Implementation of First Year Biomath Courses at the Ohio State University

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Name of Institution: The Ohio State University	
Size	about 38,000 undergraduate students
Institution Type	large state university with PhD program
Student Demographic	recent high school graduates with interests in mathematics, statistics, and/or biology
Departments and Program Structures	Six departments (Mathematics, Statistics, and four biology), plus the biology major administered by the Center for Life Sciences Education, all inside the College of Arts and Sciences
Web Pages	`http://www.stat.osu.edu/~lkubatko/CAUSEwebinar` `http://rumba.biosci.ohio-state.edu`

Abstract

With approximately 38,000 undergraduates on the main campus in Columbus, Ohio, The Ohio State University (OSU) is one of the largest schools in the nation, providing a significant challenge in the creation of a BioMathematics curriculum that will adequately serve the needs of this undergraduate population. In this article, we describe our initial steps toward this goal, namely, the development and implementation of several first-year BioMath courses for students majoring in the Biological Sciences at OSU.

STRUCTURE OF COURSES

- Weeks per term: 10 weeks (will convert to semesters in 2012)
- Classes per week/type/length: three 48-min lectures, two 48-min recitations
- Average class size: Calc I = up to 120; Calc II = up to 60; Stats = up to 40
- Enrollment requirements: Calc = standard; Stats = Calc II prerequisite
- Faculty per class, TAs: each course has 1 faculty and 2, 1, 1 TA respectively

Introduction

The Ohio State University (OSU) is one of the largest schools in the nation, with over 50,000 students on the main campus in Columbus, Ohio, approximately 38,000 of whom are undergraduates. The administrative structure of the University consists of eighteen distinct colleges, with a total of 167 undergraduate majors. The four biological science departments, housed within the College of the Arts

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and Sciences serve approximately 2,300 undergraduates who obtain one of eight majors. Also, OSU houses the NSF-funded Mathematical Biosciences Institute (MBI), which provides a link between the mathematical and biological sciences.

In collaboration with the biological science departments at OSU, the Departments of Mathematics and of Statistics have developed courses to provide a quantitative foundation for the training received by undergraduates majoring in a biological sciences (see accompanying article in this volume for details about the development of these courses). The courses include a two-quarter sequence in calculus and a one-quarter course in statistics. The calculus courses are taken by freshmen who have placed into calculus and who plan to obtain one of the eight biological science majors, and are structured so that students those who complete them are prepared to continue with the more traditional Calculus III course offered by the Mathematics Department. Two sections of the calculus sequence have been offered in every academic year since 2006-07, serving approximately 160 students each year. The course in statistics is intended to serve as a follow-up elective course; students are recruited primarily from the calculus sequence, though any student who has completed two quarters of any calculus can enroll. The statistics course has been offered during the Spring quarter every year since 2007, with approximately forty students per section.

In this article, we describe each of these courses in detail. The next section describes the structure of each course, the material covered, and projects and class activities included. The Discussion section includes reflection on what aspects of the courses worked well and what needs improvement. We then discuss some more advanced courses that have recently been added to our BioMath curriculum. We conclude with a discussion of our long-term vision for the BioMath curriculum at OSU.

Description of First Year BioMath Courses at OSU

OSU followed the quarter system rather than the semester system until the Fall 2012 semester, with an academic year thus consisted of three 10-week quarters (Fall, Winter, and Spring) with a week of final examinations following each. Quarter courses generally comprised 3-5 credit hours of instruction per week, and often consisted of a mixture of lecture' and laboratory sections. Each of the BioMath courses we developed was offered for 5 credit hours, with three 50-minute lectures taught by a full-time faculty member and two 50-minute laboratory sessions taught by Graduate Teaching Assistants (GTAs) per week. The lecture sessions were often large (ranging from 40 to 100 students), while the laboratory sessions generally had no more than 30 students. Laboratory sessions were devoted to hands-on activities and problem-solving, while lectures covered the introduction and discussion of new concepts. We now describe these courses in detail.

Calculus I and II for the Life Sciences

Both calculus courses were taught from the text *Calculus for Biology and Medicine* by Claudia Neuhauser (2003). The Calculus I course covered the first five chapters of the text, including sequences and difference equations (2 weeks), limits and continuity (2 weeks), and differentiation and applications (6 weeks). The Calculus II course covered material in Chapters 6, 7, and 8: basic integration (2 weeks), advanced integration techniques (6 weeks), and differential equations (2 weeks). Course grades were based on weekly homework and quizzes, a project, two midterm examinations, and a comprehensive final examination.

An innovative aspect of the courses was the inclusion of group projects. During the first offering of Calculus I, ten projects were designed by the instructors and GTAs. In subsequent quarters, projects have been developed and supervised by post-doctoral researchers associated with the MBI. Each quarter, several post-docs developed projects and gave a lecture advertising their projects to the students;

students then selected one of the projects to study in a group of three to five students. The post-docs arranged two additional class meetings to work with the students, who were also expected to spend time working on their own outside of class. Each project contained several questions to be addressed, and each student was required to write the solution to at least one of the questions. The group was responsible for combining the solutions to the questions to form a cohesive written report for the project as a whole. This has the advantage of giving students experience in writing in a research-like setting. The group reports contributed the equivalent of two homework assignments to each student's grade in the course. Here are examples of the projects.

Tumor growth and treatment. Differential equations can be used to model tumor growth. A tumor cell divides, generating two daughter cells with unlimited ability to reproduce. Initial rapid growth supported by abundant nutrients such as oxygen and glucose is followed by slower growth as the population size increases. Injecting anti-cancer drugs that kill a fraction of tumor cells per unit time may reduce the size of the tumor cell population. The project involves studying the differential equations to find the best strategy for reducing tumor size.

Analyzing cartilage health. In an osmotic loading experiment, chondrons (cartilage cells with encapsulating pericellular matrix, PCM) are extracted from cartilage and placed in different external concentrations of sodium chloride in water. Depending on the concentration of the sodium chloride, the chondron will either swell or shrink. We look at how the volume of the PCM changes with respect to the different external concentrations of sodium chloride in water.

Fisheries management. Humans catch fish for a variety of reasons, such as for food or for sport. While these purposes may have merit, it is important to realize that there is not an unlimited number of fish in the sea. The National Marine Fisheries Service was formed by the U.S. government to manage marine resources in the U.S. In order to do their jobs, their scientific research teams use many tools, including mathematical models. In this project we explore a hypothetical fishery model for a sea bass population within an enclosure.

The material given to the students consisted of an expanded verbal description followed by the formulation of a mathematical model for the situation. The students were then asked to solve a series of problems using the model and to interpret their results. Also, the students were provided with information concerning expectations from the groups, both for functioning of the group as a whole and for individual interactions of each student with the group. The principal mathematical tool for the Calculus I projects is the derivative; differential equations, when they occur, are accompanied by solutions that the students must verify.

In the Calculus II projects, the main tools are derivatives and integrals, and many involve solving some ordinary differential equations. Example projects are:

Brain waves with noise. An EEG (electroencephalogram) machine measures local field potentials in the brain by recording from electrodes placed on a patient's scalp. These potentials represent an electrical signal from a large number of brain cells called neurons. Monitoring the EEG recording is useful in assessing brain activity and in diagnosing conditions such as epilepsy, sleep disorders, and coma. This project examines brain wave power when the signal is noisy.

Grass management. A modern method to raise cattle consists of preventing cows from grazing in a field until the grass has reached an optimal height. When the grass is too short, it cannot recover well from being cropped. Older grass grows more slowly, may become senescent, and is less tasty to cows. In this project we examine grass growth and its optimal management.

Drug absorption. Understanding therapeutic and adverse drug reactions is important in the treatment of many diseases, particularly cancer. Two models for drug absorption and toxicity are examined to compare injected drug therapies with a polymer delivery system.

Statistics for the Life Sciences

This course, intended as an optional course to follow the calculus sequence, was taught from *The Analysis of Biological Data* by M. C. Whitlock and D. Schluter (2009). Material selected from Chapters 1 through 17 of the text was included, with additional materials provided by the instructor that built on the students' knowledge of calculus (the text does not assume Calculus). Topics included descriptive statistics and graphical methods (1 week), probability, including Bayes Theorem (1 week), discrete distributions and the analysis of categorical data (2.5 weeks), one- and two-sample inference for means and variances (2.5 weeks), experimental design (1 week), and correlation and regression (1.5 weeks).

As in the calculus sequence, assessment was based on weekly homework and in-class examinations. The lectures were in the traditional style, though activities were incorporated into a few of the sessions. The recitation sessions were divided between problem-solving sessions and activity sessions. In the activity sessions, students used the StatCrunch software (StatCrunch, 2012) to analyze biological data sets after being given an introduction to the biological setting. Results of their analyses were brought into the lecture sessions and used as examples for subsequent topics in many cases, creating continuity between the recitation sessions and the lectures. A short lab manual for the course can be found at `http://www.stat.osu.edu/~lkubatko/CAUSEwebinar`.

Examples of the data sets included in the course and with the topics they illustrate are:

Fisher's iris data. A well-known data set studied by R. A. Fisher includes measurements on characteristics of three species of irises, including sepal length, sepal width, petal length, and petal width (Anderson, 1935; Fisher, 1936). These data were used in several ways. When the normal distribution was introduced, students used it to explore the distribution of characteristics in the recitation session using the StatCrunch software. They examined histograms and normal probability plots for the data when all three species are grouped together and for each species separately. The data is later used in lecture to motivate hypothesis testing by asking whether the mean sepal width differs between pairs of species. After an example is worked in lecture, the ideas are reinforced in recitation by carrying out hypothesis tests using the StatCrunch software.

Population frequencies of human chemokine receptor gene variants. A genetic variant of the human chemokine receptor gene appears to provide strong resistance to HIV infection. This variant is found in all European populations with varying frequency. Lucotte and Mercier (1998) studied a sample of 2,522 people throughout Europe to determine their genotypes, and found an overall allele frequency for the gene variant of approximately 9%. In the recitation session, students are given this information as background to the problem (with some added discussion about what is a genotype). They then compute the expected frequency of this gene variant in various European subpopulations, and compare them to the observed data of Lucotte and Mercier (1998). Although hypothesis testing has not yet been formally introduced, the students compute quantities similar to p-values by examining the probability of observing the data given in the paper if the variant gene frequency actually is 9%. This example is used to motivate hypothesis testing later in the lecture sessions.

Old-growth forest data. This data set consists of an extensive survey of an old-growth beech-maple forest carried out at the James H. Barrow Field Station (owned and maintained by Hiram College in northeastern Ohio) during the summer of 1993 by Laura Kubatko. The goal of the data collection was to assess the diversity and distribution of tree species in the forest. The data were collected by subdividing the forest into 50m × 50m plots. Within each of sixty-seven plots, four 10m × 10m sub-plots were randomly selected to be surveyed. All tree species occurring within the sub-plots were counted and recorded. The diameter at breast height (dbh) was measured for any tree larger than 3.0 cm dbh. An interesting feature of this data set is that the forest can be divided into four distinct areas that vary in composition of species and size-class distributions due to various external stresses (e.g., chestnut blight and an area affected by a tornado in the early 1970s) and physical characteristics (west-facing slopes).

These data are used in the course to give students experience with examining and comparing distributions. When discussing summary statistics and graphical displays, students are asked to use the StatCrunch software to find graphical displays for the counts of the number of trees of each species in various areas of the forest and for the distribution of trees among size classes (based on dbh). Later, the data are used to compare areas of the forest using hypothesis tests and confidence intervals.

Discussion

Successes

Feedback from the courses has been positive. Students seemed motivated and interested in what was taught, and many commented on its usefulness to them in their future careers. The current cohort of students in the courses is generally well-prepared for this level of mathematics. As we look to expand the offerings to include a broader group of students, our approaches may need to be adjusted to accommodate differing levels of preparation among our students.

The class structure (three lectures and two recitations per week) worked well for several reasons. One is that it divides our potentially large (40-100 student) lecture sections into smaller groups, so that students can receive more individual attention. This allows for activities (such as the calculus group projects) and computer exercises (such as analysis of real data using StatCrunch in the statistics course) to be included. Another advantage of this format is that the GTAs were able to get experience teaching students from the biosciences. The GTAs were involved in developing course materials for the recitation sessions, and were therefore able to learn how to communicate with this group of students. Since the GTAs are the next generation of instructors in biomath, the early exposure to such courses with the guidance of a faculty mentor is very valuable. Although the GTAs were not given special training in preparation for teaching the courses, we worked to ensure that they were interested in teaching in this setting. All GTAs were carefully mentored throughout the quarter.

Another positive feature was the inclusion of the MBI post-docs in the calculus sequence through the development and mentoring of the student projects. The exposure of the undergraduate students to a variety of research areas in BioMathematics and the interaction with the BioMathematics community at OSU is beneficial in creating an interest in and appreciation for interdisciplinary work. Several of us have had discussions with students interested in pursuing undergraduate research projects in these areas, and we expect such interactions to continue to increase over time.

Challenges

One challenge in designing and implementing the courses was that of finding textbooks with an appropriate mix of biological motivation and mathematical rigor. We were happy with the Neuhauser text used in the calculus sequence in that it was easy to teach from, as it is similar to a traditional calculus text but infused with biological examples. However, other books (e.g., Adler 2004) that are more oriented toward biology-driven mathematics than calculus per se are also appealing. An important point to consider is that some students in these courses may decide to continue in the traditional mathematics curriculum, and thus the courses need to prepare them to do so.

It was also difficult to select the topics, both biological and mathematical, that should be covered in the courses. The topic coverage in both the Calculus and the Statistics courses was similar to what would be covered in traditional courses, though the time spent on them varied somewhat. On the biological side, the students consisted largely of freshmen who, while mathematically prepared for the courses, were just beginning their study of biology. Thus we often had to teach a fair amount of the biology underlying our examples, as well as the mathematics, which could be a bit overwhelming for the students (and for us!) at times. In the future, particularly as we convert our courses to the semester system, we hope to work more closely with faculty in the biological sciences to understand the freshmen biology curriculum better, which will allow us to use examples that utilize biological concepts to which the students have been exposed, and to gain a further appreciation for which mathematical and statistical topics will be most relevant for students in their future study and careers.

A final challenge is recruiting students to take the elective courses (Statistics and the courses described in the next section) following the calculus sequence. Because the students are freshmen, they are also taking laboratory courses in biology and chemistry, which is a substantial academic load in the first year. It may be more convenient for students to return to mathematics courses in their second or third year, when they have more flexibility in their scheduling, and we therefore expect these courses to grow.

BioMath Courses at OSU Beyond the First Year

In addition to the first-year courses, we have developed two additional courses to enhance student interest in mathematical biology at OSU. The first is an undergraduate seminar that has been developed as a result of our recently-funded NSF UBM grant for undergraduate research in mathematical biology at OSU. As part of our program, called RUMBA (Research for Undergraduates: adventures in Mathematical Biology and its Applications—see `http://rumba.biosci.ohio-state.edu` for more information), the seminar course is offered in each academic term. It meets for one hour each week and consists of talks or discussions led by PIs for the program and speakers from within the OSU BioMath community. The outside speakers have included faculty in Mathematics, Statistics, and Biological Sciences, Visiting Scholars at the MBI, and MBI post-docs. The seminar enrolls approximately fifteen undergraduates at all acamedic ranks (freshmen to senior) and a variety of majors (mathematics, biology, environmental science, pre-medicine, etc.). Student evaluations have been very positive, and we feel that the course is succeeding in its goal of increasing interest in and awareness of the field of mathematical biology.

The second new course is titled Introduction to Mathematical Biology and was taught for the first time during the 2009-2010 academic year. The topics included population dynamics (logistic growth model and Lotka-Volterra predator-prey model), epidemiological modeling, modeling of competition, neuronal dynamics, and enzyme kinetics. We expect that this course will be offered every year. We have also added a mathematical biology track within the math major. All of these recent efforts build on our earlier curriculum development to strengthen the undergraduate BioMath program at OSU.

Future BioMath Curriculum Development at OSU

Our most recent efforts in BioMath curriculum development at OSU are focused on converting our courses to the semester system which will take effect at the start of the 2012-13 academic year. Our goal is to refine them to meet the needs of broader groups in the biological sciences and the university as a whole. At present, our calculus sequence accommodates a maximum of 160 students per year, which is just a fraction of entering students planning to major in biological sciences. Students majoring in health science fields may also benefit from taking these courses rather than the traditional calculus sequence.

One reason for our success has been the presence of a group of faculty working in mathematical biology who interact with both the mathematical/statistical and biological communities at OSU. This has been facilitated by the MBI, several recent joint hires between departments (including such department as Mathematics; Statistics; Evolution, Ecology, and Organismal Biology; and Molecular Genetics), and several hires of faculty within the Mathematics Department who work in mathematical biology. As we continue to assemble a community of interdisciplinary researchers, we hope to build our curriculum further. Two areas of growth that have been discussed are the development of courses that enable students in one field to obtain a major or minor in the other, and the development of interdisciplinary degree programs, such as the BioMath concentration. The recent addition of our RUMBA program has enabled us to establish an interdisciplinary research program for undergraduates at OSU, and has thus facilitated the continued enhancement and expansion of our curriculum development.

Overall, we view our mission as helping undergraduate life science majors learn to think in a quantitative manner, whether for modeling biological phenomena or analyzing experimental data. With this goal in mind, we have enjoyed meeting the challenges of cross-department collaboration on curriculum development in a large university, and we look forward to continuing our progress.

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