Turning the Potential Liability of Large Enrollment Laboratory Science Courses Into an Asset

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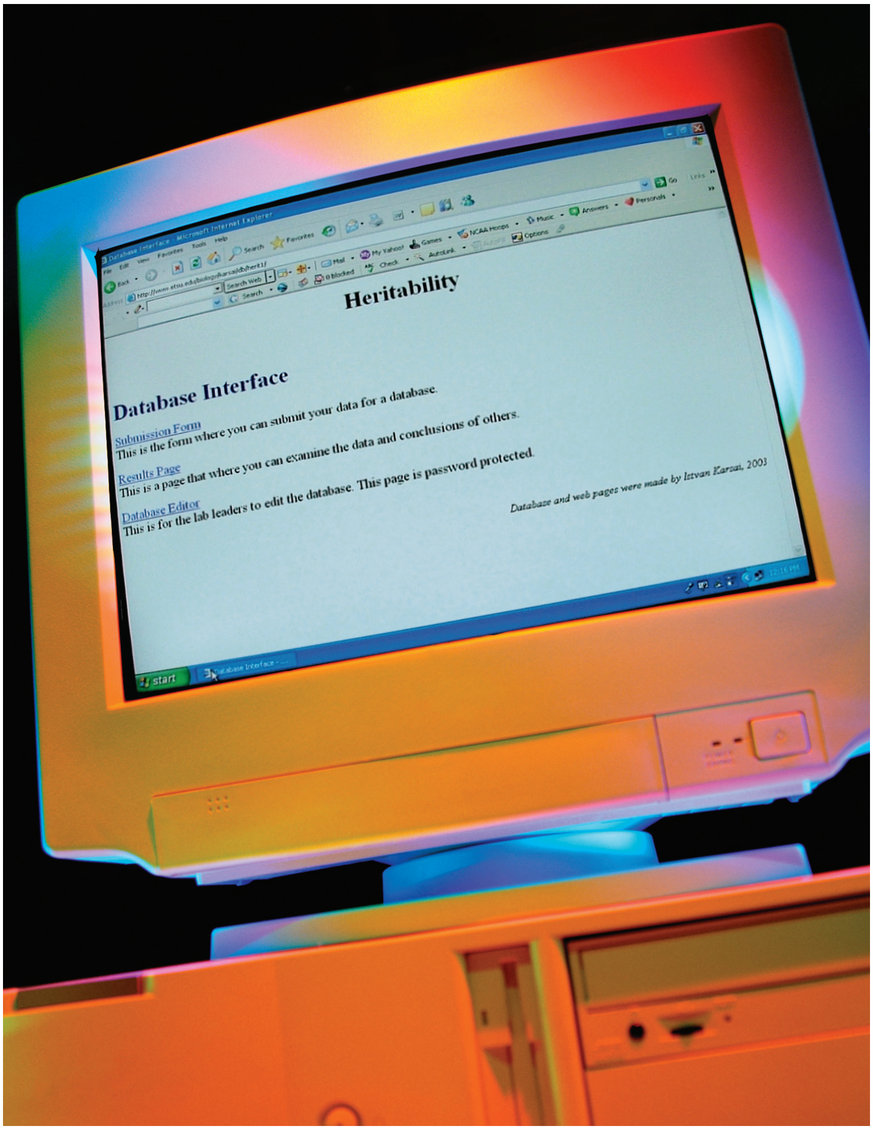
Data sharing among multiple lab sections increases statistical power of data analyses and informs student-generated hypotheses. We describe how to collect, organize, and manage data to support replicate and rolling inquiry models, with three illustrative examples of activities from a population-level biology course for science majors.

The Society for College Science Teachers' position statement on introductory college level science courses (Halyard 1993) challenges those responsible for such courses: "Laboratory activities should feature experimental procedures that require students to think about, select, generate, test, and evaluate the effectiveness of hypotheses and the scope of their results." As faculty in a university where multiple lab sections are taught by graduate teaching assistants or part-time temporary faculty, we find it difficult to provide the individual attention required to monitor projects conducted by small groups or individual students (Dimaculangan et al. 2000; Lunsford 2003; Norton et al. 1997; Ortiz 1994; Stager 1994; Tolman 1999).

Like Grant and Vatnick (1998), "we lack the resources to supervise large numbers of independently active learners that populate our introductory courses," and consequently have adopted what they call *bounded inquiry*: "…students' research questions and study subjects are instructor constrained but hypotheses…are not a priori speci-



Heritability

Database Interface

Submission Form
This is the form where you can submit your data for a database.

Results Page
This is a page that where you can examine the data and conclusions of others.

Database Editor
This is for the lab leaders to edit the database. This page is password protected.

Database and web pages were made by Istvan Karsai, 2003

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fied." We are encouraged by apparent success involving graduate teaching assistants as reported by Sundberg and Moncada (1994) and by Glasson and McKenzie (1997). Assuming that properly prepared graduate assistants in multiple-section general education science labs can implement bounded inquiry, we offer ideas for how one might take advantage of multiple sections to enhance the inquiry experience.

With support from Howard Hughes Medical Institute to enhance undergraduate education in biological sciences, we modeled a community of scholars in general education biology labs by sharing data gathered in inquiry activities. We created databases that facilitate such data sharing and management in the two-semester nonmajors course and in two of three semesters of our majors sequence. The ability to easily pool data collected by multiple lab sections, both within and among semesters, effectively converts what is often seen as a liability—the need to teach large numbers of students in multiple sections—into an asset by enhancing statistical power of data analyses so that results are more meaningful, or selecting a subset of data from a larger database to inform further analysis.

In a population-level introductory biology course at our comprehensive regional university, fall semester enrollment is typically about 100 students with five sections of lab, and spring semester enrolls about 60 with three lab sections. The same part-time temporary faculty member teaches all lab sections. We illustrate two large-enrollment-dependent approaches called *replicate* and *rolling* models for inquiry in this multiple-section environment. These models differ in how they use previously collected data: The replicate model pools data to enhance power of statistical tests, while the rolling model uses previous results to suggest which hypotheses warrant further experimentation.

Databases

When we planned how to store and manage large data sets we had several alternatives. First we created preprogrammed Excel spreadsheets where students could enter data to see in real time how different characteristics (distributions, slopes, and so on) change as data accumulate in the spreadsheet. This approach was effective for individual use, but analyzing large data sets this way is very labor intensive. We needed a central data depository to collect and store data for future use, but one that allowed multiple individuals to enter and retrieve data simultaneously from different computers. We also had to protect databases from re-editing by students or accidental deletions, but we wanted instructors to be able to edit databases to correct obvious errors. Combining an Access database with a network-based form proved the best solution to these requirements. Network security ensures database integrity. Students use a web browser to communicate with the database via a simple form.

Every lab activity has a homepage or a link (for examples see *www.etsu.edu/biology/BIOL1131.htm*). From the main link, students go to the database interface where three choices are available. The first is a submission form where students can submit data. The submission form is clear and simple, but there are explanations for how to fill in blanks. If the wrong type of data are entered, or if data are out of reasonable range, the system asks the user to correct the error before data go into the database. If all data meet the predetermined criteria, the system accepts the submission and the student receives a confirmation page where all submitted data are listed. The server that stores the database processes incoming data using FrontPage Extensis protocols.

All data are available from the results page, the second choice on the database interface page. For security reasons, the Access database is accessible only via FrontPage Extensis protocol. Data are available in a table format. Simple instructions are provided for transferring data into an Excel spreadsheet. After transfer, students can filter data as instructed (for example, based on lab sections, gender, and so on). In some cases, when complex calculations are needed, we set up an Excel spreadsheet to do these calculations. Because data can only be retrieved but not modified and saved, this is a secure data retrieval process.

The third option from the database interface page is a password-protected database editor.

Replicate model

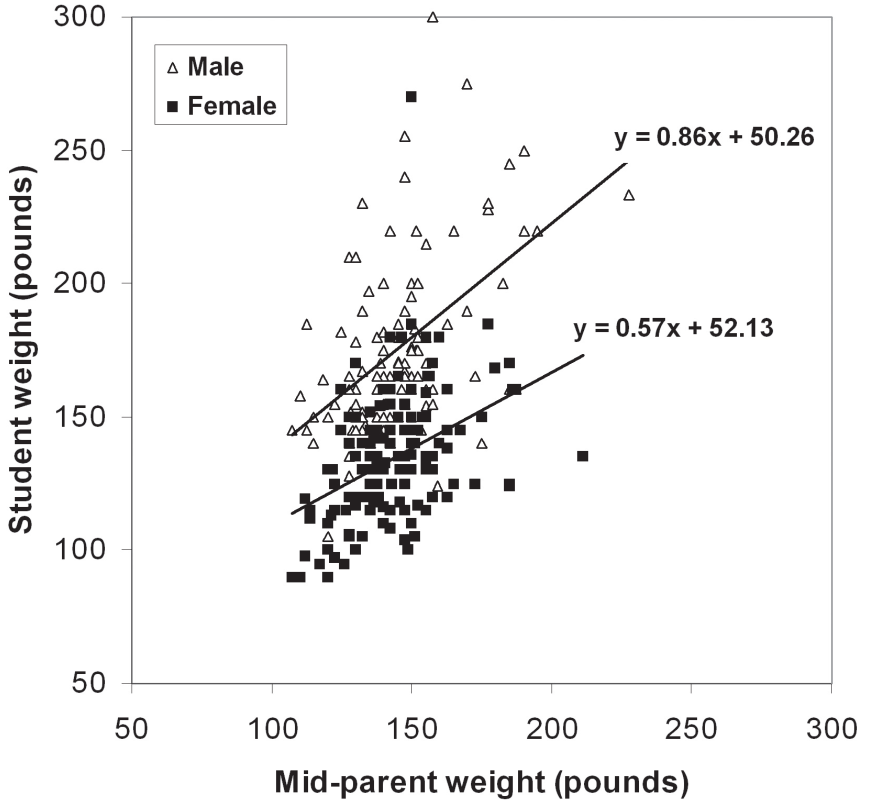
One constraint on accomplishing meaningful research in individual laboratory sections is low statistical power associated with studies that use only a few observations and relatively few replicates of experimental treatments. We have overcome this problem—and turned multiple lab sections into an asset—by combining observations of particular phenomena and experimental results from several lab sections, within and among semesters, into one statistical analysis. We have used this approach with observational studies of heritability of human height and weight, and with experiments on plant competition.

Heritability

Heritability (h^2) of continuous quantitative traits is the proportion (or percentage) of phenotypic variance in a population that can be attributed to genetic differences among individuals rather than to environmental effects. This is an important concept for understanding potential effects of selection on population means and variances for traits, such as body size and shape, behavior, intelligence, and so on, that are influenced by multiple gene loci. The ratio of the covariance (X,

FIGURE 1

Heritability of weight estimated as the slope of least squares linear regression of student weight on mid-parent weight at the same age: 86% for males (open triangles), 57% for females (closed squares). Note that the nonmetric English system of measurement was used for studies of weight because this is commonly used by Americans to discuss that variable.



Y) divided by the variance (X) is used to estimate the slope of least squares linear regressions. If X = average parent phenotype (usually called mid-parent value) and Y = offspring phenotype, we may estimate the proportion of phenotypic variance among parents that is passed on to offspring (heritability) as the slope of linear regressions of offspring phenotypes on mid-parent phenotypes of biological parents (Falconer 1981, p. 152). For one lab activity each semester, students record in a database self-reported values for their own height (inches) and weight (pounds) as well as the height and weight that their biological parents report for when they were a similar age. Such estimates—based on memory and perhaps biased for personal reasons—may not be as accurate as one might like for contributing to the human genetics literature, but as an educational activity they illustrate a method of analysis quite well.

Between fall 2003 and spring 2005, 14 sections of lab with enrollment ranging from 13 to 25 students conducted such analyses. Had they used only data collected by their own sections, the number of data points for linear regressions would have ranged from 4 to 14 for females and from 3 to 14 for males. Estimates of heritability based on such small data sets would have been quite variable: coefficients of variation (standard errors divided by estimates) for 28 estimates would average 192% for weight and 76% for height. It is difficult to interpret such variable results. Furthermore, heritability is a proportion that should range from 0.0 to 1.0 (0% to 100%), so negative estimates (7 of 56) and those greater than 100% (17 of 56) would have no meaningful biological interpretation.

To avoid such inaccuracies, students add their data to an online database to be pooled with data from previous lab sections, semesters, and years. Analysis of this much larger data set provides substantially more reliable estimates of heritability as evidenced by reduced coefficients of variation. As of this writing—using data for 116 males and 140 females from fall 2003 through spring 2005—those estimates (and coefficients of variation) expressed as percentages were: male height, h^2 = 79% (14%); female height, h^2 = 76% (10%); male weight, h^2 = 86% (17%); and female weight, h^2 = 57% (19%). We find it satisfying that these values are similar to estimates of heritability for human height and weight reported in professional literature (Brown et al. 2003).

As a graphical example, Figure 1 shows a comparison of heritability of weight for males and females. The observation that heritability for females is much less than for males suggests that variance in female weight is less affected by genetics and thus more affected by environment; this can provoke discussions of how peer pressure—part of the environment—may influence teenage females to control weight and thus express less of their genetic tendency.

Plant competition

The classic Lotka-Volterra model of interspecific competition suggests that one condition for stable coexistence at equilibrium is that the intensity of intraspecific competition must be greater than the intensity of interspecific competition (Hutchinson 1978, p. 117). This phenomenon results in niche partitioning among coexisting species when resources limit population growth for both.

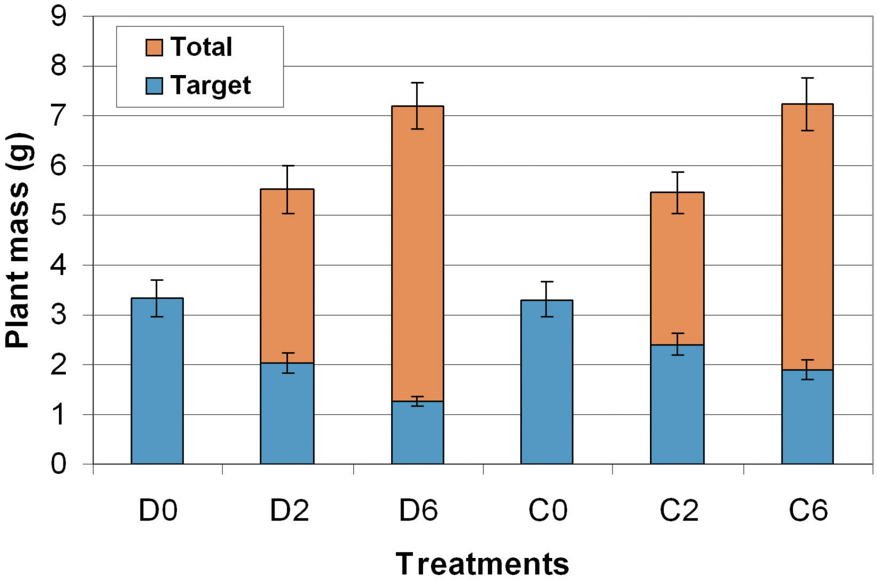
We use an additive experimental design to assess competition effects on plant growth (Harper 1977, p. 250). A target plant is surrounded by varying numbers of intraspecific (density effect) or interspecific (competition effect) competitors. In density treatments, target radishes are competing with radish neighbors; in competition treatments, target radishes are competing with barley neighbors. We chose these plant species because both seeds are readily available and germinate and develop rapidly, and they are species with widely divergent phylogenetic lineages.

One target radish seed is planted in the center of a four-inch pot in vermiculite, a relatively inert planting medium. A radish was chosen as the target because both green growth and size of the root can be used as performance indicators. Zero (control), two, or six competitors surround each target. After eight weeks in the greenhouse, target and competitors are harvested, washed of soil, dried, and measured for wet mass.

Students are asked to analyze data from their lab section and to write a lab report based on their analysis. For the first part of their analysis, students construct a stacked bar graph of the mean target mass and total biomass (target + neighbors) for each of the six treatments (Figure 2). This graph can be used as a visual aid to compare masses between different density and competition treatments. For the second part of their data analysis, students are asked to enter class data into an Excel spreadsheet and to perform a linear regression for target mass versus neighbor mass in density and competition treatments. Student *t* values corresponding to the null hypothesis of no competition (slope does not differ significantly from zero) are used to determine if increasing neighbor mass significantly reduces target mass. Another *t*-test comparing slopes of the density and competition treatments tests whether the intensity of intraspecific and interspecific competition are significantly different.

FIGURE 2

Mean plant mass (and standard errors) in density and competition treatments. D represents density treatments, C represents competition treatments; a number following D or C represents the number of neighbors.



After class, the instructor analyzes the class's data along with data from previous semesters and presents results of analysis of the larger data set the next week. Two trends have emerged from this study. First, in density and competition treatments, target mass decreases as the number of neighbors increase; that is, both types of competition significantly reduce plant mass (Figure 2). Second, target radish plants surrounded by six radish neighbors (D6) are smaller than targets surrounded by six barley neighbors (C6) (Figure 2). However, effects of intraspecific and interspecific competition on the target were similar when there were only two neighbors. Therefore, effects of intraspecific competition are more severe than effects of interspecific competition only when there are large numbers of neighbors (competitors). The other striking result that emerged from the full data analysis is that total biomass increases as number of neighbors increases from two to six. This observation has important agricultural and biodiversity implications—that mixtures can be more productive than monocultures (Tilman et al. 2001).

Rolling model

Rolling inquiry is another way to take advantage of multiple lab sections and to model a community of scholars. Students in one lab section identify a hypothesis and design an experimental test. They set up an overnight experiment, but leave it to the next section to gather resulting data and to analyze and interpret those results. In a group discussion, students in the second section then decide whether to repeat the same treatments (to enhance statistical power) or to modify them to test another hypothesis. This process continues through multiple sections and is completed when the first section

TABLE 1

Number of seeds or beads removed. Pooled data from multiple experiments.

Type 1	Type 2	X^2 value
Violet 122	Radish 43$^+$	37.82*
Violet 106	Radish w/ fat 43	26.64*
Bead 43	Bead w/ fat 22	6.79*
Seed (no fat) 96	Bead w/ fat 65	5.97*

* Significant at $p < 0.05$

$^+$ In one section, many seeds were dispersed by exceptionally strong winds.

finally gathers data from an experiment set up by the final section. All data are recorded in an online database so that each lab section can benefit from examining the larger data set to determine what hypotheses have already been tested, and which might bear repeating.

Ant preference for seeds

Students are given lecture instruction on the hypothesized ant-plant mutualism in which some plants produce seeds with an external fat body (eliasome). The energy reward of the eliasome presumably attracts ants that carry the seed to the nest and thereby act as dispersal agents (Dunn 2005). The experimental approach, suggested by Dr. B.D.J. Meeuse at the University of Washington, is conducted in the field and challenges ants with a choice between seed types. The design, referred to as a *cafeteria experiment*, has been used to show that ants of several species transport violet seeds to their nests (Culver and Beattie 1978). In the nest, eliasomes are usually removed but germination capacity is not impaired.

In a typical series of lab sections, the Monday section may choose to test the hypothesis that seeds with eliasomes are preferred over those without. They would set up a replicated experiment in which each pair of students lays out a circle of alternating violet and radish seeds. These plant species produce seeds of similar size and color but the violet seeds have an eliasome. The next morning, the Tuesday section collects data from the experiment laid out on Monday. They use a chi-square test to determine if the ants had a significant preference for violet seeds over radish seeds. If the violet seeds were preferred, the Tuesday section may choose to test whether the preference was caused by the presence of fat on the violet seeds. They may design an experiment using only radish seeds, half of which had a fat body added with a dab of Crisco. The radish seeds with fat might be preferred. If so, the Wednesday section could choose to focus more clearly on fat as attractant. They might remove the seed variable by using brown beads (of similar size to a violet seed), half of which had Crisco placed in the center cavity. If beads with fat were preferred over beads without fat, the Thursday section may then attempt to eliminate the color variable by giving ants a choice of different colored beads, all with added fat.

At the end of each series of experiments, the entire set of hypotheses, data, results, and interpretations is placed in the class database. Our results show that violet seeds are strongly preferred over radish seeds (Table 1). Ants maintain the preference for violet seeds even when radish seeds are coated with fat. However, we were surprised to learn that the fat we have used is not by itself a significant attractant when coating either a seed or a bead (Table 1).

Discussion

Replicate and rolling models provide benefits to students and instructors. The rolling approach relieves some of the tedium for instructors who must repeat the same experiment over and over. Similarly, students do not enter class already knowing the expected results garnered from conversations with peers previously enrolled in the course. Rather, students have the opportunity to test hypotheses developed through group discussions.

When we first introduced rolling models in fall 2000, a student survey asked whether this approach was more or less interesting and informative than a traditional lab; 54% chose “more.” But the same

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survey found that two projects using the rolling approach—ant dispersal of seeds, and sow bug habitat preference—received the lowest percentage of favorable responses (43% and 49% respectively) of eight lab activities. Discussion with students identified an important drawback of the rolling model: students do not get to analyze data from their own experiment. Electronic databases that allow students to review all hypotheses, data, and analyses were developed to overcome that objection. Though we have not conducted a follow-up survey, our impression is that students now feel more ownership of the entire experiment.

Accumulation and analysis of long-term data using the replicate model mitigates one of the most discouraging phrases used by science instructors: "The experiment didn't work, but if it had…." Rather than burdening students with the stigma of a failed experiment, all data are placed in a database. Experimental results somewhat removed from the mean or true value demonstrate natural variability inherent in biological systems; these data highlight the weakness of conclusions based on small sample sizes. For example, graphical presentation of heritability estimates allows students to view their class data points, regardless of location, and see that their points represent a few pieces of a larger picture. The fall 2000 survey mentioned above found that three projects using the replicate model—heritability of height, plant competition, and water flea population growth—received the highest percentages of favorable responses (74%, 84%, and 88% respectively). When asked whether combining data from the entire class was helpful or distracting, 88% of students surveyed chose "helpful."

Both laboratory-based instructional models also provide instructional benefits beyond the laboratory class. Real, long-term data, collected by students, are used in lectures to illustrate topics in evolution and population genetics. Moreover, these data have been made available to the mathematics department for use in courses in probability and statistics. ■

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