Science Standards with modeling as a core instructional tool, including simulating ecology, enzyme activity, gene regulation, etc. Students were provided with two basic models for infectious disease simulation using StarLogo Nova to serve as starting points: one with respiratory droplets and one with direct contact of agents. Introductory videos into the coding platform and links to a library of resources were provided, meaning the students were independently responsible for directing their modeling question and coding logic. One-on-one midproject conferences helped students troubleshoot all aspects of the project. Finally, students were asked to write mini case studies for their classmates. This included (i) background on the infectious disease phenomenon the model was examining; (ii) an explanation of how the variables were modified and represented through coding; and (iii) a series of recommended variable values for students to run and evaluate outcomes. At this point in the course, students had explored how pathogens may be transmitted and what human behaviors and risk factors could affect disease spread. The new goal was to make predictions as to the relative effect of modifying variables, and then use the model to confirm or deny hypotheses. For example, in a model coding a slider bar for vaccine effectiveness, students could run simulations at various rates of protection (50%, 90%, etc.) and compare results.

### RESULTS

**Activity 1: Model evaluation**

Students enjoyed exploring the four online models. With the exception of the StarLogo Nova model, the sites provided clear explanations of the demonstrated phenomena. When asked to provide their favorite and least favorite simulation and rationale, the Washington Post article had multiple votes on both ends (6/16 favorite and 6/16 least favorite). Interestingly, the rationale for both sides centered around simplicity—some students valued the linear nature and clear animations, while others found the setup confining and wished for more flexibility. The two simulations with more polished animations (Washington Post and Melting Asphalt) received a combined 12/16 “best” votes. The Harvard model was seen as too rigid and boring, although students acknowledged that it was the most authentic. The StarLogo Nova model confused many students, which was anticipated, but the goal of inclusion was to introduce the platform for the second activity. If Activity 1 is to be run alone, the StarLogo Nova model should be replaced with another, more user-friendly model.

**Activity 2: Model creation**

As an instructor, I was invigorated by the discussions and level of commitment shown by the majority of students. Students spent 5 to 25 h (average 12 h) coding, with some creating models from scratch (Fig. 1), while most used established programming for spread of an infectious disease. There were also students who struggled with the logistics and technical details of the project, since this was both their first experience of a fully asynchronous class and first exposure to any kind of coding. These issues may be avoided by providing more time for completion and requiring students to work through the scaffolded coding instruction rather than allowing them to begin immediately. Of the students completing the post-assignment survey, only 1 of 11 thought this project was not worthwhile. Providing more formal connections between coding and modeling and biology may resolve this.

Positive change in mastery of complex systems and disease spread was observed through paired pre- and post-surveys from 11 students. Qualitative analysis of an open-ended question showed increased reference to multiple core ideas: for “Variables or Factors,” 4 of 11 students (pre) to 10 of 11 students (post); “Simulate or Model,” 0 of 11 to 8 of 11 students; “Interact or Adapt,” 3 of 11 to 7 of 11
students; and “Predict,” 2 of 11 to 9 of 11 students. These positive gains corresponded with student perception. Those agreeing with or who were neutral regarding the statement “I can modify computer code to answer questions about biology” went from 1 of 11 to 10 of 11, and 6 of 11 said they enjoyed computer simulations more than a typical lab experiment. With regard to disease spread, all students were more confident in their understanding of its complex nature, the effect of human behavior, and the utility of computers to make predictions, in comparison with their responses on the initial survey.

While there is a learning curve in building and troubleshooting models, working with students individually provided tremendous opportunities for “just-in-time teaching.” Student correspondence by e-mail and virtual meetings were filled with excitement about showing me what they learned and created, with 7 of 11 students agreeing they enjoyed the project more than they thought they would.

In summary, both activities provided students with online exploration of a timely topic. These activities can be used as stand-alone projects but, paired together, they provide students with an effective introduction to complex systems, coding, and predicting infectious disease.

SUPPLEMENTAL MATERIALS

Appendix 1: Descriptions of models

ACKNOWLEDGMENTS

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REFERENCES


