



Students in Differential Equations and Epidemiology Model a Campus Outbreak of pH1N1

Meredith L. Greer^{1*} and Karen A. Palin² Departments of Mathematics¹ and Biology², Bates College, Lewiston, ME 04240

INTRODUCTION

We describe a semester-long collaboration between a mathematics class and a biology class. Students worked together to understand and model the trajectory of the pandemic HINI, pHINI, outbreak across campus in fall 2009 (4). Each course had about 30 students and was an upperlevel elective for majors. Some mathematics students had taken no college-level biology, and some biology students had taken no college-level mathematics. All students had taken at least three quantitative courses, so they had some experience working with data. Our goals were to allow students to work with and model a real data set that affected them personally (5, 6, 7), to explore how the outbreak spread within our small campus, and for students to share their areas of expertise. This project created opportunities for synthesis and evaluation (1).

PROCEDURE

The fall 2009 outbreak of pHINI on campus provided real data relevant to our students. Shortly after the outbreak, Professors Greer and Palin asked our campus Director of Health Services for these data and filed an Institutional Review Board application for this project. Data collected included incidence, isolation, vaccination status when vaccine became available, and demographics. All identifiers were removed.

Our courses were scheduled for the same time slot in the winter 2010 semester and we planned four joint meetings. Before the first meeting, each instructor asked her students to consider ways to explore the outbreak from the perspective of their discipline. Students contemplated what knowledge they would bring to the data analysis and what their colleagues in the other course could contribute.

At our first joint meeting, early in the semester, we administered a survey assessing knowledge about pHINI. Professor Palin reviewed influenza virus biology and discussed current knowledge about pHINI spread. While students were familiar with pHINI due to extensive media coverage, our discussion centered on the initial report from the World Health Organization declaring the pandemic in June, 2009 (www.who.int/mediacentre/news/statements/2009/hInI_pandemic_phase6_20090611/en/index. html), and Morbidity and Mortality Weekly Reports from the CDC documenting incidence in the US. Professor Greer introduced SIR (Susceptible-Infected-Removed) differential equations models (2, 3) (Fig. I) and showed their use with past influenza outbreaks. Students then formed small mixed groups to discuss both topics. They brainstormed use of SIR-style models and what data they would need. Epidemiology students had completed the NIH web-based training course "Protecting Human Research Participants" and shared information about ethical research protocol.

Our second joint meeting was one month later. As homework, using Health Center data, Epidemiology students had generated incidence and prevalence graphs and mapped the outbreak by residence halls to investigate transmission between students with potential for high levels of interaction. They had also estimated incidence rates to use in SIR modeling, making assumptions from knowledge of student behavior during the outbreak. During class, professors and students discussed students' assumptions about incidence and prevalence. Students considered together how factors such as student risk behaviors affected transmission. Students further discussed how the following could affect their modeling: illness duration, length of time for pHINI vaccine to provide antiviral protection, and any overlap between students immunized at vaccine clinics and those already immune due to illness.

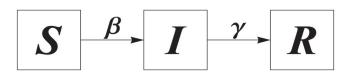


FIGURE I. A compartmental diagram for a standard SIR (Susceptible-Infected-Removed) model. Each individual in a population is in exactly one compartment (S, I, or R) at any given time. Arrows indicate movement is permitted between compartments. The parameter β governs likelihood of infection, and the parameter γ relates to length of time for an infectious individual to recover. This model can also be represented as a system of three differential equations, quantifying the changes over time in each of the three compartments S, I, and R.

^{*}Corresponding author. Mailing address: Department of Mathematics, 2 Andrews Road, Bates College, Lewiston, ME 04240. Phone: 207-786-6283. Fax: 207-753-6949. E-mail: mgreer@bates.edu.

GREER and PALIN: MATH AND BIOLOGY STUDENTS MODEL PH1N1

The third meeting was two weeks later, just past the semester's halfway point. Students in small groups used the mathematical software *Mathematica* to simulate their models. They varied parameters to best fit the data with their models (see Fig. 1). For example, students compared a fixed transmission parameter β with a time-dependent transmission function $\beta(t)$ that described higher influenza transmission on weekends, to explore increased social mixing. Students also varied γ , the recovery parameter, as duration of infectious period was not yet known from the public health literature. The mathematics students led this part of the project, but several groups had students with strengths in both subject areas, and these groups found the most interesting models to describe the outbreak.

On the last day of classes, we held our final joint meeting. The Dean of Students, the Director of Health Services, and other Health Center staff joined us. We administered the same survey as we had on the first day and two Epidemiology students presented data they had collected comparing outbreaks at other colleges with the outbreak at Bates (4). Students, professors, and visiting administrators discussed our analyses and what could be done differently in a future outbreak.

CONCLUSION

We accomplished our two major goals: to explore ways to collaborate across disciplines to address a common topic and to provide students with real-world experience with data. Our goal was not to fully analyze the outbreak that occurred at Bates; we did not have access to the data necessary to accomplish this. In the project discussed here, students worked with real data, rather than text or literature examples. They quickly realized that data are often incomplete, not all data collected are useful, and potentially useful data are not always collected. These are important realizations for those studying mathematics and biology. Since historical models for influenza spread did not fully explain what happened on our campus, our students questioned assumptions and tried new models.

Groups comprised of students from both classes worked together during the first three joint meetings. They produced ideas, predictions, and modeling results. They considered effects of thinking of the campus community as open or closed: in an open community, a significant number of people enter and leave the Bates campus, whereas in a closed community students mainly interact with each other. They wondered whether pHINI spread more easily over the weekend, due to parties and other social events. They questioned when a student had recovered and was no longer infectious, noting that symptom relief or resolution could cause students to break self-imposed isolation and return to classes.

During Mathematica simulations, groups first used a combination of epidemiological knowledge and trial-anderror to estimate best parameters for fitting a standard SIR model to the Bates data. The groups incorporated changes to the model according to which hypotheses they wished to test, such as whether certain one-time or weekly events changed infection rates.

We compared student results on the pHINI quiz (written by the biologist) given in our first and last joint meetings. Among Epidemiology students, student responses held steady or improved for all questions. For Differential Equations students, class response improved on three questions, but fewer students answered correctly on three other questions. Three unscored quiz questions asked students to make predictions, which they then examined through data analysis and modeling. These included estimating the basic reproduction number R_0 , the typical number of cases caused by a single infectious person in an otherwise susceptible population, and considering vaccination levels necessary for herd immunity in both open and closed communities.

We polled our students at the end of the semester, and then requested further feedback two years later. Some students felt the combined days were the best of the semester. These tended to be students with interest and experience in both fields. Other students saw both positives and negatives: they found the idea very interesting, but had different preferences for how we used class time, or felt their particular small group did not gel as well as they would have liked. Some of the mathematics students enjoyed the chance to see real data brought into a course that is otherwise more theoretical. One epidemiology student noted that working together in mixed groups forced students to bring their different perspectives together and that by the end of the semester, both sets of students had a "pretty good" working knowledge of both perspectives.

We saw, and students seconded, ideas for improvement. These included making it clearer, each time we met, what we hoped to accomplish. With multiple weeks between meetings, some students no longer recalled our exact goals. Further, on a given class day about half the students seemed less able to contribute: early in the semester the math students mainly learned from the biology students, and on *Mathematica* day the biology students relied on help from their mathematics teammates. Common preparatory readings, homework assignments, and class discussions may increase the abilities of all students to participate more equally.

We believe this was a solid first attempt to integrate the concepts explored in both Differential Equations and Epidemiology and to provide our students with exposure to real world situations. Students worked in teams to expand their perspectives and knowledge; for future combined courses, we would increase student preparation before joint meetings and implement more thorough assessment. After the winter 2010 semester, the professors continued the modeling and data analysis, resulting in a publication (4) and a new research direction. We look forward to other ways of integrating our courses and our scholarship, in keeping with the liberal arts tradition.

ACKNOWLEGMENTS

The authors declare that there are no conflicts of interest.

REFERENCES

- Anderson, L. W., D. R. Krathwohl, P. W. Airasian, K. A. Cruikshank, R. E. Mayer, P. R. Pintrich, et al. 2000. A taxonomy for learning, teaching, and assessing: a revision of Bloom's taxonomy of educational objectives, abridged ed. Allyn & Bacon, Boston, MA.
- Brauer, F., and C. Castillo-Chávez. 2000. Mathematical models in population biology and epidemiology, p. 281–287. Springer, New York, NY.

- Kermack, W. O., and A. G. McKendrick. 1927. A contribution to the mathematical theory of epidemics. Proc. R. Soc. Lond. 115: 700–721.
- Palin, K., and M. L. Greer. 2012. The effect of mixing events on the dynamics of pHINI outbreaks at small residential colleges. J. Am. Coll. Health. 60: 485–489. [Online.] Available from: http://www.tandfonline.com/doi/ abs/10.1080/07448481.2012.696294.
- Riegelman, R. K., S. Albertine, and N. A. Persily. 2007. The educated citizen and public health: a consensus report on public health and undergraduate education. Council of Colleges of Arts & Sciences, Williamsburg, VA.
- Steen, L. A., ed. 2005. Math & Bio 2010: linking undergraduate disciplines. The Mathematical Association of America, Washington, DC.
- Stroup, D. F., and S. B. Thacker. 2007. Epidemiology and education: using public health for teaching mathematics and science. Public Health Rep. 122: 283–291.