Journal of College Biology Teaching
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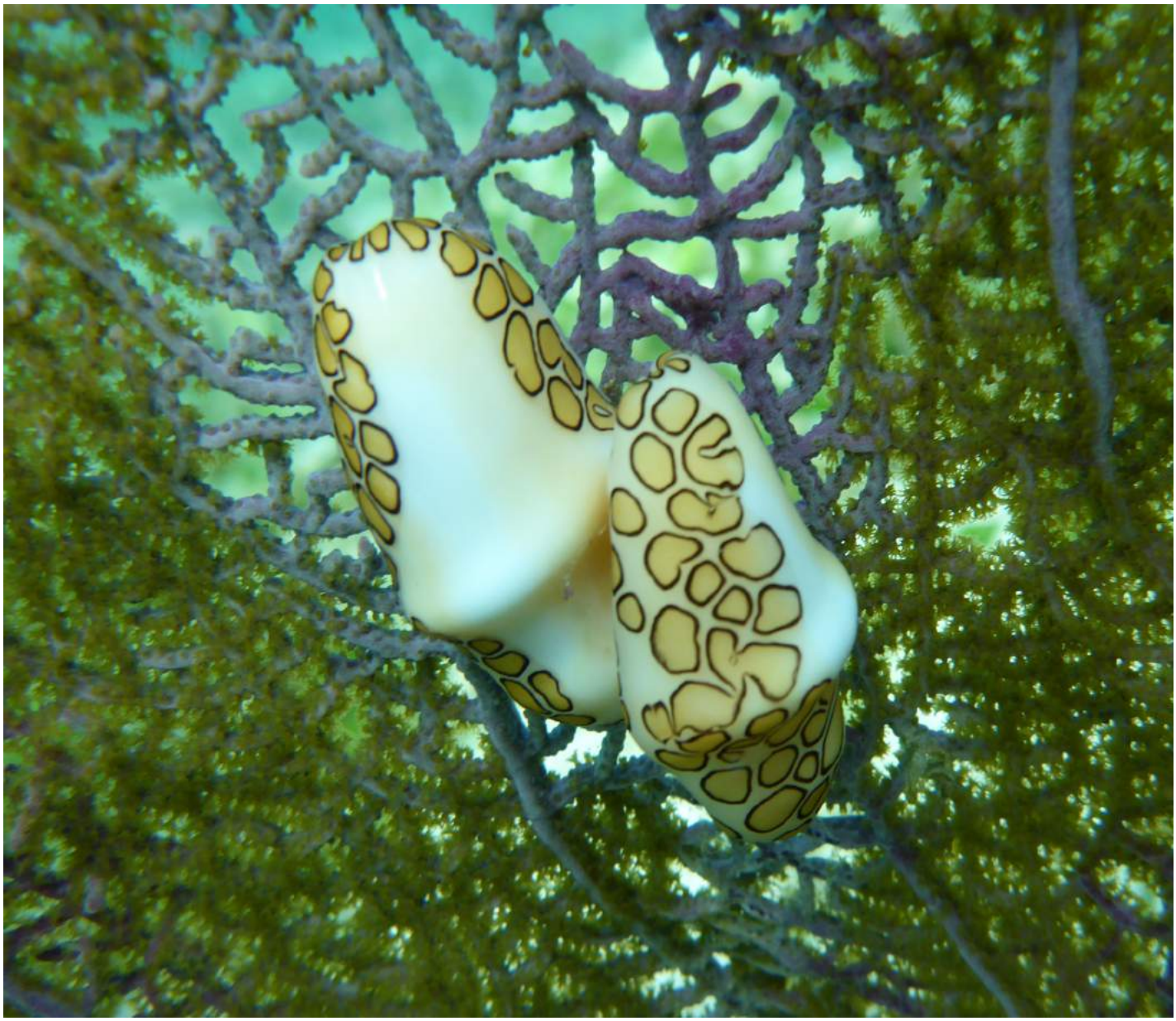

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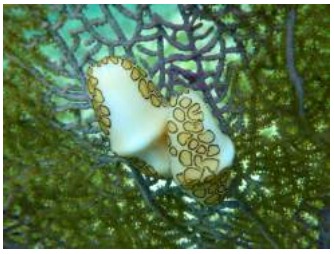

Photographer: Paul C. Pickhardt, Associate Professor of Biology, Lakeland University
Location of photo: Shallow reef within the Sapodilla Cayes Marine Reserve, Gulf of Honduras, Belize
Camera: Panasonic Lumix DMC-TS5
Date: May 27, 2018
Photo Details/Species Info:
A pair of Flamingo Tongue Snails (*Cyphoma gibbosum*) feeding on a common sea fan (*Gorgonia ventalina*).

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- incubate new and innovative teaching ideas;
- involve student research in the biology curriculum;
- advise and mentor students in and out of the classroom;
- enhance scholarship through our nationally, peer-reviewed journal, *Bioscene*.

ARTICLES

Utilizing Quantitative Analyses of Active Learning Assignments to Assess Learning and Retention in a General Biology Course

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Abstract: Numerous studies have examined the use of active learning methods in undergraduate courses, suggesting that these methods increase learning and retention as well as student engagement. In order to investigate the benefits of particular active learning assignments involving presentations of 3-dimensional simulations in an introductory biology course for science majors, quantitative analyses of the effects of these assignments on learning and retention as assessed by unit and final exam scores were performed. Same student populations and varying student populations across multiple semesters were compared using t-test analyses, single factor ANOVA analyses, and Pearson correlation coefficients. These statistical analyses determined the simulation assignments as compared to other active learning assignments resulted in no consistent significant increase in learning or retention of material covered by these assignments for same student populations and varying student populations across multiple semesters. Based on these results, the simulation assignments were replaced with other active learning assignments and additional assessment found no significant difference in the learning and retention of course material. The approach described in this study can be used for other assignments in introductory majors' biology courses, as well as other courses to assess the effectiveness of course assignments for student learning and retention.

Key words: active learning, general biology, assessment, quantitative analysis

INTRODUCTION

Moving beyond standard lecture format in undergraduate biology classrooms has been an area with much focus over the past several years (Couch et al., 2015; Waldrop, 2015). This may manifest in many different formats, from flipped classrooms to blended methods incorporating multiple approaches (Jensen et al., 2015; Sadeghi et al., 2014). Increasing both student engagement with material and overall retention and learning has long been the goal of good pedagogy, often achieved through an increase in overall active learning techniques employed in the classroom (Jensen et al., 2015; Tanner, 2013). An analysis of over 200 studies of active learning in the STEM fields found that student failure rates were 12% higher in traditional lecture style classes versus ones utilizing active learning environments (Freeman et al., 2014). A study comparing performance on ETS® Major Field Tests in Biology administered to senior students having completed a two-course sequence with or without active learning as freshmen found significant increases in overall scores for those that completed the active-learning courses (Derting & Ebert-May, 2010). Often these methods are incorporated into introductory or first-year courses, but active learning has also led to increases in exam performance in upper-level biology courses, indicating these methods can be incorporated across curricula to improve understanding and course performance (Knight & Wood, 2005).

Beyond increased student learning and retention of material, a switch to group-based, active-learning classrooms generally leads to increases in positive student attitudes toward material and courses (Goldberg & Ingram, 2012; Aguilera et al., 2017; Obialor et al., 2017; Tal & Tsaushu, 2017). However, not all instructors have perceived significant improvements in overall performance compared to standard lecture formats, indicating there is still more work to be done to consistently engage students and increase overall learning and retention (Sadeghi et al., 2014; Miller & Metz, 2014). Even without measuring increases in student performance following group-based creative activities, a recent study found improved student confidence of material after employing active learning activities (Bentley & Connaughton, 2017). Improvements in overall confidence and satisfaction of students has been shown to increase retention in biology programs, suggesting that active learning methods have impacts on students beyond potential increases in learning and assessment performances (Jeno et al., 2017).

An essential learning outcome outlined by the Association of American Colleges and Universities is "creative thinking" and their VALUE rubric on creative thinking can be utilized by schools to examine curricula for creative thinking (https://www.aacu.org/value-rubrics). Because creative thinking and activities are important features of active learning that have historically increased engagement and retention of course content, we employed creative three-dimensional simulations completed in groups in selected units of our first semester introductory biology course for biology majors. This course aims to set a foundation for future courses in the curriculum with a focus on basic biological concepts of molecules, cells, genetics, and energy. In the course, two units utilized a group simulation activity, whereas the other two units employed different types of active learning assignments. We compared test scores among same student populations over the course of a semester. In addition, comparisons were done between all sections of the course in a semester, over multiple semesters, as well as between the different instructors teaching the course over the same time period(s). Overall, exam scores did not significantly vary between topics with simulations and topics without. However, in the absence of group simulation assignments, other active learning assignments were used to provide students opportunities to work with the material, suggesting that the various active learning assignments employed in this General Biology I course were equivalent in terms of their effects on student learning and retention. Though no consistent differences were observed for the active learning assignments utilized in this course, continual quantitative assessment of assignments in biology courses and other subjects will allow for informed decisions about pedagogical methods and active learning assignments to be made in efforts to improve student learning outcomes and understanding of material presented in undergraduate courses.

METHODS

Course description

The course examined in this study was BL1250 General Biology I, an introductory course for biology majors at Rockhurst University in Kansas City, Missouri. This course, along with BL1300 General Biology II, examines basic biological concepts that will be required for upper level courses in the biology curriculum. The course goals are for students to be able to explain basic cellular and molecular structures and processes, apply knowledge to answer important biological questions, demonstrate effective study habits for learning about science, and to work successfully in groups upon the completion of the course. Though General Biology I is considered a foundation course for biology and other natural science majors, students from other fields of study are also included in this course, including a considerable number of exercise science and engineering majors and students opting to take this course as a Core requirement for degree completion. General Biology I consists primarily of freshman level students, although all levels of students can enroll in the course. The class size is typically restricted to 48 students, which also includes honors students (included in this study) that enroll in a separate course number, BL1260 Honors: General Biology I, with the classroom experience between these two courses being equivalent and shared.

Course structure

The structure of the course includes 4 units based on content, including Units: I – cell division and genetic inheritance; II – molecular genetics; III – cellular structure, function, and communication; and IV – energy, cellular respiration, and photosynthesis. Each unit is assessed through a combination of in-class activities, assignments, quizzes, presentations, and unit exams. Additionally, a comprehensive final exam is given at the end of the semester to determine understanding and retention of knowledge. Teaching approaches for this course include lecturing, in-class activities, group problem solving, case studies with associated exercises, simulations and modeling of biological processes, quizzes, problem-based discussions, group assignments, and reading reviews. Unit and final exam questions varied by semester and section of the course and were comprised of a mixture of question types written and graded by the instructors for the individual sections of the course, including multiple choice, essay, true or false, fill in the blank, matching, draw or fill in a diagram, and biological problem solving questions. Unit and final exams were assessed based on revised Bloom's taxonomy levels independently by two instructors to determine the percentage of lower (revised Bloom's taxonomy levels of remembering and understanding) and higher (revised Bloom's taxonomy levels of applying, analyzing, evaluating, and creating) order cognitive skills questions on each exam (Krathwohl, 2002).

Simulation assignment description

To increase student understanding and learning, 3-dimensional simulation assignments were included to display the dynamic and 3-dimensionality of the biological processes being examined and to integrate other disciplines and student interests with biology. In these simulation assignments, student groups of 3 or 4 were instructed to create and perform a 4 to 5 minute creative and accurate presentation, either live in class or via multimedia, related to a given topic

that incorporates the 3-dimensionality of the process assigned. Detailed rubrics for the simulation assignments were given to the students in advance (see sample rubric). For each assignment, students were instructed to incorporate a creative approach (e.g. interpretive dance, Claymation, etc.) to explain a particular process or topic (e.g. cell division, genetic inheritance, DNA synthesis, RNA transcription, protein synthesis, cellular structure and enzymatic function, cellular respiration, or photosynthesis) that was covered within particular units. For unit 1 and 3 simulations, students were assigned specific genetics problems or enzymes to ensure different approaches and information was being conveyed in the simulation presentations. The students were graded on biological process accuracy, inclusion and movement of 3-dimensional molecules, uniqueness and creativity involved in particular artistic approaches, delivery of the presentation, and inclusion of all group members in the presentations. A detailed outline of the project was due in advance of performances to ensure that the student groups had effectively incorporated the assigned biological topic with another discipline or field of study before continuing with the project. This allowed for students to receive constructive feedback before presenting to attempt to ensure understanding of the biological process and that students have met the requirements outlined for this project in the rubric.

Data collection and analysis

The data collected for this study were based on student performances on General Biology I simulation assignments, unit exams, and final exams at Rockhurst University for students enrolled in the fall 2013-2016 semesters among different sections of the course taught by three specific instructors that were consistently involved in the course throughout the period being examined. Sections of the course taught by other instructors were excluded so that the data included in this study came from sections of the General Biology I course that were taught in a similar manner during the period being examined. For each section of the course included in the study, overall performances on unit exams and questions over specific topics from the comprehensive final exams were compared to the inclusion of simulation assignments for the topics being covered. The combined number of students included in this study was 513 students, though numbers vary slightly for particular assignments and exams as not all students completed every assignment or exam and 2013-2014 final exam data was not available for one instructor.

In order to determine if the simulation assignments increased learning and retention of material covered in these assignments, unit and final exam scores were compared within same course sections and semesters; within same semesters across all course sections for all students and for the bottom performing 25% of students; based on simulation assignment topics across multiple semesters; based on instructor; and based on simulation assignment performance. Comparisons of exam scores based on simulation assignments were analyzed in Excel using paired and unpaired t-test analyses or single factor ANOVA and p values were used to determine any significant differences (using a cutoff of $p < 0.05$ for significance) with respect to the use of simulation assignments in General Biology I courses at Rockhurst University that occurred during the fall semesters from 2013-2016. Correlations between simulation assignment and exam performances were analyzed in Excel using Pearson product-moment correlation coefficient analysis. This methodology allowed for comparisons of student performance with and without simulation assignments using same student populations, as well as among multiple semesters to determine whether these assignments increase learning and retention in larger populations of multiple groups of students.

RESULTS AND DISCUSSION

Analysis of unit exam scores within same student populations with and without simulation assignment

Previous studies have indicated that active learning and creative thinking enhance student learning and retention, and therefore, two creative three-dimensional simulation assignments were added to a General Biology I course in attempts to increase student engagement with material covered in this course, as well as enhance understanding of basic biological processes. The biological topics covered in the simulation assignments corresponded to information from two of the four units of the course, with the other two units of the course not implementing these simulation assignments but rather including other types of active learning.

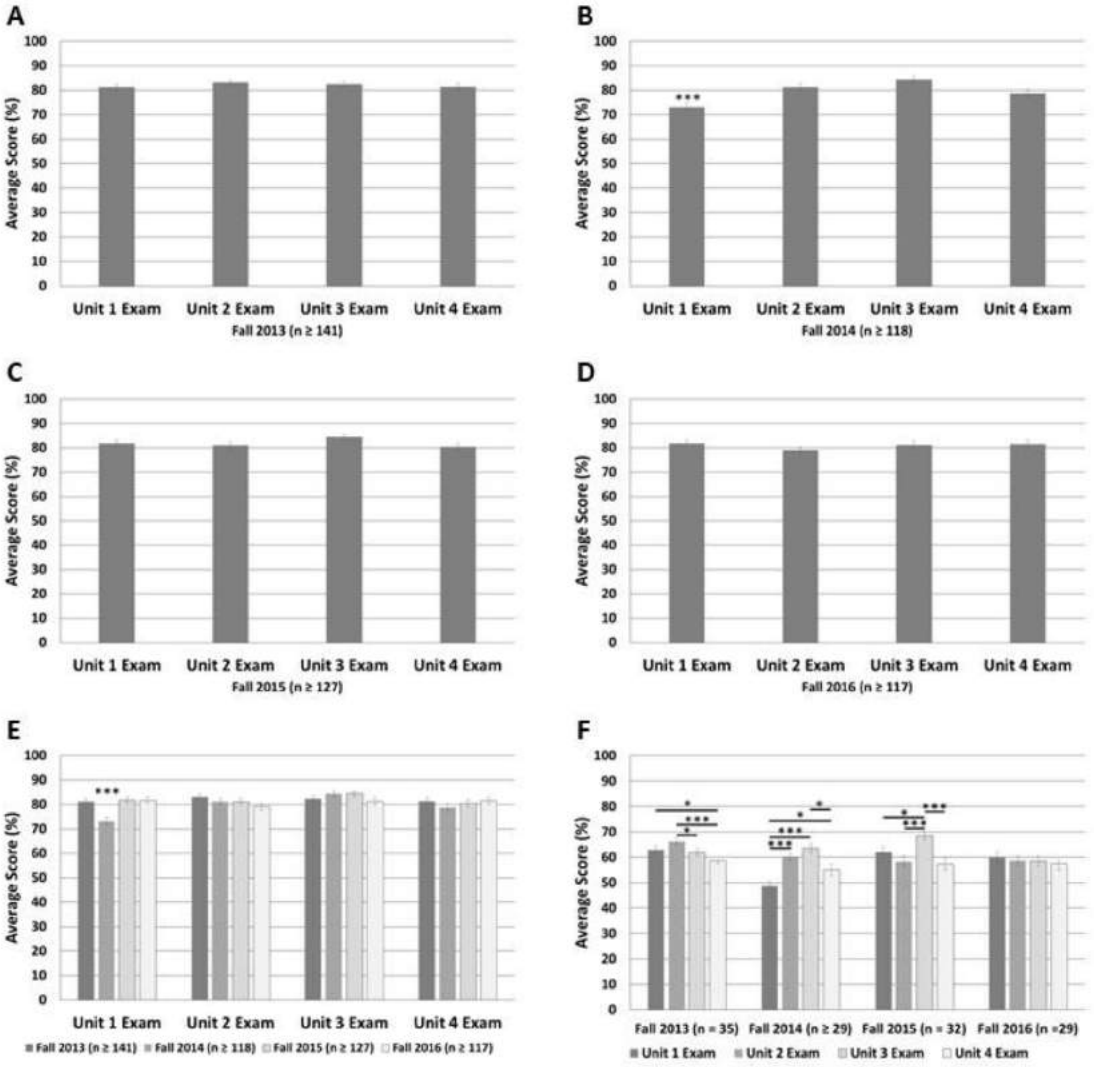
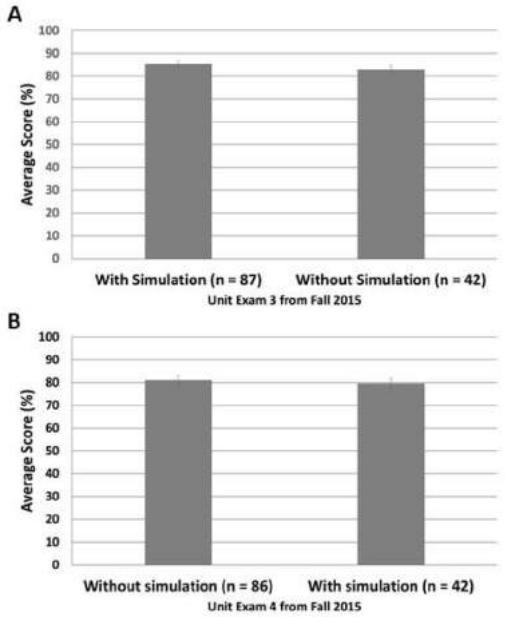


Fig. 1. Comparison of average unit exam scores in General Biology I by year for: A. Fall 2013; B. Fall 2014; C. Fall 2015; D. Fall 2016; E. Fall 2013-2016 combined; and F. Fall 2013-2016 combined for bottom 25% performing students. Asterisks indicate a significant difference between exam scores, with (* $p < 0.05$; ** $p < 0.005$; and *** $p < 0.0005$). The asterisk in B indicates a significant difference between exam scores for unit 1 and units 2-4 for fall 2014. The asterisk in E indicates a significant difference in unit 1 exam scores when comparing 2014 to all other years examined. Error bars indicate standard error of the mean (SEM).

To assess the effectiveness of these simulation assignments, unit exams for the course were used as a measure of understanding of material covered in the simulation assignments, as well as material that was not covered in the simulation assignments. Student performance on unit exams were compared for same student populations for the fall 2013, 2014, and 2015 semesters. Unit exams that assessed material covered in the simulation assignments were compared to unit exams that assessed material not covered in the simulation assignments within each semester using a one factor ANOVA analysis.

When comparing units of the course with simulation assignments (units 2 and 4) versus units without simulation assignments (units 1 and 3) for the fall 2013 semester, no statistical difference was observed between unit exam scores for units 1 through 4 of the course (Fig. 1A). For the 2014 semester, a significant decrease in unit exam percentages was observed for unit 1 of the course as compared to the other 3 unit exams (Fig. 1 B). As unit 1 of the course for the fall 2014 semester did not contain a simulation assignment, this finding led to a change in the units of the course that contained the simulation assignments, with all 4 sections of the course including a simulation assignment for unit 1 in fall 2015. However due to instructor preference, the second simulation assignment from the fall 2015 semester covered material from unit 3 of the course for 3 of the 4 sections of the course and unit 4 for the remaining section of the course. Comparison of fall 2015 unit exam scores determined that there was no statistical difference between unit exams (as observed in fall 2013), regardless of which units of the course included simulation assignments covering the material (Fig. 1C). Dividing the unit 3 and 4 exam

Fig. 2. Comparison of average unit exam scores in General Biology I in fall 2015 for content covered by a simulation assignment and content not covered in a simulation assignment for: A. Unit 3; and B. Unit 4. Error bars indicate standard error of the mean (SEM).



scores into students that performed simulation assignments versus students that did not perform simulation assignments over the material in a particular unit of the course for fall 2015 did not display any significant difference between student populations (Fig. 2A and 2B). As mean exam performances were typically near 80%, differences for particular groups of students, such as low-performing students, could potentially be difficult to observe. To determine if the simulation assignments were resulting in an increase in performance for the lower-performing students in the course, we compared average unit exam scores for the students that performed in the bottom 25% on the exams (Fig. 1F). Though some variation was observed in lower-performing students' scores, no consistent differences were observed that varied with the inclusion of the simulation assignments, suggesting that simulation assignments were not leading to an improvement in performance for those that had the most potential for improvement. With the exception of one unit exam for the fall 2014 semester, overall these results suggest that the simulation assignments did not result in significant increases in understanding of material covered by these assignments when assessed by course unit exams (Fig. 1E).

Differences among unit exams could potentially confound any observed effects of the simulation assignments. Therefore, unit and final exams were compared based on revised Bloom's Taxonomy

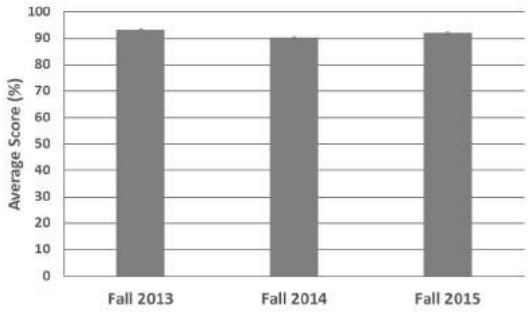
Table 1. Comparison of the percentages of points allotted to lower order cognitive skills (LOCS) and higher order cognitive skills (HOCS) questions on each unit and final exam for General Biology I for fall 2013-2016 semesters.

		Fall 2013	Fall 2014	Fall 2015	Fall 2016
Unit 1 Exam	LOCS	0.447	0.476	0.414	0.398
	HOCS	0.553	0.524	0.586	0.602
Unit 2 Exam	LOCS	0.706	0.794	0.754	0.742
	HOCS	0.294	0.206	0.246	0.258
Unit 3 Exam	LOCS	0.816	0.759	0.916	0.751
	HOCS	0.184	0.241	0.084	0.249
Unit 4 Exam	LOCS	0.889	0.973	0.948	0.893
	HOCS	0.111	0.027	0.052	0.107
Final Exam	LOCS	0.672	0.699	0.724	0.701
	HOCS	0.328	0.301	0.276	0.299

levels (Krathwohl, 2002) by determining the amounts of lower order cognitive skills (LOCS) and higher order cognitive skills (HOCS) questions on each exam. Though the levels of LOCS and HOCS questions differed between the different unit exams within the same semester, the percentage of points allotted to LOCS and HOCS questions on same unit (e.g. unit 1 exams) and final exams across different semesters were fairly consistent with the exception of the fall 2014 unit 4 and fall 2015 unit 3 exams (Table 1). However, it is important to note that increased percentages of HOCS questions on particular exams do not always correlate with increased difficulty (Dunham et al., 2015), as shown in our data with average unit 1 exam scores (with the exception of fall 2014) not significantly different than the other unit exams though unit 1 exams contained a higher percentage of HOCS questions. Additionally, differences between instructors of course sections could result in differences in student performance on unit exams, as each individual instructor wrote and graded exams for the sections separately. However, comparisons between average student performances on unit exams based on the instructor of the course section were performed for each individual unit exam, with no consistent statistical difference based on instructor observed (data not shown).

Though average performances on unit exams did not vary significantly with the inclusion of the simulation assignments, it is possible that individual student unit exam scores may vary with individual performance on the simulation assignments (Fig. 3). Therefore, performance on simulation assignments were compared with individual unit exam performances using Pearson correlation coefficient. For fall 2013-2015, no strong correlation was observed between performance on simulation assignments and performance on unit exams ($r \leq$ 0.205 for all simulation and unit exam pairs). These

Fig. 3. Comparison of average performance on simulation assignments in General Biology I for fall 2013, 2014, and 2015. Error bars indicate standard error of the mean (SEM).



results suggest that higher scores on simulation assignments did not correlate with increased unit exam scores. However, since the simulation assignments were performed in groups and all group members received the same grade on the simulation assignment, some group members could have benefited more from the simulation assignments, possibly through the process of leading the group, which may have resulted in increased unit exam performances for particular students and not for other students. As efforts of individual group members on simulation assignments were not individually measured, this analysis cannot distinguish between these possibilities.

Analysis of unit exam scores across multiple semesters to allow for comparison of same units of assignments

Comparison of unit exam scores across semesters did not find any significant differences between unit exam scores, with the exception of the fall 2014 unit 1 exam score that was lower as compared with the fall 2013 and fall 2015 unit 1 scores (Fig. 1E). Though an increase in unit 1 exam scores was observed between fall of 2014 (no simulation) to fall 2015 (simulation), the observation that there was no significant change in unit 1 exam scores when comparing fall 2013 (no simulation) to fall 2015 (simulation) would suggest that the increase in scores between fall 2014 and 2015 might not be due to the inclusion of the simulation assignment in fall 2015 for unit 1 of the course. All other unit exam percentages did not significantly vary between the fall 2013, 2014, and 2015 semesters in this course.

With analyses of unit exam scores as compared to inclusion of the simulation assignments not suggesting significant increases in performances on unit exams, the simulation assignments were removed in the fall 2016 semester due to time constraints inside and outside of the class, in lieu of other active learning components in all units of the course. No significant difference was observed between performances on unit exams in fall 2016 when no simulation assignments were assigned (Fig. 1D). Comparison of unit exams from the fall 2016 semester with unit exam scores from fall 2013-2015 semesters found no significant difference in exam scores for all units of the course, with the exception of the fall 2014 semester for unit 1 of the course (as previously described) (Fig. 1E). These findings indicate that the specific simulation assignments utilized were not likely having a large impact on student learning of the material in each of the units of the course that included these assignments.

Analysis of material retention within same student populations with and without simulation assignments

In order to examine retention of material, performances on final exam questions from each unit of the course were compared based on the inclusion of simulation assignments for the fall 2013 through 2015 semesters. For fall 2013, no significant difference was observed between performances on questions from various units on the final exam (Fig. 4A). For the fall 2014 and 2015 semesters, differences were observed between performances on specific units of the course (Fig. 4B and 4C). However, significant differences were also observed between the four units of the course in fall 2016 when no simulations were assigned (Fig. 4D). Therefore, the differences in performances on questions from various units of the course seem to vary, but these variations might be due to factors other than the presence of the simulation assignments.

When comparing performances on questions from the final exams that assessed material from units with simulation assignments as compared to those without simulation assignments, again no significant difference was found for fall 2013, but significant differences were observed for the fall 2014 and 2015 semesters (Fig. 5). Interestingly, performance on questions assessing topics covered by the simulation assignments was significantly lower in 2014 and higher in 2015 as compared to questions assessing material not covered by simulation assignments (Fig. 4B, 4C, and 5). Therefore, we did not observe a consistent increase in retention of material covered by simulation assignments to the final exam as compared with material not covered by these simulation assignments. As this analysis is comparing retention in same student populations, these results could suggest that the simulation assignments might improve retention in some groups of students, but not in others. However, no strong correlation was

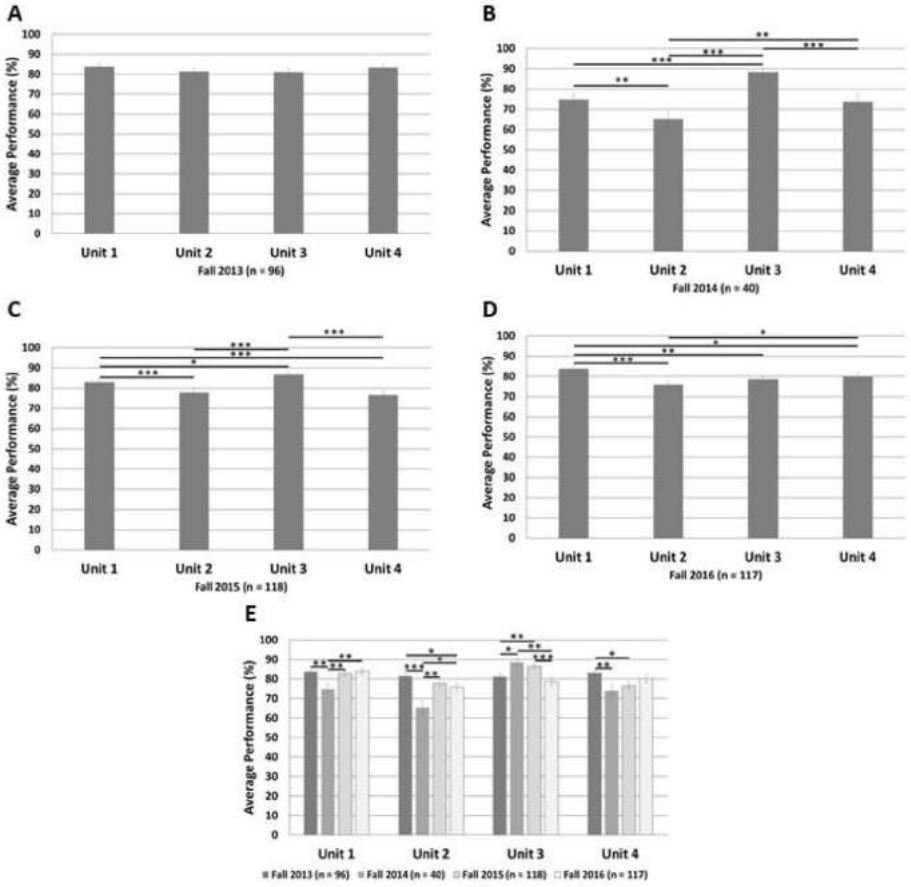


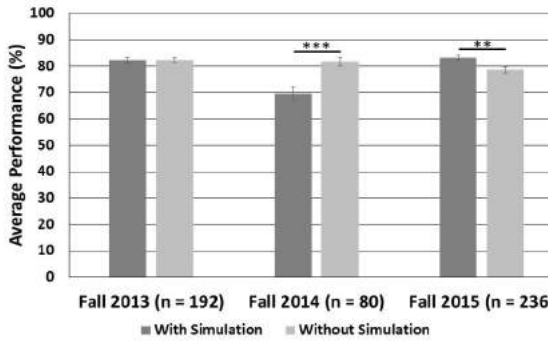
Fig. 4. Comparison of average performance on final exam questions covering material from each unit of the course in General Biology I for: A. Fall 2013; B. Fall 2014; C. Fall 2015; D. Fall 2016; and E. Fall 2013-2016 combined. Asterisks indicate a significant difference between exam scores, with (* $p < 0.05$; ** $p < 0.005$; and *** $p < 0.0005$). Error bars indicate standard error of the mean (SEM).

observed between simulation performance and final exam performance ($r \leq 0.185$ for all simulation and final exam pairs). Alternatively, the simulation assignments may have no effect on retention of material to the final exam for each population of students examined. Though no consistent improvement was observed in retention through the completion of the course, it is important to note that this study did not assess long term retention, as it is possible that students completing the simulation assignments may retain the information covered in these creative assignments longer than individuals that did not participate in these presentations.

Analysis of material retention across multiple semesters to allow for comparison of same units of the course with and without simulation assignments

After removal of the simulation assignments from all sections of the course, retention of material between the time at which the material is covered and final exam were examined again. Comparison of performances on questions from individual units of the course with the presence or absence of the simulation assignments from the fall 2013-2016 semesters did not find any significant difference, with the exception of unit 3 of the course (Fig. 6). Interestingly, comparison of unit 3 with and without simulation assignments did not display a significant difference for the 2013-2015 semesters (data not shown). Though overall final exam performance in fall 2016 was not statistically different from the fall 2014 and fall 2015 semesters (Fig. 7), the average performance specifically on unit 3 questions from the fall 2016 final exam was significantly lower as compared to the fall 2014 and 2015 semesters (Fig. 4E). There was no significant difference between average performances on unit 3 questions from the final exam when comparing the fall 2013 and 2016

Fig. 5. Comparison of average performance on final exam questions covering material from units of the General Biology I course from fall 2013-2015 that contained simulation assignments and did not contain simulation assignments. Asterisks indicate a significant difference between average performances, with (* $p < 0.05$; ** $p < 0.005$; and *** $p < 0.0005$). Error bars indicate standard error of the mean (SEM).



semesters (Fig. 4E). However, the fall 2013 overall final exam performance was significantly higher than all other semesters examined (Fig. 7). As student populations vary each year, it is possible that these significant variations in learning and retention of material could be due to changes in student populations or exposure of students to the material prior to covering the various topics in the General Biology I course. However, average composite ACT scores for entire populations of incoming freshmen classes (not only students enrolled in General Biology I) were similar at 25.5 for fall 2013 and 2014 and 25.6 for fall 2015 and 2016, which might suggest similarity in general academic preparation for the student cohorts for each academic year from 2013-2016. One difference that was noted was the overall

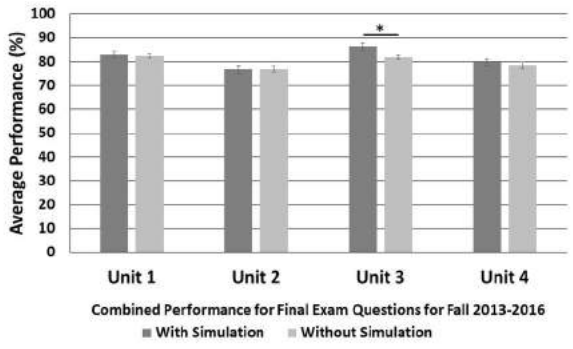


Fig. 6. Comparison of combined average performance on final exam questions covering material from each unit of the course in General Biology I for fall 2013-2016 sections based on the inclusion or exclusion of the simulation assignments. Asterisks indicate a significant difference between average performances, with (* $p < 0.05$; ** $p < 0.005$; and *** $p < 0.0005$). Error bars indicate standard error of the mean (SEM).

reception of the simulation assignments, as determined by feedback on formal student course survey questions asking students about aspects of the course that contributed to learning and aspects of the course that could be changed, varied from 2013 to 2015. In 2013, numerous students commented that the simulation assignments contributed to their learning of the material and few students provided negative feedback. However, by fall of 2015, the trends shifted some, with many students commenting that the simulation assignments did not benefit their learning or that these assignments should be removed. As active learning assignments tend to increase engagement, increases in student learning, retention, and course performance in active learning environments all might be a result of the increased engagement. Therefore, by including other active learning assignments that the students valued more as student opinions of these simulation assignments changed over time, any observable increase in performance due to including simulation assignments might have been attenuated due to the replacement of the simulation assignments with different active learning assignments that continued to engage our student population.

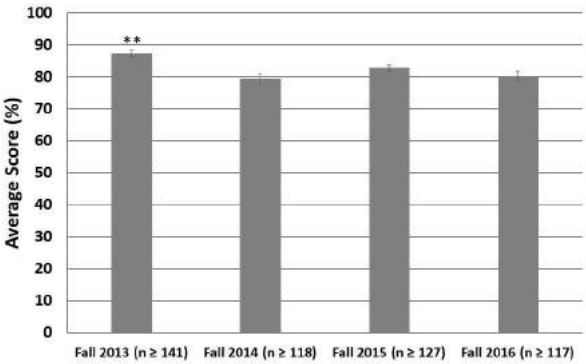


Fig. 7. Comparison of average overall final exam performance in General Biology I for fall 2013-2016. Asterisks indicate a significant difference between average performances, with (* $p < 0.05$; ** $p < 0.005$; and *** $p < 0.0005$). Error bars indicate standard error of the mean (SEM).

CONCLUSIONS

Through quantitative analyses presented in this work, we were able to determine the overall effectiveness of a specific active learning assignment in terms of learning and retention of material in a General Biology I course. Our results suggest that this particular assignment did not consistently increase overall student learning or retention of material covered by these assignments. It is important to note that these studies did not investigate whether individual students gained from

the simulation exercises, as these assignments were completed in groups where participation and engagement in the simulation exercises were not directly measured. Though the particular active learning assignment in this study did not appear to increase class learning and retention, we did not examine the difference in student performance with and without active learning components in the classroom. When the simulation exercises were not assigned for units of the course, other active learning assignments were given that covered the material. Therefore, the students generally performed similarly in an environment when active learning methods were employed. As various assignments will have differential effects on student learning and retention, this study provides an example of how assignments can be assessed to ensure that we are utilizing tools that will continue to improve student learning, retention, and positive experiences in the classroom.

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This study (#2018-01) has been approved by the Rockhurst University Institutional Review Board.

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Improving Scientific Literacy through a Structured Primary Literature Project

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Abstract: Emphasizing scientific literacy in the core science curriculum promotes informed students within a liberal arts education. In our Introduction to Biology course, which enrolls predominantly humanities majors in their final science course of their academic careers, we designed a project to advance these analytical processes through the deliberate dissection of primary literature. This project, completed over the course of one semester, includes both a written analysis and an oral presentation of a primary scientific article of the students' choosing. The students are guided through this iterative process from article selection to the completion of products. Within this work we detailed the objectives and created complementary tools to stimulate the progression of higher order cognitive skills and assist faculty in assessing the interpretations of applied biological concepts. Surveys from faculty and students suggest that this project and its supporting materials are useful to improve scientific literacy and improve critical thinking skills. Whether the audience is non-STEM majors or scientific minded persons, this project can be utilized to enhance critical analysis skills. Overall, we found this student-led group activity allowed for exploration of the scientific process outside of the classroom environment, which facilitated a more hands-on approach to developing increased scientific literacy in undergraduate students.

Key words: scientific literacy; metacognitive progression; scientific communication; primary literature analysis

INTRODUCTION

Increasing scientific literacy is an important goal in undergraduate science courses (Gormally et al., 2012). Rather than memorizing facts and information, applying knowledge through critical analysis stimulates higher-order cognitive skills (Zoller, 1993). These skills reinforce course objectives and support the assessment of a deeper conceptual understanding. It is this understanding that can be applied in a larger context for students to exercise metacognitive skills when examining scientific literature. Biological courses can cultivate informed decision makers by practicing skills in scientific interpretation and communication (McPhearson et al., 2008).

Critical thinking requires students to move beyond consumption of knowledge and into the analysis, evaluation, and synthesis of ideas. Faculty can foster these skills when training students to evaluate and discriminate the components of primary literature. Some have approached this goal by achieving information literacy in biology (Porter et al., 2010) by analyzing published data and discoveries from one particular laboratory over a period of years (Hoskins et al., 2007). Others have integrated a cell biology laboratory project with a literature analysis (Woodham et al., 2016) or drawn conclusions from figures in a specifically assigned paper (Round & Campbell, 2013). These and others have demonstrated that upper-level biology courses benefit from the incorporation of primary literature module threads (Sato et al., 2014) or discipline specific article dissection (Kovarik, 2016). While this concept of literature analysis is not entirely new (Gillen, 2007), our study concentrates on the deliberate progression of critical thinking skills (reading, evaluation, and synthesis) and strategic communication in a topic which may be otherwise unfamiliar to students. Previous work mentions the general gap of comprehensive tools to assess these guided development strategies to enhance higher cognitive learning (Crowe et al., 2008). Studies have examined this process in biology major courses (Varela et al., 2005), but few have implemented this universally in a predominately non-science majors population. We sought to address this gap in an introductory biology course, an audience of primarily humanities majors, by designing a semester-long project to deliberately dissect primary scientific literature and communicate findings in oral and written forms.

Table 1. Assessment mechanisms of taxonomy progression. Students advance their analytical skills through specific actions during this project. [Select actions modified from Bloom's-based Learning Activities for Students (Crowe et al., 2008).]

Goal: Cultivate critical thinkers who can solve ill-defined problems	
Cognitive Progression	**Key Action**
Knowledge/Comprehension	• Identify & define key terms • Describe background and experimental design in own words
Application/Analysis	• Create flowchart or diagram to summarize a key experimental method • Assess effectiveness/appropriateness of statistical methods and analytical tools used
Synthesis	• Generate a new hypothesis or propose additional experiment
Evaluation	• Prepare a written & verbal assessment of the article analysis

We exposed students to primary literature through a highly-structured analysis on an article of their choosing. The objectives of this small group project, accounting for 11% of the total course grade, were detailed in hand-outs and grading rubrics provided to all students (Appendix 1) at the beginning of the course. Students were to summarize and identify the purpose of the study, outline a key method to examine, and evaluate the experimental design. This assessment of higher order thinking skills, in a step-wise manner to maintain student engagement, can further scientific comprehension and application. With the goal of improving strategic communication, this capstone project concluded with an oral presentation, geared towards improving applied scientific literacy.

MATERIALS & METHODS

Development of the Project & Guidelines

As the American Association for the Advancement of Science describes, the scientific competencies of applying the process of science and effective communications should be practiced in a variety of oral and written methods as "a standard part of undergraduate biology education" (Brewer & Smith, 2011). Embedding contemporary research articles into a biology course is one such mechanism to develop these competencies. Our program goal is to cultivate critical thinkers who can solve ill-defined problems. Problem solving requires an initial factual foundation, the ability to design an experimental strategy, and assessing whether the approach was appropriate to address the research question (Sensibaugh et al., 2017). Thus, we used published research as a means to practice the scientific process.

We approached enhancing metacognitive skills by building on the Blooming Biology Tool (Crowe et al., 2008), which describes this progression from describing or summarizing concepts in lower-order cognitive skills to higher-order interpretations of data. Students began by examining the relative merit of the selected study by analyzing whether the experimental design was a suitable test for validating the hypothesis. Through the deliberate guided progression from knowledge to the synthesis and evaluation of materials, we desired to establish a mechanism to practice critical thinking skills. Table 1 illustrates this progression beginning with the initial description of the experiment in students' own words. Students were encouraged to relate course knowledge to experimental descriptions, conditions, or variables encountered in the classroom. The generation of a concept map or chart focused on one key method required synthesis and using higher-level cognitive skills. Additionally, directed comments on the statistical models encouraged inter-disciplinary STEM applications. Finally, the synthesis of the chosen study and the generation of a novel hypothesis and follow-on experiment moves students from consumers to producers of knowledge. Each of these activities are included within this project to guide the cognitive progression of scientific literacy. As further described in Appendix 1, the assessment of student progression and performance is prescribed in both narrative form and a rubric, available to all students and faculty during the first class. The second objective was to communicate this analysis in written form. Through this product, faculty can identify significant misconceptions that students have on topics or improper interpretations or conclusions from a particular experiment. In partnership with our Writing Center, faculty can also identify students who struggle with written communication and provide additional resources early within the student's academic progression to address shortfalls. The final goal was for students to present scientific data to their peers during in-class presentations at the end of the course. Thus, students could apply their course knowledge using the selected study as a vehicle to summarize, dissect, and critique or propose further lines of investigation. Together, these goals sought to advance scientific communication and literacy.

Study population and classroom implementation

In an undergraduate biology course for non-majors, students often have little experience in reading primary scientific literature. The majority of

our students (n = 550) were first or second year humanities majors enrolled in a one-semester undergraduate biology course over the period of one academic year. Prior to the study, exemption was granted by USMA IRB CLS17-001. Students were randomly divided between fifteen sections each semester consisting of 16-21 students. Nine faculty were allocated to teach the course, six senior doctoral faculty with more than five years of experience, and three junior faculty with masters' degrees and less than five years of experience. Senior faculty taught one to two sections per semester while junior faculty instructed three to four sections.

Over the course of the semester consisting of 40 lessons and 8 laboratories, students were required to select and analyze one primary literature article in a topic of their choosing. Faculty familiarized students with the project during the first lesson by providing detailed handouts and grading rubrics (Appendix 1), standardizing the expectations and assessment over the course of the semester. The project was divided into four portions: 1) article selection; 2) written analysis; 3) slide submission; and 4) oral presentations.

Assessment

1) Assessment: group designation and article selection

Groups were self-designated on sign-up sheets, available within Appendix 1 (Enclosure 1). Students worked in groups of two to three with their initial task to select a primary literature article. While the article topic was not prescribed, article selection was accomplished early in the semester to verify primary sourcing as well as the feasibility for the target audience. Students were encouraged to choose a topic of interest; written in a manner they were able to understand and interpret.

A common issue for our cadets, 78 of 550 students, was difficulty identifying primary literature. Instructors stressed examples of primary literature in class and shared tips on searching the library databases. While article selection was a low stakes event, a ten-point allocation, it was useful for faculty to both confirm that the article was primary research and that it was to a level of which non-science majors would be able to interpret. Five points (of the 10) were designated for providing a copy to the instructor for review by the designated time with the remaining five points for the article being from primary literature. Once instructors confirmed the selection of a primary article the groups were directed to proceed with their analysis over the course of the semester.

2) Assessment: written analysis

Students had the first half of the course to read and reflect on their chosen article in preparation of their written submission. Instructors used the rubric (Appendix 1, Enclosure 2) to assess student analysis and interpretations. In an iterative fashion, these comments and rubrics were returned to students to incorporate in the preparation of a slide packet for oral presentations at the end of the course. The writing assignment was challenging as most students had not previously assessed primary literature and even fewer had communicated scientific findings in written form. Faculty assessment was facilitated by rubric criteria considering the level of insight and thoroughness of their effort. The written analysis was divided into sections worth 125 of the total 220 project points. Students were specifically directed to address the article organization, hypothesis, references, introduction, and study design. An in-depth analysis of one key method and materials allowed groups to explore the findings, statistics, and the biological relevance of the results. Importantly, students examined the interpretation and potential bias or issues within the study as they generated a novel hypothesis and experiment to continue the work. A memorandum with instructions for each of these sections assisted students in viewing the article in a scientific context (Appendix 1). Enclosures within this appendix further specify the content and grading of each category specified within the instructional memorandum. For example, in summarizing the article abstract, students were tasked to describe the article in common terms as if they were speaking to nonscientists. When identifying the hypothesis, students referenced course material in an effort to tie classroom instruction to their project. As the materials and methods section can be unfamiliar to non-science majors, students selected one key method and created a flowchart describing this method.

Keeping the focus on the scientific question, students dissected the study design, results, and discussion sections. We were interested in the "how" and included specific questions and guidance to avoid students simply paraphrasing the corresponding sections. For example, in the results section, students identified a key figure and explored the statistical tests performed by the authors and the main findings. They could apply their mathematics coursework and determine if the tests were appropriate. Within the discussion section, groups considered the coherency of the author's story, how easily they were able to interpret results, if they felt the study supported author's claims, identified new questions that emerged, and made suggestions on how to address those questions in future experiments.

3) Assessment: slides

The slide assessment was subdivided into slide submission and instructor assessment, specified within Appendix 1, Enclosure 3. Five points were specified for the timely upload of slides. Fifty points were allocated for the quality and content of the slides themselves. Students were assessed not only on the overall design and appearance but also in how they summarized their article analysis findings. Groups consolidated their ideas on the scientific

	Select Article	Written Analysis	Oral Presentation	Slide Upload	Slide Assessment
Max Points	**10**	**125**	**30**	**5**	**50**
Average (pts)	9.2 (+/- 1.3)	113.3 (+/- 9.3)	27.5 (+/- 1.5)	5.0 (+/- 0.1)	46.7 (+/- 2.0)
Average %	92.4%	90.7%	91.6%	99.1%	93.3%

Table 2. Student performance on the five specific graded portions of the project. Average scores for each portion are shown (+/- standard deviation of the average) along with the average percentage for that event. (n=183 groups totalling 550 students over the course of two semesters).

design and approach as they described the hypothesis, experimental methods, and results. Finally, groups proposed a future experiment and novel hypothesis for the respective field.

4) Assessment: oral presentations

Presentations received a maximum of thirty points with criteria focused on the clarity of their talk, overall bearing, and the incorporation of figures. Specifically, the focus was to communicate findings by integrating their ideas and figures with seamless transitions between members of the group. The final criterion was whether students adhered to the established time limits.

Collection of data

Data collection on student performance for each category of the project was extracted from the Academy Management System (AMS) database, an internal Academy grading system (West Point, 2017). Instructors separately entered scores for the article selection and verification of primary literature (10 points); written analysis (125 points); slide upload (5 points); slide assessment (50 points); and oral presentation (30 points). Results are shown in Table 2. All students within the same group received the same scores. Similarly, student responses to end-of-course feedback survey questions (Table 4) were anonymously collected within AMS. Data regarding the strength of agreement to question prompts was automatically compiled from all responses.

The instructor assessment of this project was through faculty surveys on a scale of 1 to 5, with five being the most effective. This survey focused on whether students were able to distinguish primary literature and apply the scientific method before and after the project (Table 3). Additionally, faculty were asked to describe the usefulness of the provided rubrics and instructions and whether this project was effective at improving literacy and critical thinking skills.

RESULTS

Within our study, students who followed the guidance and assessment metrics scored very well (Table 2). Students that lost points did so mainly for not clearly answering questions or omitting answers entirely. Points were also deducted for misinterpreting data. Instructors assessed and returned feedback on the written submissions (90.7% +/- 7) to the groups (n=183) prior to their presentations. Improved adherence to rubrics evidenced an increase in the average scores for the slide assessment (93.3% +/- 6) and for oral presentations (91.6% +/- 2) compared to the written submissions. With a variety of topics covered, oral presentations stressed the importance of conveying

Table 3. Instructor assessment of Article Analysis Project. Faculty were surveyed on a scale of 1 to 5 for their responses to questions indicated. (1 = strongly disagree; 2 = disagree; 3 = neutral; 4 = agree; 5= strongly agree). Average scores are reflected (+/- sd, n=7).

Students were able to:	Prior to Project	After Project
Distinguish primary literature	2.5 (+/-0.5)	4.0 (0)
Apply the scientific method	2.2 (+/-0.2)	4.0 (0)
Project Design		
Students self-selecting topic was useful		5.0 (0)
Grading rubrics were useful for assessment		5.0 (0)
Instructions were sufficient for students		4.5 (+/-0.5)
Project is effective in improving scientific literacy		4.5 (+/-0.5)
Project is effective in improving critical thinking skills		4.5 (+/-0.2)

Table 4. End of course feedback. Students were surveyed at the end of the course as to their thoughts on learning attributable to their instruction (n=279 students).

	Strongly Agree	Agree	Neutral	Disagree	Strongly Disagree
This instructor encouraged students to be responsible for their own learning.	151	115	12	1	0
This instructor used effective techniques for learning, both in- and out-of-class assignments.	129	120	21	7	2
In this course, my critical thinking ability increased.	94	109	55	17	4
After taking this course, I can apply multiple disciplines to solve ill-defined problems.	115	126	32	6	0

scientific findings in an understandable manner to increase awareness (thus scientific literacy) for the subject at hand. The slide decks were also assessed on timely upload to our server (99% +/- 1). The presentation was limited to ten minutes and the audience was able to ask the group questions at the conclusion. The ability of students to answer questions was considered in the student's final presentation grade.

A secondary mechanism to assess improvement in scientific literacy was through course-end feedback. Faculty surveys suggest that the ability to distinguish primary literature and apply the scientific method increased following project completion (Table 3). While the faculty survey is limited to our internal cohort, it would be of interest to see how similar institutions apply this project and assess the usefulness of provided informational tools and rubrics. Faculty that penalized cadets for not adhering to published project guidelines or submitting secondary items provided the baseline for the pre-project ability to distinguish primary literature. Preliminary faculty feedback suggests that this project is an effective approach to improve scientific literacy and critical thinking skills. Additionally, in free-response text, instructors noted that students who chose topics that interested them or selected articles written in a manner they could interpret were more enthusiastic and appeared more comfortable answering questions during their oral presentations. Students (Table 4) were surveyed on their improvements in learning throughout the course and their ability to solve complex, ill-defined problems. While the faculty feedback directly relates to the project, it is possible that student gains or motivation are due to unrelated aspects of the course.
on learning attributable to their instruction (n=279 students).

DISCUSSION

Reports have suggested that biology curriculums need to promote critical thinking using primary literature (Tabor & Jakobsson, 2004 and Varela et al., 2005). Building on preliminary coursework, this guided approach provides the framework for students to apply preliminary coursework in a biological topic of their choosing, following the scientific process from the original question to conclusions. With careful consideration of the methods employed, as well as any bias or statistical implications, students become informed readers rather than passive consumers of knowledge.

We found this student-led group activity allowed for exploration of the scientific process outside of the classroom environment, which facilitated a more hands-on approach to developing increased scientific literacy. Moreover, this project encouraged the progression from lower- to higher-order cognitive skills. In the future, we plan to incorporate this into our advanced biology courses for STEM majors and suggest that it can be adopted by courses desiring to improve analytical skills and promote scientific literacy.

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NOTE TO EDITOR

The work was reviewed and approved as exempt under IRB USMA DCLS 17-001. The views contained within are those of the authors and do not reflect the official policy or position of the Department of the Army, Department of Defense, or the US government.

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SUPPLEMENTAL MATERIAL
APPENDIX 1. Analysis of Primary Literature Instructions with Grading Rubric

Memorandum of Instruction for Improving Scientific Literacy through a Structured Project
Subject: Primary Literature Project Guidelines for Introduction to Biology

1. Scientists publish and distribute their experimental findings and conclusions from original experiments in primary research. Authors describe how their research is relevant to the scientific community and propose future experiments. These articles undergo a peer review process, where editors and other scientists evaluate the soundness of the experimental design and interpretations along with relevance and novelty within the field. In contrast, secondary literature or sources are items that summarize primary literature through review articles and meta-analyses. Secondary sources can include magazines, textbooks, or websites. While these may be trusted sources, they do not meet the criteria for primary literature.

2. Review articles (secondary literature) are a great place to begin research and often summarize several aspects of primary literature, presenting them in one location. One must, however, take this analysis and go to the referenced primary source(s) before formal conclusions can be drawn, based on experimental data.

3. This is a group project, no more than three students per group. Each student within the group will receive the same grade for all submissions. This project is subdivided into four objectives: 1) Identify formal groups. 2) Select one primary research article and provide a copy to your Instructor via SharePoint. 3) Perform an analysis and prepare written products further described below. 4) Prepare and present your analysis to the class.
Students are encouraged to choose a topic that interests them and an article written in a manner you are able to understand and interpret. To determine your topic of interest, it is useful to scan the table of contents of journals such as Cell or Nature. Following topic selection, there are several databases to begin searching for relevant articles. While not all inclusive, databases such as PubMed (www.ncbi.nlm.nih.gov) or Science Direct (sciencedirect.com) allows one to query journals which offer free access to recently published articles. The specificity of search terms will increase the targeted return of relevant articles. For example, someone interested in fungi could enter "white nose fungus in bats" as opposed to "animal fungus". Ideally, specific search criteria will yield several articles to further interrogate. Access to some primary articles require coordination through library resources. Allow adequate search time or seek freely available articles for the project.

4. The grading rubrics are available as enclosures. These identify the assessment criteria for the article analysis and slides for the in-class presentations.

5. Each group will examine a primary article on a biological topic of their choosing and prepare a written commentary, according to the following specifications. Points will be assessed, as indicated below in parenthesis, and according to the grading rubric located at Enclosure 2. In addition, five points will be assigned for overall format and aesthetics and five points for appropriate citations (internal and works cited). The use of passive voice, misspellings, and grammatical errors will result in additional point deductions in the sections in which they appear.

A. *Title & Abstract. (5 points) Read the abstract and summarize the main idea and purpose of the paper using your own words in 2-3 sentences. Use common terms as if you were talking to a family member or friend.*
B. *Problem Statement/Hypothesis. (5 points) Referring to Lesson 1, describe whether this was discovery science or hypothesis-driven science. In your own words, identify the hypothesis. State the problem and question within the field this work attempts to address/answer. Be specific as articles often seek to examine one small aspect of a very large field.*
C. *Reference Section. (5 points) Examine the reference section of the article. Are the author(s) citing their own previous work(s) or current work of other scientists? Are there any disclosed or perceived conflict(s) of interest?*
D. *Introduction. (10 points) This is where background information is presented for those who may be unfamiliar with the area. In no more than one paragraph, summarize the key background information regarding the topic.*
E. *Terms. (5 points) Within the Introduction, identify and define five key terms that are used. These terms should be vital to understanding the paper and your analysis.*

F. *Overall Study Design. (15 points) 1) How did the researchers attempt to answer their research question/evaluate their hypothesis? Provide an overview of the experimental/study design keeping in mind the research question. 2) What controls were used and why?*

G. *Material & Methods. (20 points) The Materials & Methods section describes how the authors performed the research so others may replicate the same experiments. Considering the overall study design, select one key method from the paper and create an ORIGINAL (i.e. your own) flowchart or diagram that describes the key method. Include as much detail as necessary. This should clearly explain what was done and how. A reader should be able to understand your flowchart and explanation without referencing the paper. Include any conditions (time, temperature, etc.) and reagents (concentrations, chemicals, subjects) so that you could take this into the lab/field and repeat the experiment using your flowchart or diagram.*

H. *Results. (15 points) The Results section presents experimental data. To fully evaluate scientific claims, the results section is the most important for discerning validity of claims. Identify the most critical table or figure presented within the paper for further analysis. Specify which figure is being analyzed and answer the following questions: A) What is the main finding from the data? B) How large is the population size (n)? C) Is there a statistically significant difference (focus on the p–value) in the treatment versus control group? Keep in mind there may not be a treatment and/or control group. D) What statistical test was performed and what is the likelihood of a false positive or false negative result? Keep in mind not all experiments will include this information. E) Explain how the results are biologically relevant to the problem statement or hypothesis.*

I. *Discussion. (35 points) The Discussion section is the authors' mechanism to convey their findings and interpretations. They also discuss the significance of their finding and propose additional studies. Within this section, A) Do the authors present a coherent story? Why or why not? B) How do you, as the reader, interpret the results? Are they aligned with the authors? C) Have they presented sufficient evidence to support their claims? D) Do they identify areas of potential weakness in their experimental design? If so, what are the weaknesses? If not, what do you think are weaknesses? E) Describe how this article is novel in either content or experimental approach and how it is important to the scientific field. F) What new questions emerge from the results of this experiment? Include your questions and any the authors bring up. G) In your own words, describe one future experiment or line of inquiry that the authors (or you) could take on this topic.*

6. Scientific literacy is not only in written form but involves critical analysis and oral presentation. As such, each group will prepare a 9-11 minute summary of their respective article. Groups will present their data to the class using PowerPoint. Presentations will be assessed on format, content, and delivery.

7. Grades will be assessed for each main objective during the semester. The total points (220) are allocated as follows:

Group selection	0 points	Lesson 6
Provide copy of primary article	10 points	Lesson 7
Article Analysis	125 points	Lesson 25
Submit Slides to Instructor	5 points	Lesson 39
**due NLT 0600 Lesson 39		
Slide Assessment	50 points	Lesson 39
Presentation Assessment	30 points	Lesson 39/40

//original signed//
XXXXXXXXXXX
Course Director

Encl
1-Group Sign-up Sheet
2-Article & Analysis Rubric
3-Grading Rubric Slides & Presentations

Encl 1- Group Sign-up Sheet

Primary Article Group Analysis Sign-up Sheet

Section _____

		Identify formal group (LSN6)
Group #1	Names	*
Group #2	Names	*
Group #3	Names	*
Group #4	Names	*
Group #5	Names	*
Group #6	Names	*

*Denotes group leader. Leader is responsible for submitting items to instructor and coordination.

Encl 2- Article & Analysis Rubric

	Max Point		Criteria	Assessed Points	Total/notes
Group & Article Selection	**10**				
		5	Provide copy of article that group will analyze		
		5	Article is from primary literature		
Article Analysis	**125**				
		5	**Overall design and appearance:** 0—disorganized & difficult to follow 1-2—adequate organization, somewhat difficult to follow 3-4—organization and images aid understanding 5—professional appearance with text greatly increasing understanding of topic		
		5	**Appropriate citations (internal and works cited):** 0—no references presented 1-2—limited references using somewhat consistent formatting but missing two or more internal citations 3-4—several well-presented references in consistent format but missing one to two internal citations 5—fully referenced		
		5	**A: Describe abstract in common terms:** 0—no abstract discussion 1—topic is not introduced in general terms 2—description present but unclear 3—relevant background provided 4—clear understanding of topic with some synthesis 5—excellent background provided		
		5	**B: Hypothesis** 2—correctly specify discovery or hypothesis-based approach 3—identify problem statement/hypothesis		
		5	**C: Analyze reference section for completeness/conflict of interest:** 0—analysis not included 1—only states no conflict of interest 2—only mentions reference section 4—examines 1-2 references 5—full consideration of references and analysis of conflicts of interest		
		10	**D: Summarize introduction of topic:** 0—no introduction 2—topic is not introduced in general terms 4—description present but unclear 6—relevant background provided 8—clear understanding of topic with some synthesis 10—excellent introduction provided		
		5	**E: Identify and define five key terms**: 1—for each term and definition		
		15	**F: Study design:** (8) Overview of experimental/study design 0—no discussion of experimental design 2—briefly mentions study design without any description 4—discussion present but not clear or informative with two misinterpretations		

		6—clear understanding of design with some synthesis or slight misinterpretations 8—excellent description of study design with clear understanding and interpretation (4) Analyze controls used 0—not discussed 2—mention controls but not discussed 4—correctly identifies and discuss controls (3) Why those control are important 1—simply states that controls are important 2—relates controls to the particular type of experiment 3—correctly relates controls to the particular type of experiment and states why that particular control was selected		
	20	**G: Materials & Methods:** (5) Thoroughness of flowchart 0—flowchart not included 2—flowchart included but missing two or more key components from study 4—flowchart clearly labeled, concise design 5—chart is clearly labeled, concise design, contains legend (5) Ability to use flowchart at bench 0—unclear 2—three or more mistakes or missing items 3—two or more mistakes or missing items 4—chart clear but missing one item 5—chart is concise and easily translated to lab use (5) Clearly describe what was done 0—unclear 1—does not use common verbiage 2—confusing wording or excessive grammatical errors 3—clear wording but two or more grammatical errors 4—clear with one grammatical error 5—clear with correct grammar (5) Clearly state conditions 0—no reference to experimental conditions 1—conditions mentioned but not correlated within flowchart 2—conditions have two or more errors or missing one key component 3—conditions have two or more errors 4—conditions mentioned 5—conditions clearly described and discussed within diagram ***Note, direct copying of the Materials and Methods paragraphs will results on a zero on this portion (20 points).*		

	15	**H: Results from a particular figure** (5) Identify the main finding 0—no identification 1—state finding without discussion 3—state finding with sufficient discussion 5—findings clearly and concisely stated (2) Sample size 0—does not discuss sample size 2—clearly states sample size (3) Statistical significance 0—does not discuss statistical significance 2—states statistical significance of finding 3—relates significance to original hypothesis (2) Statistical test and false positive/negative 1—identifies the type of test used 1—discuss the potential for false positive or false negative results (3) Biological relevance of results 0—no relation of results to hypothesis 1—states results are relevant without context 2—relevance mentioned but in general terms 3—results related to original hypothesis		
	35	**I: Discussion:** (5) Coherent story 2—states the article was coherent 3—explains why the article was/was not clear 5—excellent discussion of the flow, content, and results of study (5) Interpretation of results 2—references results only 4—results and their interpretations are discussed 5—coherent mention of how authors interpreted and applied their results to hypothesis (5) Sufficient evidence 2—states sufficient evidence was presented 4—relates strength of evidence to conclusion 5—synthesizes evidence to describe whether sufficient results convince the reader (5) Weakness in experiments 2—states no weakness in experiments 4—identifies one potential issue with experiments (design or conduct) 5—identifies two or more potential issues with experimental design or conduct (5) Novelty of article 1—states experimental design is novel 3—minimally identifies why article is novel 5—relates why article is novel compared to other published studies (5) New questions		

		1—restates question from paper 3—generate your own research question 5—restates question from paper and generates own novel research question (5) Future experiment 2—identify one future experiment 3—identify one experiment and hypothesis 5—identify one experiment, hypothesis, and resources necessary to complete experiment		

Encl 3 Grading Rubric Slides & Presentations

	Max Points		Criteria	Assessed Points	Total/notes
Slides	**5**				
		5	Digitally submitted via SharePoint NLT 0600 Lesson 39 [all or nothing]		
Slides (Instructor Assessment)	**50**				
		10	**Overall design and appearance:** 0—disorganized & difficult to follow 2—illegible portions on slides 4—adequate organization, somewhat difficult to follow 6—organization and images aid understanding 8—slides flow with complete titles and labels 10—professional appearance with text greatly increasing understanding of topic		
		5	**Citations (internal and works cited):** 0—no references presented 1—missing works cited 2—somewhat consistent formatting but missing two or more internal citations 3-4—several well-presented references in consistent format but missing one to two internal citations 5—fully referenced		
		5	**Introduce topic and background:** 0—no introduction 1—introduction is not concise 3—description present but unclear 5—clear understanding of relevant information presented		
		5	**State problem statement/hypothesis** 2—correctly specify discovery or hypothesis-based approach 3—identify problem statement/hypothesis [points are all or nothing]		
		5	**Describe the overall experiment/paper** 2—mention goal of paper 4—mention goal of paper, relevant background provided 5—clear goals, background, & results		
		10	**Methods** (4) Focus on one key method 2—include figure from paper 4—include figure from paper and designed flowchart (4) Describe how/what was done from one key method 2—minimal description of what was done 4—description conveyed in succinct manner (2) Controls and comparison/treatment group within key figure 1—identify control(s) 2—clearly identify control(s) and experimental group(s)		

		5	**Discuss results of this overall experiment** 1—summarize one conclusion 3—summarize findings and conclusion 5—summarize findings and mention novelty of results		
		5	**Discuss how overall findings relate to original problem statement/hypothesis and future inquiry** 2—relate findings to hypothesis 3—include future experiment(s) 5—include future experiment and pose a novel hypothesis		
Presentations (Instructor Assess)	**30**				
		10	**Quality of oral presentation (clear, concise, avoid speech filler)** 2—excessive speech fillers 4—minimally effective at conveying information 6—message somewhat clear but trouble answering questions 8—clear, concise, with one to two errors 10—confident, concise, effective		
		5	**Overall bearing/demeanor** 1—one or more member disengaged 3—sufficient posture and bearing 5—excellent bearing and demeanor		
		5	**Use of appropriate figures** 0—includes memes or inappropriate figures 1—displays figures but does not refer to them 3—casually refers to figures 5—fully integrates slides into presentation		
		5	**Flow of data among group** 2—obviously not rehearsed 4—smooth transition with one awkward pause 5—seamless transitions		
		5	**Time requirement** 2—exceeds prescribed time 5—within time limits		

INNOVATIONS

How to Teach the Hardy-Weinberg Principle Using Engaging, Non-trivial Evolutionary Scenarios

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Abstract: As a foundational evolutionary concept, the Hardy-Weinberg principle should be taught enthusiastically in introductory biology courses. In a companion Perspectives paper, I made the case that students are often given limited or incorrect information on the HW principle due to a lack of mastery or confidence on the part of their teachers. The purpose of this Innovations paper is to identify where errors are most-often made in the set-up and solutions of HW problems. The centerpiece of this paper is a set of six biological scenarios to which students need to apply the HW principle to answer interesting evolutionary questions. I provide explanations for solving the problems (including Excel instructions with formulas to perform chi-square tests), and I identify several teachable moments that are likely to arise in the discussion of the solutions. The use of this problem set and the pedagogical strategy described in this paper significantly improved students' performance on HW problems in my introductory biology class, and I expect that they can benefit other teachers at least as much.

Keywords: chi-square test, evolutionary mechanisms, Hardy-Weinberg principle, introductory biology, population genetics, problems

INTRODUCTION

The Hardy-Weinberg principle (HWP) is among the more challenging concepts taught in introductory biology courses. The probabilistic nature of the HWP makes analysis of evolutionary scenarios deceptively difficult for students, as well as teachers who are not specifically trained in quantitative analyses (Mertens, 1992; Masel, 2012; Brewer & Gardner, 2013). As a result, the exercises that students are given to apply the HWP tend to be over-simplified, and the students' understanding and appreciation of the HWP ends up being superficial and fleeting (Masel, 2012; Smith & Baldwin, 2015).

My goals in writing this and the companion Perspectives paper are to encourage introductory-biology instructors to teach the HWP enthusiastically and to provide them with the means to do so confidently. This paper begins with general guidance on teaching students to analyze evolutionary scenarios using the HWP, based on a strategy I have developed over many years of teaching introductory biology. This strategy includes the option of using chi-square tests to make statistically supported inferences. The rest of the paper focuses on a HW-problem set that includes six scenarios that I have used in my introductory biology courses. I explain the rationale for each scenario, the mathematics used to analyze the problems, and hypotheses for how evolution would most likely cause the patterns in the data. Throughout, I provide guidance on avoiding the most common mistakes made by students, as well as by teachers, in applying the HWP.

PROCEDURE

General Guidance on Teaching Hardy-Weinberg Problems

The strategy that I teach students to use in solving HW problems involves a four-step process (Fig. 1). The first step is to identify the relevant information given (generally about phenotypes, but maybe about genotypes or alleles) that can be used to calculate the actual (i.e., observed) allele frequencies and genotype frequencies in the population. It is very important to stress that the actual allele frequencies can always be calculated if one knows the genotype frequencies, but the reverse is not true: The actual genotype frequencies in a population cannot be calculated from the allele frequencies alone. (Note the one-way red arrow from the genotype-frequency box to the allele-frequency box in Step 1 of Fig. 1). A very common mistake in HW problems is that students plug the allele frequencies into the HW equilibrium equation (see below) to try to calculate actual genotype frequencies (Smith & Baldwin, 2015).

The second step is the calculation of the HW equilibrium (HWE) genotype frequencies from the actual allele frequencies (i.e., p^2, $2pq$, and q^2; Fig. 1). The third step is to compare the actual genotype frequencies with the HWE genotype frequencies. This comparison can be done with or without the aid of statistical analysis (e.g., chi-square test). Without statistical analysis, students can still make qualitative

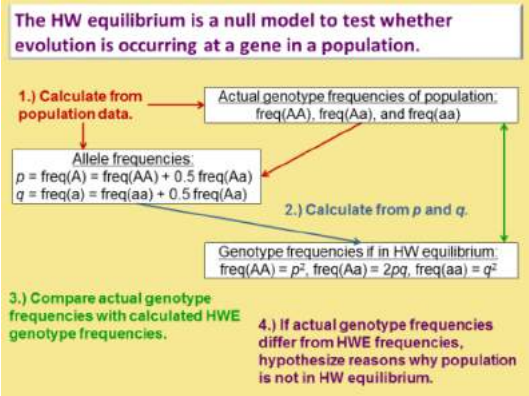

Fig. 1. Lecture slide used to overview strategy for solving Hardy-Weinberg problems.

statements such as whether there are more or fewer heterozygotes in the population than predicted by the HWE frequencies. The fourth step is to compare any discrepancies between the actual and HWE genotype frequencies with patterns expected if any of the assumptions of the HWP are violated. These patterns allow students to propose hypotheses about what mechanisms are the most likely to be causing the evolution observed in the population. Ecological information about the organisms given in the text of the problem should guide students toward explanations of how these mechanisms might act in terms of the biology of the system.

Group Activity on Hardy-Weinberg Scenarios

In the most-recent version of my introductory Biological Diversity course, I employed the six-scenario problem set using a group activity. Before presenting the problem set, I lectured briefly on the historical context and development of the HWP. I used a textbook example of the inheritance of coloration in cats (Raven et al., 2014) to illustrate the four steps shown in Fig. 1. I then had the class of 24 students break into six groups of four students, and I handed each student a sheet with six evolutionary scenarios (i.e., "HW problems"). These scenarios are based on actual biology, but the numbers were fabricated to achieve my pedagogical goals. Each student-group volunteered to be responsible for solving one of the problems and presenting it to the class during the next meeting. Students spent the rest of the class period solving their problem together. They were provided with colored markers and a flipboard to work on their presentations. While they were working, I rotated among groups to check their progress and give hints as needed so that they would not present wildly erroneous information to the rest of the class. Most groups finished preparing their presentations for homework, and I strongly encouraged students to work on the other five problems on their own so that they could get the most value out of watching the presentations of the other student groups during the next class meeting.

Use of Chi-Square Tests in Hardy-Weinberg Problems

Because my course was the second of a two-semester sequence of introductory biology, I knew that the majority of my students had been exposed to analyzing genotype frequencies (in the context of Mendelian genetics) in the prerequisite course. Therefore, I required students to analyze their data by performing a chi-square test using calculators and a chi-square probability table (Table 1), as they had done in the previous course. Alternatively, chi-square tests can be performed in a relatively straightforward manner using Excel. I have provided a generic Excel table (Fig. 2) that can be used to quickly calculate all of the information needed for Steps 1-3 in most HW problems. The orange-shaded cells show the formulas for the calculations using Excel syntax (i.e., exactly what would be typed into the cells). The pink-shaded cells (C5:C7) are where data on the number of individuals of each phenotype or genotype would be entered. (Be sure that students enter counts of individuals into these cells—rather than frequencies or proportions.) The generic information in the unshaded cells should be replaced with the information specific to the problem (e.g., the phenotype names in Column A and convenient abbreviations for the alleles for the genotypes in

Table 1. Table of chi-square (X^2) probabilities and associated *P*-values. Use this table to perform a chi-square test of the null hypothesis that observed genotype frequencies in a sample population did not differ from Hardy-Weinberg equilibrium (HWE) frequencies. First find the row for the number of degrees of freedom in your test. Then find the columns between which your calculated X^2 value falls. Drop to the bottom (shaded) row of these columns to find the range of *P*-values associated with your X^2 and df. If $P < 0.05$, then you should reject the null hypothesis, and you can infer that the genotype frequencies in your sample population are not at HWE.

df	Null hypothesis is supported ←							→ Null hyp. is rejected		
	Chi-square values (X^2)							Chi-square values (X^2)		
1	0.00016	0.0039	0.064	0.455	1.074	1.642	2.706	3.841	5.412	6.635
2	0.0201	0.103	0.446	1.386	2.408	3.219	4.605	5.991	7.824	9.210
***P* =**	**0.99**	**0.95**	**0.80**	**0.50**	**0.30**	**0.20**	**0.10**	**0.05**	**0.02**	**0.01**

Fig. 2. Excel table for performing a chi-square test of the null hypothesis that a population is in Hardy-Weinberg equilibrium for a given gene. Data on observed numbers of individuals are entered directly in the pink-shaded cells (C5-C7). The formulas in the orange-shaded cells calculate the information needed for the chi-square test.

	A	B	C	D	E	F	G	H	I
1									
2									
3			Number	Number		$\frac{(Obs. - Exp.)^2}{Expected}$		Frequencies	
4	Phenotype	Genotype	Observed	Expected	Observed - Expected			p =	=C5/C8+C6/C8/2
5	Homozygote 1	*AA*	N_{AA}	=C8*I6	=C5-D5	=(E5^2)/D5		q =	=(C7/C8+C6/C8/2)
6	Heterozyogote	*Aa*	N_{Aa}	=C8*I7	=C6-D6	=(E6^2)/D6		p^2 =	=I4*I4
7	Homozygote 2	*aa*	N_{aa}	=C8*I8	=C7-D7	=(E7^2)/D7		$2pq$ =	=2*I4*I5
8	Sums:		=SUM(C5:C7)	=SUM(D5:D7)	=ROUND(SUM(E5:E7),1)	=SUM(F5:F7)		q^2 =	=I5*I5
9	X^2 =	=F8	df =	=(COUNT(D5:D7)-1)*(2-1)-1	0	=CHISQ.DIST.RT(F8,D9)			

Column B).

There is substantial flexibility in how much guidance you choose to give your class depending on how much time you have to spend on these problems. For example, you could provide them with Excel tables with formulas already filled in, you could provide them with a printout of a blank table with only headings, or you could let them figure out for themselves how to tabulate the data. If you do not want to involve computers, you can have students make statistical inferences by hand-calculating chi-square (χ^2) values and degrees of freedom (df). Students can then compare these values with the values in a chi-square-probability table to find the *P*-value range for their test (e.g., Table 1).

The *P*-value range identified using the table (or the precise value calculated by Excel) can be interpreted as the likelihood of finding actual genotype frequencies as divergent from the HWE frequencies by random chance alone. By convention, if the *P*-value is < 0.05, then we can infer that the null hypothesis (viz., that the population is in HWE) can be rejected; that is, the actual genotype frequencies are "statistically significantly different" from HWE. Therefore, the population can be inferred to be undergoing evolution at the gene of interest. If the *P*-value is ≥ 0.05, then we cannot reject the null hypothesis, and there is not sufficient evidence to conclude that the population is evolving.

One common area of confusion in applying chi-square tests for HW problems is the appropriate number of degrees of freedom to use. In general, the degrees of freedom in a chi-square test are calculated as the number of columns (*c*) minus one, times the number of rows (*r*) minus 1, or df = (*c*-1) x (*r*-1). This is the formula that Excel uses to determine the df for a chi-square test when using the built-in function "=CHITEST( )" in which the range of cells containing the counts are entered as the argument in parentheses. For comparing actual to expected genotype frequencies, there will always be two columns—one for actual counts of individuals and one for expected counts of individuals under HWE. Thus, the df calculation reduces to just the number of rows - 1. For three genotypes, there would be three rows of data, and the df would thus be 2, or df = (2-1) x (3-1). Equivalently, a commonly taught approach to calculating df for chi-square tests in HW problems is simply to subtract 1 from the number of genotypes under consideration (cf. McMurran, 2010).

While this approach is convenient and may help avoid a class-wide discussion of the statistical/philosophical rationale behind degrees of freedom, it actually perpetuates a critical error. Simply put, the degrees of freedom available for any statistical test is reduced by the number of parameters that must be estimated from the data. For calculating the expected genotype frequencies, one must generally estimate allele frequencies (*p* or *q*) from the data. This estimation uses up one degree of freedom. Therefore, in a typical HW problem, the appropriate number of degrees of freedom for a chi-square test involving three genotypes would be 1 (or, df = 3-1-1) (Hartl & Clark, 1989; Freeman & Herron, 2004).

This statistical issue can be easily rectified by using a different Excel function: "=CHISQ.DIST.RT(_, _)" in which the calculated χ^2 and the df are entered as the arguments in parentheses. While conceptually a bit more difficult, this correct approach offers few additional practical difficulties in statistically analyzing HW problems than the typical, incorrect approach. An exception is when the problem involves only two genotypic categories instead of three. In such a case, the degrees of freedom will equal 0, which precludes a valid application of a chi-square test. The second scenario in the problem set below illustrates such a case in which a chi-square test cannot be applied to analyze the data. Instead, students are limited to making qualitative, rather than quantitative, inferences in that scenario.

Set of Six Hardy-Weinberg Scenarios

The question set that I used is displayed in Appendix 1. In this section, I overview the rationale behind the scenarios, explain the solutions, and provide hints and caveats for each of the six problems. A summary of the intermediate and final quantitative answers for each problem is displayed in Excel-table format in Fig. 3. (An Excel file with formulas entered into the cells is also available from

Fig. 3. Excel tables showing the intermediate calculations, X^2, df, and *P*-values for analyses of the six Hardy-Weinberg scenarios shown in Appendix 1.

1) Sickle-Cell Anemia

Phenotype	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.6625
normal	*SS*	75	87.78125	-12.78125	1.8610	q =	0.3375
carrier	*Ss*	115	89.4375	25.5625	7.3061	p^2 =	0.4389
sickle-cell anemia	*ss*	10	22.78125	-12.78125	7.1708	$2pq$ =	0.4472
Sums:		200	200	0	16.3379	q^2 =	0.1139
X^2 =	16.3379	df =	1	P =	5.29934E-05		

2) Bitterness in Dandelions

Phenotpye	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.5
mild	*bb*	5	31.25	-26.25	22.0500	q =	0.5
bitter	*BB + Bb*	120	93.75	26.25	7.3500	p^2 =	0.25
Sums:		125	125	0	29.4000	$2pq$ =	0.5
X^2 =	29.4000	df =	0	P =	#NUM!	q^2 =	0.25

3) Copper Tolerance in Bent Grass

Phenotype	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.775
Cu-tolerant	*TT*	55	60.0625	-5.0625	0.4267	q =	0.225
Cu-tolerant	*Tt*	45	34.875	10.125	2.9395	p^2 =	0.6006
Cu-sensitive	*tt*	0	5.0625	-5.0625	5.0625	$2pq$ =	0.3488
Sums:		100	100	0	8.4287	q^2 =	0.0506
X^2 =	8.4287	df =	1	P =	0.003693443		

4) Flower Color in Morning Glory

Phenotype	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.6227
white	*WW*	388	290.785333	97.21467	32.5006	q =	0.3773
purple center	*Ww*	158	352.429333	-194.4293	107.2634	p^2 =	0.3877
purple	*ww*	204	106.785333	97.21467	88.5018	$2pq$ =	0.4699
Sums:		750	750	0	228.2657	q^2 =	0.1424
X^2 =	228.2657	df =	1	P =	1.4242E-51		

5) Pigmentation in Water Boatmen

Phenotype	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.35
pigmented	*AA*	20	12.25	7.75	4.9031	q =	0.65
pigmented	*Aa*	30	45.5	-15.5	5.2802	p^2 =	0.1225
albino	*aa*	50	42.25	7.75	1.4216	$2pq$ =	0.455
Sums:		100	100	0	11.6049	q^2 =	0.4225
X^2 =	11.6049	df =	1	P =	0.000657783		

6) *Delta-32* Mutation

Phenotype	Genotype	Number Observed	Number Expected	Obs. - Exp.	$(Obs. - Exp.)^2$ / Expected	Frequencies	
						p =	0.7
HIV-susceptible	*SS*	500	490	10	0.2041	q =	0.3
HIV-susceptible	*Ss*	400	420	-20	0.9524	p^2 =	0.49
HIV-resistant	*ss*	100	90	10	1.1111	$2pq$ =	0.42
Sums:		1000	1000	0	2.2676	q^2 =	0.09
X^2 =	2.2676	df =	1	P =	0.132104339		0

the author. This file has the data that I used in my class for the scenarios, but these data can be modified as desired, and the statistics will be automatically recalculated.)

Scenario 1: Sickle-Cell Anemia

Sickle-cell anemia is a classic example of a disease caused by a recessively expressed mutation that is found in higher-than-expected frequencies due

to a phenomenon called "heterozygote advantage." Specifically, carriers of the disease (i.e., heterozygous individuals) have an increased resistance to malaria, which is a deadly disease prevalent in tropical areas in which sickle-cell anemia is also common. Thus, while individuals homozygous for the sickle-cell gene are selected against (i.e., they are likely to die before reproducing), individuals heterozygous for the gene are favored by selection because they are less likely to die of malaria before reproducing.

The numbers of individuals possessing the different genotypes are given in the text of the problem. (If using the Excel table, enter these in Cells C5-C7, Fig. 2.) With these numbers of individuals, the genotype frequencies and then the allele frequencies can be calculated using the formulas in Step 1 of Fig. 1 (or Cells I4 and I5, Fig. 2). In Step 2 (Fig. 1), the HWE genotype frequencies are calculated from the allele frequencies (Cells I6-I8, Fig. 2). The numbers of individuals in the sample that would be expected if the population is at HWE are then calculated from these genotype frequencies (Cells D5-D7, Fig. 2). Then the actual numbers of individuals of each genotype are compared with the number of individuals we would expect from a population of the same sample size if the population is at HWE (Step 3, Fig. 1).

With the numbers of individuals given in this problem, there are fewer than half as many recessive homozygotes as expected at HWE (10 vs. 23, Fig. 3), slightly fewer dominant homozygotes than expected (75 vs. 88), and more heterozygotes than expected (115 vs. 89). Qualitatively, these results are consistent with strong selection against individuals with the sickle-cell phenotype, and selection in favor of heterozygous carriers.

An obvious question is whether these differences from the HWE expectations are substantial enough to be of biological interest. This is where a chi-square test proves to be very useful. Using Excel, the CHISQ.DIST.RT function (Cell F9 of Fig. 2) returns a *P*-value of 0.000053 (Fig. 3; or if you use the chi-square probabilities in Table 1, then $P < 0.01$), which is well below the traditional cutoff of < 0.05 for statistical significance. Thus, the genotype frequencies are highly significantly different from those predicted by the HWE null hypothesis, and we can reject this null hypothesis and infer that evolution is occurring at the sickle-cell gene in this population. The pattern of evolution found in the genotypes is indeed consistent with the hypothesis of heterozygote advantage.

In this scenario on sickle-cell anemia, some students might answer that genetic drift is responsible for the deviation of the genotypic frequencies from HWE. As detailed in the companion Perspectives paper, the biological and stochastic processes that result in genetic drift are always acting in every population of organisms. Therefore, students might argue that genetic drift is a reasonable answer for *any* of the scenarios in the problem set. After all, one cannot prove for certain that genetic drift alone did not cause a deviation in genotype frequencies of any magnitude from HWE expectations. The rebuttal to such arguments involves a rational appeal to likelihood (i.e., perhaps, common sense). Specifically, the employment of a chi-square test enables a quantitative and objective assessment of the likelihood that drift is solely responsible for a deviation of genotype frequencies from HWE expectations.

In general terms, the *P*-value from a statistical test indicates the probability of finding a deviation from the null hypothesis as large as you observed by random chance alone (what statisticians call "sampling error"). In terms specific to the context of population genetics, the evolutionary mechanism that causes random departures in genotype frequencies from HWE is genetic drift. The probability of genetic drift causing a deviation from HWE as large as was observed in a population is embodied in the *P*-value. Specifically, the lower the *P*-value, the less likely it is that genetic drift alone was responsible for the deviation, and thus the more likely another evolutionary mechanism was also at play. The identity of that mechanism should be hypothesized from the background information given in the text of the scenario.

For this scenario on sickle-cell anemia, the *P*-value for the chi-square test of the null hypothesis that the genotype frequencies were at HWE was 0.000053. Therefore, the chance that genetic drift alone would cause the observed deviation in genotype frequencies from HWE was only about one in 20,000. While a student could still argue that we cannot 100% prove that genetic drift was not solely responsible, the low probability of that outcome makes that answer relatively untenable. A much better answer to this question would include an explanation of the evolutionary mechanisms (e.g., natural selection and heterozygote advantage) that are consistent with the observed patterns in deviations of genotype frequencies from HWE predictions in the specific scenario.

In any given generation, genetic drift may act either to accentuate or obscure the influence of other evolutionary mechanisms on the deviations of genotype frequencies from HWE expectations. However, the smaller the *P*-value is, the more confidently we can infer the influence of another evolutionary mechanism through the noise that is caused by genetic drift.

Scenario 2: Bitterness in Dandelions

In this scenario, it is the allele frequencies that are given; these can be entered directly into Cells I4 and I5 of Fig. 2. We cannot calculate the actual frequencies for all three genotypes because we don't

know how many of the 120 bitter plants are heterozygous and how many are homozygous. Nevertheless, a careful reading of the scenario will show that we do not need to know all the genotype frequencies to address the specific question—at least qualitatively. We can still calculate HWE genotype frequencies from the allele frequencies (Step 2 of Fig. 1; Cells I6-I8 of Fig. 2). We know that the number of mild plants expected under HWE is the number of individuals homozygous for the mildness allele (Cell D5, Fig. 2), and that the number of bitter plants expected under HWE is the number of heterozygotes plus the number of individuals homozygous for the bitterness allele (Cells D6+D7 of Fig. 2).

In Step 3 (Fig. 1), we just need to compare the ratio of mild:bitter plants observed (5:120) with the much higher ratio expected under HWE (31:94). A chi-square value can be calculated from these data (χ^2 = 29.4; Fig. 3). This χ^2 value is much higher than all of the critical values for statistical significance shown in Table 1. However, a valid chi-square test cannot be performed on these data, because the df for such a test would equal zero. Note that Excel will return an error message (#NUM!) if one asks it to perform a chi-square test with df = 0. Therefore, students will be required to interpret the results without the benefit of a statistical test. The inclusion of a scenario in which a chi-square test is not an option can serve as a topic of discussion regarding students' confidence in statistical tests, as well as the difference between biological significance and statistical significance.

Even without a statistical test, students can see that there were 24 times as many bitter dandelion as mild dandelions in my yard, while if the population was in HWE, there would only be three times as many bitter dandelions plants as mild ones. The most reasonable explanation for the discrepancy in the actual phenotype ratio from that predicted by HWE is that natural selection acted against the mild phenotype. If students need hints to hypothesize a mechanism, ask them what kinds of animals one might find in yards. Among these animals, several are bound to be herbivorous (e.g., rabbits, slugs, and insects), and these animals may perceive the palatability of dandelion greens just as we do. Herbivores feed on (and thus reduce the fitness of) mild dandelions, while bitter dandelions survive and reproduce. In answering the question posed in the scenario text, one could conclude that rather than being unlucky, I was not thinking enough about evolution by natural selection.

Scenario 3: Copper Tolerance in Bent Grass

In this scenario, the numbers of individuals of each genotype in the sample are given, which allows for simple calculation of the allele frequencies (Cells I4-I5, Fig. 2). The HWE genotype frequencies are then calculated from the allele frequencies (Cells I6-I8, Fig. 2). The numbers of individuals expected for each genotype under HWE are then calculated by multiplying these HWE genotype frequencies by the number of individuals (100) in the sample (Cells D5-D7, Fig. 2).

A comparison of these expectations with the actual numbers of individuals shows that the number of copper-susceptible individuals at the abandoned mine site is lower than the HWE expectation (0 vs. 5, Fig. 3). This result is easily explained by natural selection in the abandoned copper mine acting against the individuals that are susceptible to copper poisoning. However, the number of copper-tolerant homozygotes is also a bit lower than the HWE expectation (55 vs. 60). This result is not consistent with natural selection for copper tolerance being the only evolutionary mechanism in action.

The more surprising result is that the number of heterozygotes observed was greater than HWE expectations (45 vs. 35). The clue to understanding this result is knowledge that grass is wind-pollinated. Some bent-grass plants in the abandoned mine site are likely to be fertilized by pollen that blows in from plants adjacent to the mine, where copper-sensitive individuals are more fit than copper-tolerant individuals. Such pollen would carry the susceptibility allele. Thus, gene flow from a non-mine site is a likely evolutionary mechanism responsible for the larger-than-expected number of heterozygotes in the abandoned-copper-mine site. Seeds originating from the low-copper populations adjacent to the mine are also likely to be dispersed by wind into the abandoned mine site. These seeds would likely be homozygous for the susceptibility allele. However, plants that grow from such seeds in high-copper soil are likely to die before maturity, and thus homozygous susceptible plants are not likely to be found in a sample of mature individuals from the abandoned mine site.

Scenario 4: Flower Color in Morning Glory

In this scenario, there is incomplete dominance for flower-color phenotype. Thus, the genotype frequencies are directly reflected in the phenotype frequencies, which are easily obtained from the numbers given in the text of the problem. I used *p* to represent the frequency of the white allele, and *q* for the purple allele—though the choice of letters is arbitrary. The allele frequencies are calculated from the observed numbers of individuals (Cells I4-I5, Fig. 2), and HW-equilibrium genotype frequencies are calculated from the allele frequencies (Cells I6-I8, Fig. 2). The numbers of individuals in the sample that would be expected if the population is in HWE are then calculated from these genotype frequencies (Cells D5-D7, Fig. 2).

A comparison of these expectations with the actual numbers of individuals shows that the observed numbers of both types of homozygotes were much greater than the expected numbers (Fig. 3). In contrast, the number of heterozygotes observed was much smaller than expected under HWE (158 vs.

352). With such a large sample (750 plants), these deviations from HWE were very highly statistically significant ($P = 1.4 \times 10^{-51}$, Fig. 3). This pattern of an excess of both homozygotes is a hallmark of assortative mating, wherein individuals with similar phenotypes mate with each other and avoid mating with individuals of different phenotypes.

Hypothesizing a mechanism that would cause this pattern requires a recognition of how morning glory plants "choose" mates. The hint to how this occurs is given in the first sentence of the text of the problem. Specifically, it is the bumblebees that transfer pollen among plants, and thus they are choosing which plants are mated. To forage efficiently, bumblebees may form a search image for one color or the other. For instance, an individual bee may find purple flowers to be rewarding, and thus may go from one purple flower to another. Another bee may focus on just white flowers. The result is that purple alleles tend to match up with other purple alleles, and white with white, which results in a preponderance of offspring homozygous for flower color.

Scenario 5: Pigmentation in Water Boatmen

This scenario is perhaps the most challenging of the set, as its setup is more complex than the others, and because the answer is not as simple as one evolutionary force acting consistently in one direction. The text of the problem clues students in to the fact that the pigmentation gene is indeed evolving in the tanks. Specifically, the phenotype ratios have changed over time in the tanks, going from extreme ratios to 50:50. Students will also probably realize that the predatory fish are the drivers of the evolution. However, the scenario is not as simple as fish always preferring to eat pigmented individuals or always preferring albino individuals. This scenario involves frequency-dependent selection, where the fish will favor whichever prey phenotype is the most common.

The actual frequencies at the end of the experiment are the important numbers to compare with the HWE frequencies. From the information given, it is a simple matter to figure out that each tank ended up with 50 albino (all homozygotes), 30 heterozygous pigmented, and 20 homozygous pigmented water boatmen. These values can be used to calculate the actual allele frequencies (Cells I4-I5, Fig. 2). The allele frequencies are then used to calculate the HWE genotype frequencies (Cells I6-I8, Fig. 2), which are then used to calculate the expected number of individuals of each genotype at HWE (Cells D5-D7, Fig. 2). A comparison of these expectations with the actual numbers of individuals shows that number of both homozygous-pigmented and homozygous-albino individuals were greater than expected (Fig. 3). This deviation from expectation was statistically significant ($P = 0.00066$), which indicates that evolution is indeed occurring on this gene, even when the two phenotypes are equally common in the tanks.

Natural selection by the predatory fish is the most likely explanation for the deviation from HWE in this problem. However, neither phenotype has a consistent advantage. That is, if fish always preferred pigmented insects, then the number of pigmented insects would be less than the HWE expectation. Likewise, if fish always preferred albinos, then the number of albino insects would be less than the HWE expectation. The fact that both homozygotes were more frequent than expected shows that they both experienced selective advantages. However, they experienced them at different times—when each was the minority phenotype. Thus natural selection always favors the rare phenotype, such that the two phenotypes become equally common over time—a hallmark of frequency-dependent selection. The text in the setup of the scenario should lead students to the conclusion that the fish prefer to eat the more-common phenotype, even though they may not yet have the language to explain it as "frequency-dependent selection."

This pattern of the both homozygotes being more common than expected, at the expense of the heterozygotes, is also consistent with assortative mating (as observed in the question on morning glories). Therefore, students might hypothesize that pigmented individuals prefer to mate with other pigmented individuals, and albino individuals with other albinos. However, assortative mating by itself does not explain why the two phenotypes always became equally common in the experimental tanks. The text of the scenario intentionally did not mention anything about mating. In fact, the time scale involved is likely so short that the fish ate the insects before the insects completed their life cycles. Nevertheless, these details were not specified in the text so that students would have more flexibility in hypothesizing about evolutionary mechanisms, which could then generate more critical thinking and discussion.

Scenario 6: Delta-32 Mutation

This scenario may be the most interesting to students because it is about human health. (Be aware, however, that it involves topics that may be uncomfortable for some students.) The genotype frequencies are given in this problem, so the allele frequencies can be readily calculated (Cells I4-I5, Fig. 2). From the allele frequencies, the HWE genotype frequencies can be calculated (Cells I6-I8), and the expected number of individuals with each genotype (Cells D5-D7) can then be compared to the observed numbers (Cells C5-C7).

Qualitatively, there were more individuals homozygous for the Delta-32 mutation than expected under HWE (100 vs. 90). However, this difference was not statistically significant, with a chi-square test *P*-value of 0.13 (Fig. 3). Thus, there is not definitive

evidence that this population is evolving at the *CCR5* gene due to natural selection. Instead, the discrepancy in the observed data with the HWE expectations could easily be due to genetic drift alone. Nevertheless, this failure to reject the null hypothesis does not mean that the Delta-32 allele is not advantageous in some fashion. Individuals homozygous for the mutation may be likely to survive longer than sexually active gay men without the mutation. However, fitness involves not just survival, but reproduction to pass along the genes. Gay men may be unlikely to pass on their genes, whether or not they have the Delta-32 allele. Or, people may reproduce before contracting HIV and thus may pass along the non-mutated allele to their offspring before natural selection for mutation has a chance to take place. Finally, the Delta-32 mutation may provide other immunity benefits, but natural selection was not strong enough to be statistically significant in this sample of 1000 individuals.

This example on the Delta-32 allele provides a good opportunity for discussing the limits of using the HWE test to detect the action of natural selection. Specifically, the strength of selection must be quite high, or the sample population must be very large, for selection to result in a statistically significant departure in genotype frequencies from HWE within a generation (Hartl & Clark, 1989). Nevertheless, even weak selection can have a substantial effect on the allele frequencies of a population over very long periods of time. Thus, methods other than testing for HWE are often more useful for finding evidence of evolution by natural selection.

CONCLUSION

In the first introductory biology course in which I used this problem set, the students' scores on a set of questions based on a HW scenario on the final exam improved by 20% compared to scores on the same question in the last biology course in which I did not use the problem set (one-way ANOVA: $F_{1,57} = 5.82$; $P = 0.02$). I expect that the improvement in the exam performance would have been even greater if I had done two things: 1) insist that every student turned in a written attempt at each of the six scenarios, and 2) remind students to review these problems prior to the final exam—rather than just studying material covered in professor-led lectures, which is something that several students admitted to doing on their course evaluations.

In addition to the objective benefit of higher exam scores, my use of this problem set provided several subjective benefits. For example, the relatively complex scenarios required students to employ quantitative reasoning and higher-order cognitive skills. The activity also provided students a chance to work cooperatively and make an oral presentation to the class—both important skills that are not generally practiced in the traditional lecture structure of most introductory biology courses (Gokhale, 1995; Prince, 2004). It is my hope that other instructors will be willing to use or modify this problem set for their own courses, including the Excel template for performing chi-square tests.

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Appendix 1. Hardy-Weinberg problem set: six evolutionary scenarios.

1. In a population of humans in a village in central Africa, doctors took blood samples from 200 adolescent boys to study sickle-cell anemia, which is a recessively inherited disease caused by a mutation in a single gene coding for hemoglobin production. In the sample, 115 boys were found to be carriers (heterozygote) for sickle-cell anemia, and 75 were homozygous for the normal-hemoglobin allele. Is there evidence for evolution in the sickle-cell anemia gene in this population? If so, what might be causing the evolution?
2. Dandelion greens can be purchased in spring at farm markets and green grocers. The greens generally have a mild flavor, and they are considered a healthy addition to salads. However, dandelions in the wild can taste quite bitter, depending on the alleles present for one gene (the bitterness gene). Mildness is a recessive phenotype, such that leaves from heterozygotes are just as bitter (and unpleasant tasting) as leaves from plants that are homozygous for the bitterness allele. Out of curiosity, I had a genetic analysis done from a sample of the huge dandelion population in my yard. The genetics lab reported that the frequency for the mildness allele was 50% in my dandelion population. Instead of mowing, I decided that it was worth harvesting all of my dandelion plants one spring to sell the greens at the local market. Out of 125 dandelion plants, it turned out that 120 had bitter leaves, and thus only five produced leaves worth eating. Should I have been surprised at my misfortune, based on a population-genetics perspective? If so, what is a likely explanation for the preponderance of bitter-leaved dandelions in my yard?
3. A species of bent grass has a gene that controls whether it is tolerant of (or susceptible to) copper poisoning. The more copper that is present in soil, the greater the survival and reproductive advantage tolerant plants have over susceptible plants. When copper levels are particularly high, susceptible plants die as seedlings before reaching reproductive maturity. In contrast, where soil-copper levels are normal, susceptible plants grow and reproduce much better than copper-tolerant plants. Bent-grass reproduction does not rely on animals, as its pollen and seeds are both carried by wind. The tolerant phenotype is inherited in a completely dominant fashion over the susceptible phenotype. In an abandoned copper-mine site, a sample of 100 mature bent-grass individuals was taken to a genetics lab, and the genotypes for copper tolerance were identified: 55 homozygous tolerant and 45 heterozygous. Is there evidence for evolution of the copper-tolerance gene in this population of bent grass at the abandoned mine site? If so, what might be causing the evolution? Is there evidence for more than one evolutionary mechanism acting?
4. Many species of morning glories produce large, showy flowers that are attractive to bumblebees. Consider a species whose flowers are either entirely white, entirely purple, or mostly white but with purple just at the center of the flower. These colors are determined by one gene with two alleles, and heterozygotes have white flowers with purple centers. Any given plant may have many flowers, but all of its flowers are the same color phenotype. A graduate student sampled a population of 750 morning glory plants and found the following phenotypic frequencies: 388 white, 204 purple, and 158 white with purple centers. Is there evidence for evolution at the flower-color gene in this population? If so, what might be causing the evolution?
5. Surface-swimming aquatic insects called water boatmen occur in two color morphs: pigmented and albino. The albino phenotype is recessive to the pigmented phenotype. In a series of cattle-tank experiments, a predatory fish was placed into each tank along with 1000 water boatmen. The water boatmen were a mixture of different proportions of albino and pigmented individuals, ranging from a low of 10% albinos to a high of 90% albinos. The experiment was terminated for each tank when 100 water boatmen remained in the tank. At the end of the experiment, the water boatmen percentages consistently ended up at half pigmented and half albino, regardless of the starting percentages. Electrophoresis determined that roughly 30% of the water boatmen were heterozygous for color in each tank. Did evolution at the pigmentation gene occur in these tanks? Does evolution continue to occur after the phenotypic ratios reach 50:50?
6. Recently, a deletion mutation in the *CCR5* gene on chromosome 3 of humans has been identified and named the Delta-32 mutation. There is evidence that individuals who are homozygous for this mutation may be resistant to infection by certain strains of the HIV virus. In a study of 1000 sexually active gay men in England, 100 men were found to be homozygous for the Delta-32 allele, while 500 men had no copies of the Delta-32 allele. Is there evidence for evolution of the gene in question in England? If so, what might be causing the evolution?

PERSPECTIVES

On Hardy-Weinberg in Introductory Biology: Teaching this Fundamental Principle in an Authentic, Engaging, and Accurate Manner

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Abstract: The Hardy-Weinberg principle (HWP) is a fundamental model upon which much of the discipline of population genetics is based. Despite its significance, students often leave introductory biology courses with only a shallow understanding of the use and implications of the HWP. I contend that this deficiency in student comprehension is too-often a consequence of teachers of introductory biology having an insufficient mastery of the HWP, as well as a lack of proficiency in quantitative analysis in general. The purpose of this Perspectives paper is to correct some common misconceptions about the HWP so that teachers of introductory biology will have more confidence that they are communicating this important principle correctly to their students. A companion Innovations paper provides a problem-set of six real-world Hardy-Weinberg scenarios, along with explicit instructions on quantitatively analyzing the scenarios.

Keywords: evolutionary mechanisms, Hardy-Weinberg equilibrium, introductory biology, population genetics

The Centrality of the Hardy-Weinberg Principle in Evolutionary Biology

The Hardy-Weinberg principle (HWP) often serves as the foundation for students to build an understanding of how evolution works in populations of organisms. Nevertheless, applying the HWP tends to be one of the more difficult and thus least favorite topics for introductory biology students, due in part to the abstract (probabilistic) nature of the HWP, students' preconceptions that biology should not include mathematics, and students' lack of appreciation of the variety of real-world biological scenarios to which the HWP can be applied (Mertens, 1992; Winterer, 2001; Brewer & Gardner, 2013; Smith & Baldwin, 2015). It does not help that instructors of introductory biology are often not specialists in population biology and may be just as uncomfortable with the quantitative aspects of HW problems as their students are (Masel, 2012). As a result, the teaching of the HWP tends to be superficial, and students often move on to higher-level biology courses with no deeper knowledge of the HWP than remembering a partial list of assumptions and the formula "$p^2 + 2pq + q^2 = 1$." Worse yet, biology departments may decide to remove the teaching of HW from introductory courses altogether (Masel, 2012).

I contend that it is a disservice to students to give superficial treatment to the HWP in an introductory biology course for several reasons. First, this topic serves as an entrée into the increasingly important discipline of population genetics. Failure to do it justice may result in a missed opportunity to attract or retain students whose interest in biology tends more to the macro-scale than the cellular and molecular perspectives that constitute much of the course matter in introductory biology. Second, the HW perspective provides students with an appreciation that evolution is a phenomenon that happens continuously and that can be studied in real time (Winterer, 2001). Third, using the HWP to analyze real (or creatively contrived) data provides an excellent way for students to employ the scientific method, including using simple statistics to test hypotheses. Thus, analysis of evolutionary scenarios using the HWP provides teachers an opportunity to answer the pedagogical call to incorporate quantitative activities into lecture courses (NRC, 2003; AAAS, 2011; Hoskinson et al., 2013; AAAS, 2015; McLaughlin & Metz, 2016). Fourth, solving problems where the HWP is applied in an authentic way (not just plugging values into a formula) requires students to use higher-order cognitive processes (e.g., analysis and evaluation in Bloom's taxonomy) (Crowe et al., 2008).

The Hardy-Weinberg Equilibrium

A central question throughout the history of the study of evolutionary biology is why genetic variation persists within populations. The work of Gregor Mendel, which was rediscovered by the scientific community in 1900, put to rest the widely held belief in blending inheritance in favor of particulate inheritance, in which phenotypes are expressed in either a dominant or recessive form. Still, many biologists reasoned that populations ought to evolve to the point where dominant phenotypes completely replace other phenotypes, thus eliminating genetic variation within populations.

Within a decade of the rediscovery of Mendel's work, the English mathematician Godfrey Hardy and the German physician Wilhelm Weinberg demonstrated analytically how and why populations maintain more than one allele for many genes, rather than one allele always spreading to fixation (Hardy, 1908; Weinberg, 1908; Raven et al., 2014). Hardy and Weinberg demonstrated that, for a gene with two alleles (in a sexually reproducing population of diploid individuals), the proportion of individuals of different genotypes will tend to stabilize at specific frequencies that are determined solely by the frequencies of the alleles in the population—a model now referred to as the "Hardy-Weinberg principle."

The HWP is often seen as consisting of two main components (i.e., implications or conclusions) (Hartl & Clark, 1989; Freeman & Herron, 2004; Masel, 2012). The first is that the allele frequencies for a gene will remain constant across generations within a population—as long as certain conditions are met. To illustrate, consider a gene with two alleles ("A" and "a") at respective frequencies of p and q in a population. These frequencies will remain at p and q as long as no force is acting to change them. Because "evolution" is often defined as a change in allele frequencies in a population over time, and these forces of change are considered "evolutionary mechanisms," this first implication is at risk of being stated in a circular fashion (e.g., "Evolution requires the action of evolutionary mechanisms") that belies the novelty of this conceptual insight.

The second main component of the HWP is perhaps of more practical use. It states that the frequencies at which the genotypes will stabilize are p^2 for AA, q^2 for aa, and $2pq$ for Aa. These genotype frequencies are referred to as the "Hardy-Weinberg equilibrium" (HWE) frequencies, and a departure from these frequencies can be seen as evidence of the action of one or more evolutionary mechanisms. Note that the first component of the HWP has to do with allele frequencies across generations, while the second component has to do with genotype frequencies within a generation.

Why Populations may Deviate from Hardy-Weinberg Equilibrium

Mutation

There are several biological phenomena that can cause a population to depart from HWE for a gene. Most simply, a gene-copying error can cause an allele to change into a different allele in an individual (e.g., "A" mutates into "a"). Such a mutation instantly changes the allele frequencies, and thus the genotype frequencies, within the population. However, mutations are so infrequent that the changes in allele and genotype frequencies they cause in a single generation are generally not statistically detectable. Thus, by themselves, mutations are not likely to lead to substantial deviations of genotype frequencies from HWE. Nevertheless, mutations are essential for the creation of genetic variation within populations, which is the raw material on which evolution acts.

Gene Flow

The HWP is strictly meant to apply to closed populations. The introduction of alleles caused by emigration of individuals from a population, immigration of individuals into a population, or fertilization of gametes by gametes that have arrived from other populations (e.g., in airborne pollen) can cause a change in allele frequencies for one or more genes in a population. These phenomena of mixing of alleles between populations—commonly called "gene flow"—can result in genotype frequencies that differ from HWE.

Non-random Mating

The HWP is also only meant to apply to populations in which alleles for a gene recombine randomly during sexual reproduction. This random mixing will occur only if individuals in the population do not preferentially mate with individuals that share their genotype (i.e., assortative mating) or preferentially with individuals that have a different genotype than their own (i.e., disassortative mating). Although non-random mating within a population will not change the allele frequencies, it can cause the genotype frequencies for one or more genes related to mating preferences to differ substantially from HWE frequencies. Specifically, assortative mating will cause an excess of homozygotes, and disassortative mating will cause an excess of heterozygotes, relative to HWE frequencies for a given gene.

Natural Selection

If individuals of different genotypes in a population produce different numbers of offspring (i.e., genotypes vary in fitness), allele frequencies will change from one generation to the next, and genotype frequencies will differ from HWE, for any gene that is correlated with fitness. Specifically, a genotype with higher-than-average relative fitness will occur at a higher frequency than would be predicted by the HWE, while a genotype with lower-than-average relative fitness will occur at a lower frequency than the HWE prediction. These differences in fitness among genotypes—whether caused by natural, sexual, or artificial selection—are the most important causes of deviations from HWE in terms of driving adaptive evolution within a population. In practical terms, however, deviations from HWE caused by natural selection tend to be relatively small compared to deviations caused by non-random mating (Hartl & Clark, 1989; Masel, 2012). Therefore, the intensity of the selection must be rather high, or the sample very large, in order to infer that deviations from HWE frequencies due to natural selection are statistically significant.

Genetic Drift

Finally, the genotype frequencies for any given gene will rarely exactly match the HWE frequencies

due to random chance alone—a phenomenon most commonly referred to as "genetic drift." The unpredictability of such departures from HWE frequencies may be intuitively understood by students, as it can be related to concrete probability examples such as the flipping of coins. For instance, if a coin is flipped 100 times, students would not be surprised if it landed on "heads" 52 times or 46 times. Analogously, students have little difficulty with the notion that genotypic frequencies can differ slightly from HWE just due to sampling "noise." Nevertheless, students' misunderstandings of the subtleties involved in genetic drift, and thus overall importance of genetic drift as a mechanism of evolution, belie the seeming simplicity of the concept of noise. In fact, even advanced students tend to harbor misconceptions about the causes or significance of genetic drift (Andrews et al., 2012; Price et al., 2014).

Genetic drift has probabilistic, stochastic, essentially random effects on allele and genotype frequencies. Statisticians would equate such effects with the phenomenon of sampling error. While such technical terms may be clear to experts, their esoteric and nuanced meanings can be a major source of confusion for students (Masel, 2012; Wang, 2016). As a result, students may come to miscomprehend genetic drift as merely a statistical artifact or an error in sampling technique, rather than a major driver of evolution in natural populations. In addition, they may lose sight of the fact that genetic drift is caused by actual biological processes—the random joining of gametes and chance events in the lives of individuals that may affect their survival or reproductive success (Price et al., 2014).

Genetic drift differs from the other major evolutionary mechanisms mentioned above because it is constantly occurring in every population of every species. Thus, changes in allele frequencies due to genetic drift are inevitable. In some generations, the effect of genetic drift on allele and genotype frequencies may be quite small, while in others, the effects may be dramatic. For instance the allele frequencies can change drastically within a single generation in a population whose size is severely reduced due to a natural disaster, or in a new population that is established by a small number of individuals—phenomena respectively referred to as a "genetic bottleneck" and a "founder effect." These phenomena highlight the fact that the relative effects of genetic drift are greater the smaller a population is, even though random, stochastic changes in allele and genotype frequencies occur in small and large populations alike.

The HW Equilibrium as a Null Hypothesis to Test for Evolution

Although Hardy and Weinberg merely aimed to demonstrate how multiple alleles could be maintained for genes in natural populations of organisms, their principle became one of the most useful tools of evolutionary biologists. The great power of the HWP is as a null hypothesis to test whether a population is undergoing evolution at any particular gene of interest. Specifically, if the genotype frequencies depart from the HWE expectations within a generation, then we can infer that the population is undergoing evolution. The magnitude and direction of the departure can inform which mechanism of evolution may be occurring (e.g., selection, immigration, or assortative mating), and the inferences about evolutionary mechanisms can be supported by information on the ecological setting in which the population is living.

The relatively simple arithmetic involved in working with the HWP has helped to make "Hardy-Weinberg problems" a staple of introductory biology courses, even in secondary schools. However, this simplicity in mathematical calculations belies the nuance and sophistication required in creating and accurately interpreting HW problems that involve authentic evolutionary scenarios.

What is Wrong with the Typical HW Problems Presented to Students?

Below, I focus on two categories of shortcomings that I have most commonly observed in HW problems that are written for students in introductory biology courses. The first has to do with the simplicity, banality, and lack of intellectual engagement required by the problems. The second shortcoming results from a conflation of the two main components of the HWP, resulting in a misunderstanding of the time-scale on which the HWE genotype frequencies are meant to apply.

Superficiality of Problems

Despite the rich potential for examining evolutionary mechanisms, most of the HW problems presented to students treat the HW principle in simplistic, superficial manner (Smith & Baldwin, 2015). Specifically, students are asked to solve problems in which they are given frequencies of phenotypes and/or alleles (usually % of homozygous recessive individuals) in a population and asked to calculate the genotype frequencies, given that all assumptions of the HW principle are met. Thus, they are taught merely to plug values into the HW equations: $p + q = 1$ and $p^2 + 2pq + q^2 = 1$. The solution of such problems entails the employment of only lower- to mid-level cognitive skills, such as memorization and application (Crowe et al., 2008). Moreover, this approach promotes a false impression about evolution in natural populations. That is, focusing on problems in which populations are assumed to be in HWE reinforces the notion that populations in nature are always in HWE. Not only is this notion false, these practice problems ignore the truly interesting aspect of the HWE: that departures from HWE indicate evolution in action!

A better pedagogical strategy for posing Hardy-Weinberg problems is to introduce scenarios in which the HWE frequencies are violated (McMurran, 2010). Enough information on numbers of individuals with particular phenotypes or genotypes must be provided so that students can calculate the actual allele and genotype frequencies they will need to address the question. The question should require them to compare the actual data to the HWE expectations to infer whether they differ. If they differ, then students can propose explanations as to what evolutionary mechanism is most likely to be causing the difference. Some information on the natural history of the organisms and the ecological setting experienced by the population should be given in the text of the problem to provide sufficient hints for the students to generate explanations. For examples of these sorts of scenarios, refer to the companion Innovations paper on Hardy-Weinberg problems in this issue. That paper contains six real-world problems with detailed solutions (including chi-square tests) that can be used as-is or easily adapted to suit an instructor's particular goals.

Time-Scale Issue

The suggestion to provide students with more realistic scenarios to which they can apply the HW principle to make inferences about evolution is certainly not novel. However, many well-intentioned teachers write problems that perpetuate the misconception that the HWE frequencies can be applied to genotypic data *across* generations (Smith & Baldwin, 2015). In reality, the HWE genotype ratios are meant to apply to allele and genotype frequencies *within* a generation. That is, the allele frequencies from one generation cannot be validly used to calculate HWE genotype frequencies that are then compared to observed genotypic frequencies in a subsequent generation—though students are often instructed to do just that (McMurran, 2010).

This mistake of applying the HWE across generations seems to arise from teachers focusing all their efforts on coming up with evolutionary scenarios that violate one of the assumptions of the HWP (viz., no mutations, no natural selection, no gene flow, random mating, and "infinite" population size), but not considering whether applying the HWE frequencies is even the best way to analyze the evolutionary scenario they created.

A scenario in a typical "HW" problem either provides (or requires students to calculate) allele, genotype, and/or phenotype frequencies for a gene of interest over a series of generations. To test whether evolution occurred in the population, students need to assess whether there has been a change in the allele frequencies in the population over time. A straightforward way to address this question would be a chi-square test of whether the relative numbers of individuals of the various genotypes (or phenotypes) in the first generation are significantly different from the relative numbers of individuals of the same genotypes (or phenotypes) in the final generation. If the chi-square value is statistically significant (i.e., $P < 0.05$), then students can infer that evolution has occurred for the gene of interest. Clues from the set-up of the problem can be used to hypothesize which mechanism of evolution (e.g. natural selection, gene flow, or genetic drift) was most likely to have caused evolution in this scenario.

Note that no application of the HWE genotype frequencies was necessary for the evolutionary analysis described in the previous paragraph. However, trouble often arises when students are required to apply the HWE frequencies to this sort of scenario (in which allele and genotype frequencies are available across generations). Specifically, students are often instructed to calculate HWE genotype frequencies from initial allele frequencies, then compare these equilibrium frequencies to the final genotype frequencies. If the final observed genotype frequencies differ from the initial HWE frequencies, then students infer that evolution has occurred. This sort of analysis may sound reasonable, and it would seem to fulfill the teacher's goal of teaching the HWE frequencies in the context of analyzing evolution. However, this analysis violates a fundamental aspect of the HWP: it uses allele frequencies from one generation to calculate HWE expectations for a different generation (which may well have different allele frequencies).

Despite this common mistake, it is possible for students to employ the HWE frequencies in a valid fashion to this scenario to test for evidence of evolution. Specifically, they could use the actual allele frequencies from the last generation to calculate HWE genotype frequencies, then compare these HWE frequencies to the observed genotype frequencies in the last generation. In fact, it would be valid to use the allele and genotype frequencies *within* any of the generations to test for evidence of evolution in this scenario. The inclusion of multiple generations of frequencies is actually superfluous if the sole goal is for students to apply the HWE frequencies to test for evolution.

These two approaches to looking for evidence of evolution (that is, by analyzing changes in allele frequencies across generations and by analyzing departures from HWE genotype frequencies within a generation) can be seen as complementary strategies, each with their own strengths. For instance, if the fitness differences across phenotypes are slight, then departures of actual genotype frequencies from HWE genotype frequencies may be too small to detect the action of evolution. However, the change in allele frequencies after many generations of individuals experiencing the same intensity of selection may be quite appreciable (and statistically significant).

In other cases, comparing the actual genotype frequencies with the HWE frequencies may indicate

that natural selection is acting within generations, even if allele frequencies do not change across generations in the population. For instance, consider a gene with two alleles ("B" and "b") for which both types of homozygotes (BB and bb) are equally common, have equal fitness, and mate randomly with respect to genotype. Heterozygotes (Bb) also mate randomly, but they reproduce at only half the rate as the homozygotes. The allele frequencies in this population may remain the same from generation to generation (i.e., $p = q = 0.5$), but the population will never be at HWE because there will always be an excess in the proportion of both homozygotes and a deficiency in the proportion of heterozygotes.

CONCLUSION

In this Perspectives article, I have identified HW-related topics where students (and teachers) are likely to harbor conceptual misunderstandings. (In a companion Innovations article, I illustrate these misconceptions with empirical scenarios and highlight common computational mistakes.) Awareness of these problem areas should help provide teachers with the tools required to teach the Hardy-Weinberg with confidence, and thus instill among their students a better appreciation for how evolution works at the population-genetics level. With the knowledge that evolution can be observed and measured in contemporary populations, introductory-biology students may be inspired to pursue the study of evolution in higher-level courses in the biology curriculum.

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ACUBE 61st MEETING ABSTRACT SUPPLEMENT

Association of College and University Educators 61st Annual Meeting

October 20-22, 2017

Hosted By

COLULMBIA COLLEGE

ACUBE Gratefully Acknowledges the Support of the Following Exhibitors at the 61st Annual Meeting

KEYNOTE ADDRESS

When Group Work Doesn't Work: Insights from Students
Peggy Brickman

College faculty are increasingly abandoning the traditional mode of delivering content in lectures to incorporate more active learning that encourages students to work in groups with their peers to solve problems and learn through collaboration and exploration. Group work and collaboration can profoundly increase students' motivation and achievement, but instructors confess that they rarely adhere to procedures to insure equity and shared contributions required for true collaboration. This seminar will review research recommendations for effective procedures to plan, monitor, and intervene so that students of diverse abilities and backgrounds can all benefit from collaborative group work no matter the class size or discipline.

PRESENTATIONS, WORKSHOPS and POSTERS

PRESENTATIONS

Field Ecology with Pokémon Go
Kirt Moody, *Columbia College*
The "augmented reality" function of the Pokémon GO AP provides an opportunity for students to spend actual time outside in the real environment, sampling for virtual organisms, and then using appropriate mathematics to describe their abundance, distribution, and population characteristics. This session will introduce and demonstrate the AP and provide instructions for collecting data and testing hypotheses involving population density, species diversity, and demography.

The Effect of a Year of Introductory Biology Education on Acceptance of Evolution and Associated Factors
Ryan D.P. Dunk and Jason R. Wiles, *Syracuse University*
The ubiquity of evolutionary theory in biology makes it nearly impossible to fully understand or engage in biological investigation without a thorough understanding of evolution. Thus, full participation in biology is hindered by a failure to accept evolutionary biology. Previous work of ours was among the first studies to combine a number of educational, psychological, and sociodemographic variables into a single working model of the factors that influence acceptance of evolution. Previous work of ours has shown that in undergraduate students, a knowledge of the nature of science, religiosity, and openness to experience all have a stronger independent effect on acceptance of evolution than knowledge of evolution. Here, we sought to further investigate the role of such factors in a longitudinal time frame. Pre and post surveys were compared using normalized change to determine which variables have the most significant relationship with changes in evolution acceptance. In addition, multivariate ANCOVA models were generated for the pre-course and post- course data. Interestingly, many of the variables that lost significance over the year were demographic factors and were replaced by variables that are tied to education. Religiosity, understanding the nature of science, and evolutionary knowledge were significant predictors of evolution acceptance in both models. This study will form a baseline that will allow further research to explore the similarities and differences between different groups in acceptance of evolution. Additionally, this research has direct potential applications to curriculum development.

Using Movies to Demonstrate Topics in Epidemiology and Ethical Challenges
Janet Cooper, Rockhurst University
Movies, such as And the Band Played On and Contagion have been helpful in highlighting the steps in an outbreak investigation discussed in the Principles of Epidemiology in Public Health Practice (US Health and Human Services Self-Study Course SS1978). These movies also prove useful in discussing ethical challenges and issues confronting work in Microbiology today. After viewing these videos, students are asked to write a reflection on the steps in an outbreak investigation as presented in the movie and are also prompted with various questions related to identifying issues dramatized in the movies or to identify the most memorable scene in the movie or their most favorite and least favorite characters. The answers to these questions have been coded for specific issues and tallied over the years. Four issues

have emerged consistently in the student reflections, 1) lack of funding (19%), 2) conflict between the French scientists and Dr. Gallo (18%), 3) failure of blood banks to acknowledge the potential that AIDS could be a blood-borne disease (16.9%) and 4) failure to close bathhouses (16.5%). When asked which movie would be better to show in a Microbiology course, the class is split although many students confess to having a difficult time choosing between the two movies. Fifty-four percent of students chose And the Band Played On while 46% would rather watch Contagion. Reasons cited for preferring "And the Band Played On" include: it is more historical and more relevant and showed the impact of AIDS on society while those who favor Contagion believe it is more engaging and fast-paced and does a better job of demonstrating the transmission of the virus. They also can relate more with the actors since they are more familiar to them than those in And the Band Played On. Using these reflections have allowed discussion of the issues or challenges students raise as well as highlighting student misconceptions relating to the history of the AIDS outbreak and the study of epidemics.

A Suite of Metacognition Mini-Lectures
Alan R. White, *University of South Carolina*
Don't study harder; Study smarter. This session will present a series of Metacognition Mini-Lecture learning modules that introduce principles of brain science and how human memory works. The mini-lectures can be incorporated into courses in any discipline. They present evidence-based learning strategies and explain why those learning strategies work in light of the brain's design. We know a lot about how the human brain works to store and recall memories during the process of learning. These principles of brain science can be applied to teaching, learning, note-taking, studying and test-taking. This process of "thinking about thinking" is known as metacognition. Both instructors and students need to be familiar with metacognition, which can help us align learning activities and practices with how our brains work. Metacognition can encourage us to use evidence- based practices that are more effective because they are based on the science of learning and take advantage of how the brain learns. This doesn't make studying and learning easier, learning is always hard, but it can make the time spent studying more effective so that the same amount of time spent learning can lead to better learning results. Metacognition Mini-Lecture Modules: 0. Intro to Active Learning, 1. Bloom's Taxonomy, 2. Modes of Thinking; Short-Term & Long-Term Memory, 3. Chunking & Transfer of Memory, 4. Forget to Learn; Spaced Repetition & Distributed Learning, 5. Recall; Self-Testing, 6. Fluency & Illusions of Competence, 7. Dealing with Procrastination, 8. Sleep & Exercise, 9. Evidence-Based Study Practices, and 10. Test-Taking Strategies

An Interdisciplinary Approach to Enhance the Math and Problem-Solving Skills of First-Year Students
Marlee Marsh, Adrienne Oxley, Madeleine Schep, and Virginia Johnson, *Columbia College*
Columbia College science and math faculty have designed, developed, and begun evaluating a first-year enhancement program titled Interdisciplinary Math and Problem-Solving (IMAPS) seminar. Our hypothesis is that IMAPS will improve mathematics and quantitative problem-solving skills in first-year women and underrepresented minorities (URM) who are underprepared in mathematics and will provide them with a foundation to succeed in college-level STEM courses. Science faculty will implement and test the innovative IMAPS model to assess its ability to improve mathematics and quantitative problem-solving skills; increase students' self-efficacy, resilience, and persistence in STEM; and provide contextual and active learning experiences in alignment with the learning styles of women and URM. The objectives are to demonstrate improvements in first-year students' mathematics achievement, problem-solving skills, and academic persistence, as assessed by academic performance, retention, engagement, and commitment to a STEM career. An interdisciplinary team of biology, chemistry, math and computer-information science faculty will give an overview of the project and the results thus far.

Election Campaign of Cell Organelles to Promote Student Engagement in Introductory Biology Course
Lynn Rumfelt, *Gordon State College*
First semester Introductory Biology courses for non-science majors are designed to cover organization and structures of prokaryotic and eukaryotic cells. This requires the students to know a fair amount of detailed information. It has been challenging to teach this material in a way they find fun, interesting, and are able to learn on their own. To accomplish the goal of making learning this material fun and interesting, I used a class activity based on a modification of published work that was given before any instruction on the content was given by the instructor. A double-section of students self-organized into groups of four then randomly chose a cell organelle/structure provided by the instructor. The student's researched, wrote, and presented a two minute campaign speech arguing for election of their organelle and arguing against five other organelles so theirs may be elected the most important organelle/structure in the cell in 2017. An art component was included by requiring creation of a campaign poster showing the greatness of their organelle candidate. A rubric was used to

grade the poster and presentations. Results: all students were engaged with the process and analyses of the formative and summative assessments will be discussed.

A CEREUS Approach to Investigating Ecological Responses to Global Change in Biology Classrooms
Alisa Hove, *Warren Wilson College*
The CEREUS (Consortium Exchanging Research Experiences among Undergraduate Students) Project addresses a recognized area of STEM need by creating inquiry-driven curricular modules, implementing new instructional strategies, and assessing student achievement and attitudes across multiple types of higher education institutions. This project establishes a place-based educational network utilizing regional environmental issues to impart botanical knowledge while encouraging high-order cognitive processes, advancing quantitative literacy, teaching analytical techniques, honing scientific communication skills, cultivating more positive student attitudes towards plants and STEM, and improving persistence in STEM majors. Our four-institution group utilizes the expertise of project P.I.s and research students to create classroom-based research modules, focused on investigating responses of Southern Appalachian ecosystems to global change. To date, over 300 students in upper- and lower-division biology courses from the four partner institutions have participated in CEREUS modules. All students participating in the project have shown significant decreases in plant blindness and many of the courses have significantly increased students' views about their ability to conduct scientific investigations. These measures of student success indicate the CEREUS course modules produce students who are more likely to persist in botanical fields and are better prepared for the STEM workforce.

Creating a Reflexive Practice – Applying Your Scientific Skills to Increase Student Engagement
Melissa M. Haswell, *Davenport University*
There has been a push in higher education for students to make meaningful connections with the material they are learning instead of merely submitting to a knowledge transmission-based learning environment. One way to accomplish meaningful learning is to encourage a dialogue between instructors and students, described as praxis (Vella, 2002). Praxis is the active application of knowledge or skills that evolve from reflection on previous actions, which is essential for creating a learning atmosphere inclusive to all students. Praxis aligns with the current reform initiatives in science education, such as the use of the scientific teaching method, because it allows faculty members to record and reflect their approach to teaching, much like maintaining a laboratory notebook in scientific research. The method of scientific teaching is based on the "making teaching more scientific" by using the core essence behind scientific discovery in order to help students identify the interconnectedness of the various biological concepts (Handelsman et al., 2007, p. 1). However, if instructors are not able to engage in regular self-reflection regarding their teaching practice are they able to provide students with the ability to identify the nuances of interconnected concepts on their own? This session will share the results of a preliminary qualitative study regarding work on instructor self-reflection in the classroom and create a platform for a round-table discussion regarding this topic.

Teaching the ecology of emerging infectious diseases using a case study about the current Lyme Disease epidemic in the U.S
Laurieann Klockow, *Marquette University*
In a typical microbiology course designed for pre-med or allied health students, students learn about pathogens that infect and cause human disease. This approach to teaching infectious diseases neglects to recognize how these diseases emerge and spread throughout communities. Taught in this way, students fail to recognize how physical and social environments impact the emergence and spread of infections and consequently do not connect what they learn in class to outbreaks they may hear about in the news. In this workshop, I will demonstrate the case study about Lyme disease that I designed and implemented to engage students in learning about the ecology of infectious disease. Lyme disease has been in the news lately as its incidence has tripled in the last 15 years according to the CDC and is estimated to affect 300,000 Americans annually. This lesson uses as its case study, an NPR news story containing interviews with two disease ecologists, Rick Ostfeld and Felicia Kessing, who describe their novel way of predicting Lyme disease incidence by measuring mice populations. The activities in this lesson follow the experiments performed by these ecologists to explore the factors that have led to the recent surge in Lyme disease. In small collaborative groups, students analyze data figures from publications by the Ostfeld and Kessing labs (along with others) to construct an understanding of the ecology of Lyme disease and predict how changes to the ecosystem would affect Lyme disease incidence. As more and more instructors try to enhance their lecture-based classes with active learning, interactive case studies like the one you will experience in this workshop can be an effective way to engage students in collaborative problem solving and in connecting course content to the "real world". This case study lesson could be relevant to those teaching microbiology, ecology, public health or biology for non-majors.

Inquiry-based Teaching in the College Classroom: The Nontraditional Student

Daniel Kiernan and Christine Lotter, *University of South Carolina, Sumter*

Decline in the economic realm often bolsters an increase of nontraditional student enrollments in colleges and universities (Windolf, 1992). This trend is especially positive for states such as South Carolina that have a lower number of bachelor's degree holders compared to most other states (State Rankings). Many of these nontraditional students, who do not desire to major in some scientific area, find themselves struggling in required science courses. Over the last decade, science departments of higher education have been adjusting their curriculum to include inquiry in the college science classroom. Although inquiry-based teaching has been shown to be very academically positive in science classrooms from K-12 and up, "at the college level the data are mixed as to whether increasing inquiry instruction can significantly change students learning or attitude toward science" (Brickman, 2009, p. 3). To help delineate this controversy, more data is needed regarding the effectiveness of inquiry on student conceptual understanding and attitude toward science. Further, little research has addressed student academic and attitude changes when entire college science courses are transformed from traditional approaches to more inquiry-based approaches. Finally, research on how to improve the learning of nontraditional, non-science major students taking science courses is absent from the literature. The proposed investigation intends to begin to address this gap in the literature. The overarching question of the following research project is: Does a science curriculum that is inquiry-based versus a science curriculum that is more traditionally-based, produce more positive academic results in nontraditional, non-science major, college students?

Genetics for pre-health undergraduate students in the era of advanced genomics and personalized medicine

Khadijah Makky, *Marquette University*

In modern medicine and patient centered treatment, clinical applications of genetics have evolved beyond just understanding the cause of rare inherited diseases. With advancements in the field of genomic and genetic testing, many believe that future healthcare providers should have the ability to understand and analyze personalized information based on a patient's genetic profile in addition to physical symptoms they may present with. This transformation has prompted a shift in medical education, with genetics coursework being central to this shift. What can biology educators do to prepare undergraduate students for their future careers as health care providers? What educational practices will best help our pre-health undergraduate students? Do we have to reform genetics classes at the college level in order to better prepare our pre-health students? In the Department of Biomedical Sciences at Marquette University, we offer a human medical genetics course that follows the medical knowledge competencies proposed by the Association of Professors of Human and Medical Genetics (APHMG). In this round table discussion, the curriculum offered by Marquette will be shared, and feedback and information from other institutes will be solicited.

Service Learning in Life Sciences: To Do or Not To Do?

Judith Maloney and Laurieann Klockow, Marquette University

Service learning is a pedagogy that can have a positive impact on both academic and civic learning. It enables students to connect course content to real life situations, engage in experiential learning, and reflect on their own personal values. While it is widely used in the humanities, its use in life sciences classes is not prevalent. Perceived difficulties of incorporating service learning into life science courses include time constraints, assessment of service learning, identification of relevant community service experiences, and integration of service learning with course content. To explore these issues, we will describe our development and implementation of a service learning component into two different upper level biology classes, a physiology class, which used a presentation service learning model, and an infectious disease class which used a placement service learning model. At the completion of each course, students were surveyed on the impact of service learning on their understanding of course content, personal development and civic engagement. Survey results, along with analysis of reflection papers indicate that the service learning experience, whether it was the presentation or placement model, had a positive effect on these learning goals. In this workshop, we will describe our experiences, as well as discuss the benefits and challenges of implementing service learning in a life science course.

Course Predictors of Success versus Performance in STEM

Melissa Eslinger and Timothy Hill, *United States Military Academy, West Point*

Teaching Introduction to Biology to non-STEM majors at the United States Military Academy is an interesting opportunity to engage humanities majors in the process of science. While the students elect to take biology, they are face with challenges when drawing conceptual applications of previous coursework in chemistry, math, and physics. Instructors are the key "tour guides" for mapping these concepts across the liberal arts curriculum. We

initially began exploring the target audience of cadets choosing biology as their final science course based on their predictors of academic success, the West Point college entrance examination rank (CEER) score. This composite predictor includes multiple areas such as standardized exams, high school endeavors, and overall candidate scores. CEER facilitated categorization of the enrolled cadets into at-risk, average, and scholar populations. We further examined their performance across the core requirements of chemistry, math, and physics based on final course averages and see a direct correlation between the course predictors and actual performance. We also compared the CEER scores to individual events and cumulative performance in biology to determine educational gains. These events included a Biology Concept Assessment Tool (BCAT), final exam percentage by course focal areas, and individual demographics. To ensure standardization across the course, we also compared faculty education and teaching experience to analyze differences in performance by cadets as well as gender and athlete status. Interestingly, the CEER score is most predictive of performance in STEM coursework at the at-risk population and extreme ends of the scholars. Taken together, our data supports that pre-admission assessments are useful predictors for STEM performance. These predictors can identify students who may benefit from additional intervention and remediation opportunities to ensure successful academic progress towards graduation as well as provide quantitative evidence for deliberate curriculum adjustments.

To Infinity and Beyond: Wrestling With Biology Curricula in the Coming Decades.
James Clack, *Indiana University - Purdue University*
Most biology curricula are somewhat archaic course structures that may be decades old. Given the rapid rate at which higher education is evolving, what strategies might we use to better structure course offerings in order to meet the needs of today's (and tomorrow's) students as well as their future employers? Several examples of innovations at various levels of the curriculum will be presented for critique and comparison with participants' current curricula. It is the aim of this round table discussion to facilitate discovery of innovative means of restructuring current curricula and to do so in a manner that will also allow more seamless future reorganization.

How to Offer an Online Science Course with an Authentic Hands on Lab Experience
Jan Benedict, *eScience Labs, Inc.*
Designing formal group work to ensure equity.
Peggy Brickman, *University of Georgia*
Join eScience Labs for an information session on designing and implementing your online lab course. Four Steps: syllabus alignment, reviewing content, customizing the lab kit to meet course objectives and student budget, and learning management system integration. Future employers are clamoring for colleges to help students gain group work skills. Instructors hope group work will encourage students to share and exchange reasoning and tackle assignments with real world complexity and relevance. Student achievement can improve through peer collaboration, but the process is not guaranteed. Many instructors have no idea how to support effective collaboration, organize student groups, deal with conflicts that arise, and a host of other practical issues that can turn group work into an ineffective and frustrating exercise for all. This interactive, practice-oriented session will focus on how to avoid the common
pitfalls that derail group work and methods for structuring groups to ensure equity even in large enrollment classes. Participants will get an opportunity to view software that can help set up groups and also provide a mechanism for peer evaluation and notification of the instructor if there are problems within the group. Time will also be set aside for participants to modify group activities so that they adhere to best practices for ensuring true collaboration.

WORKSHOPS
Teaching the Experimental Process with New Labs from SimBio
Eli Meir, *SimBio*
Dr. Eli Meir (SimBio's founder) will demonstrate two new labs from SimBio that both help students with their ability to describe and carry out well designed experiments. Understanding Experimental Design, the culmination of a multi-institution NSF cyberlearning grant, provides students individualized feedback as they design and construct experiments to solve an engaging biological mystery. A new version of our Keystone Predator lab uses a simulated intertidal system to offer helpful feedback as students generate and test hypotheses about how direct and indirect effects impact community structure. Bring your laptops - Eli will have USB drives with evaluation software so you can play along.

Transforming your classroom into an active environment by adding Universal Design for Learning.
Dawn Tamarkin, *Cell Zone, Inc. and Springfield Technical Community College*
Active learning has been shown to improve learning in biology classes. Yet, there are those who question whether active learning excludes some learners. In this presentation we will learn how to develop active learning approaches using an inclusive methodology to improve the potential for active learning to increase learning for more students. Universal Design for Learning (UDL) is a method for developing

classroom approaches to include more learners, regardless of background, disability, or primary language. The UDL approach often leads to active classrooms, since more students learn that way. In this workshop you will be given the opportunity to learn about UDL to find an approach that could help you transform your classroom. In particular, you will get to try to work through the most challenging topics that you teach to come up with better, more inclusive, approaches. The goal of this exercise is that you will leave this workshop with new ideas tailored to your own classroom to improve your students' success. While you are working on new approaches for your own classroom we will also try out some UDL classroom activities which have been very successful in my classes. You will have an opportunity to select activities from among the following topics depending upon how much time we have: biological molecules, cells, microscopy, membrane structure, membrane transport, mitosis, the genetic code, and genetic engineering. Some of those classroom activities are available through Cell Zone, Inc., but others are simply classroom activities that I will share with you.

Teaching Like a Pro in Your First Years
Rebecca Burton, *Alverno College*, Conrad Toepfer, *Brescia University*, and Jason Wiles, *Syracuse University*
Join a conversation exploring topics such as effective pedagogy, classroom management, excellent resources, authentic assessment, and the road to tenure and promotion. The conversation is led by past winners of the ACUBE Excellence in Teaching Award.

Natural Selection in the Ebola Outbreak: Integrating Multimedia and Primary Literature into Undergraduate Biology Education
Mark Randa, *HHMI BioInteractive*
In this workshop, participants will see how to scaffold learning by pairing multimedia, a hands-on classroom activity, and primary literature to improve student understanding and engagement. In HHMI's, "Think Like a Scientist: Natural Selection in an Outbreak," computational geneticist Pardis Sabeti and disease ecologist Lina Moses bring us to the front line of the Ebola epidemic and explain the science behind how this event became the largest Ebola outbreak in history. The short film reveals the invisible world of viruses and portrays some of the most dramatic moments of the recent Ebola crisis. Participants in the workshop will watch a segment of the film and then actively work through a classroom activity in small groups where they will analyze and interpret DNA sequence data and follow the Ebola virus transmission in a small set of patients in Sierra Leone. The session will conclude with a primary literature tie-in using resources from Science in the Classroom.

Pre-Health Student Advising: Successes and Challenges
Laura Salem, *Rockhurst University*
At Rockhurst University in Kansas City we have a large population of students interested in health care careers. During this session we will share information about 1) communication strategies with students, 2) establishing partnerships with local and regional health professional programs, and 3) advocating for support for Pre-Health advising within the University.

POSTERS

Gamification of a Nursing Microbiology Course: Design and Initial Impacts on Attitude, Anxiety and Student Performance
Wendy A. Dustman and Julie Shearer, and Rolando Marquez, *Georgia Gwinnett College*
Gamification of curriculum isn't just about using games in the classroom – it integrates game elements and game-thinking in course design to engage students, promote learning, motivate their actions as learners, and develop problem-solving skills. Using elements of game play (earning of experience points [XP], completion of quests, PvP battles, etc.), students' educational journey was transformed to make the learning experience more compelling while encouraging development of problem-solving skills, classroom engagement, and a drive to exceed minimum goals. In a "gamified" course, rewards and incentives, rather than fear of poor grades, are anticipated to motivate student-players to continually improve, or "level-up", as well as add to the sense of enjoyment of participating. The course structure of "gamified" Nursing Microbiology sections was modeled after a multiplayer role-playing game (like World of Warcraft) where fighting "monsters", performing "quests", "farming to level up", and working in "guilds" were regular events. Game terminology (e.g., quests, raids, etc.) was substituted for standard terms (e.g. assignments, exams, etc.) in the course syllabus. Challenges (individual and/or cooperative), were related to course goals which reflected real-world applications of the content as often as possible. An overall team competition was implemented to enhance cooperative learning and teamwork skills. While the actual content coverage, as well as many of the learning activities and assessments, remained unchanged from previous traditional section offerings, the manner in which the course was delivered and the ways in which the students reacted was different. The instructional design of the experimental ("gamified") section compared to a traditional section will be presented along with an initial summary of data collected to examine the effects of participating in the "gamified" vs. traditional design on student motivation, anxiety level, and academic performance itself. Assessment

of impacts of the alternate course design include free response learner satisfaction surveys (free response), the Colorado Learning About Science Survey (CLASS) – Biology (Likert scale response), and a comparison of pre-/post- performance on key content questions (multiple choice).

Teaching A Non-Majors Biology Online Lab Course

Daniel Kiernan and Pearl Fernandez

We designed an online Human Biology laboratory course as a companion course for the Human Biology lecture course for non-majors. The aim was to have the same learning outcomes in the online course as in a face-face laboratory course. The labs were a mixture of dry, wet and virtual labs. End of the course student evaluations revealed that the students were able to relate the online labs to their day-day lives, and the learning outcomes of the course were achieved.

Assessment of Misconceptions and Prior Knowledge in a Microbiology Course Using a Concept Inventory

Julie Grainy and Jennifer Walker, *University of Georgia*

Microbiology courses are often taught by diverse faculty with varying teaching styles. Our objective was to create an assessment tool to evaluate student understanding of important concepts across all introductory microbiology courses at a doctoral university. Concept inventories are tools to identify misconceptions at the start of a course and measure learning gains at the end of a course. Several inventories have been developed for STEM subjects, but there is a need for a microbiology concept inventory. In this study, a microbiology concept inventory was developed, refined, and validated. The ASM Curriculum Guidelines were utilized to develop a list of fundamental concepts students should learn in an introductory microbiology course. A multiple-choice inventory was developed and tested with a novice group of students at the beginning of a course, as well as with a group of microbiology experts for comparison. The novice group was predicted to earn concept inventory scores indicative of a lack of knowledge in the majority of the concepts and reveal any misconceptions. Students were prompted to explain why they chose a certain answer, and common incorrect responses were recorded. As expected, the results of the inventory identified incomplete understanding of certain concepts. Furthermore, there was a significant increase between the scores of the novice and expert groups, supporting the inventory validity. These preliminary results provide evidence for this inventory as a valuable assessment tool. The data from the first version of the concept inventory, including information from experts, influenced the improvement of a refined version that was implemented this summer and fall. Once fully refined and validated, the concept inventory can be used to identify gaps in understanding at the start of a course, which can be addressed with targeted active learning strategies. The effectiveness of interventions can be assessed with a concept inventory at the end of the course. This study provides the foundation for further development of the concept inventory into a useful tool for faculty as they improve their curriculum to enhance student learning.

Career Exploration Assignments increase Student Confidence in Career Path Planning

Latanya Hammonds-Odie, *Georgia Gwinnett College*

At Georgia Gwinnett College (GGC), an open access, 4-year public college in the University System of Georgia, many senior Biology majors are unable to answer fundamental questions about the next steps that they will take to attain their stated career goals. These students entered college professing a career goal, but many have done little to investigate their next steps post-graduation. In this individual, practical action research project, I have incorporated targeted assignments to encourage students to assert some personal agency and to engage in the process of career exploration to be able to articulate a strategic career plan. Twenty Biology majors were enrolled in the Research Methods in Biology course at GGC in spring 2016. All of the students enrolled in the course were invited and agreed to participate in this study. Over the course of the semester, students completed assignments (five written) and activities (two workshops) designed to bolster student confidence in their ability to complete specific career exploration tasks. Students recorded their level of confidence or comfort with these specific tasks on the end-of-semester questionnaire using a modified five-point Likert Scale for thirteen items. The questionnaire was designed to allow students to reflect on their confidence/comfort level at the beginning of the semester. Data was collected from students enrolled in two upper-level courses for Biology majors was analyzed using Chi-squared tests as the statistical tool. The demographics of these students paralleled the demographics of the overall diversity of the GGC student population in terms of gender, race and ethnicity with the exception of percentage employed full time and age. Overall, the general trend in the data from the thirteen students revealed that student confidence/comfort in their ability to complete each of the tasks increased from the beginning of the semester to the end when the means and the ranges are compared. This makes sense as the intervention included specific assignments related to these tasks. We should consider including these types of tasks in the Biology major curriculum at GGC.

An Investigation of Potential Trends in Anatomy and Physiology I & II Final Grades Between Male versus Female Students

Kara Cashwell, Nicole Faison, Ashley Higgenbothem, and Virginia Baker Haynes, *Charleston Southern University*

The ratio of female to male students has been growing for decades with the current statistics suggesting that nearly 60% of college students are female while 40% are male. Additionally, the female students on campus are outperforming their male peers academically. We wondered if this trend was reflected in the courses Dr. Baker has primarily taught since 2011 (Anatomy & Physiology I and II). Therefore, we posed the following question: Have female students academically outperformed their male classmates in Dr. Baker's A & P I and/or II courses from 2011-2016, as the current research suggests they would? Interestingly, the data shows that while female students have, on average, earned a higher A & P I final grade than male students by approximately 5.2 points ($p<1$), this difference is no longer see in A & P II final grades. This study lays the groundwork for further analysis of A & P performance comparison amongst male and female students which provides valuable insight for both the larger discussion on academic performance but also the trends on CSU's campus where the steady growth of the Nursing, Kinesiology, Athletic Training, and Biology programs has led to an increase in the number of A & P students taught each year.

Two-Course Collaboration for Understanding Conservation Genetics

Alissa Hulstrand and Erik Olson, *Northland College*

In our experience, we have found that students often have a hard time applying the skills and knowledge from one course to another, even if these skills are tightly woven in the professional field. A specific dearth is in understanding the role of genetics and molecular biology to making and implementing conservation and management decisions. We proposed a collaboration between two courses in different majors—Wildlife Ecology and Management, a Natural Resources course, and Methods in Molecular biology, a Biology course—for student-led projects to bring together an understanding of both wildlife conservation strategies and applications of molecular techniques. Students in Methods in Molecular Biology became the "experts" in fundamental molecular biology skills and served as leaders for small groups of students from the other course. Students in Wildlife Ecology and Management became "experts" in studying populations and making conservation decisions and brought those skills to the group. The group project used non-invasive genetic sampling of scat opportunistically found on Oak Island in the Apostle Islands of Northern Wisconsin. The students were asked to identify the species and sex of the organism belonging to each scat using a series of molecular techniques, as well as describe the uses of the data and the advantages of non-invasive genetic sampling. Based on qualitative responses by the students, we have identified strengths and weaknesses of the project. The major learning gains came from students in the Methods in Molecular Biology course, who were able to practice their skills independently and teach/lead a small group in performing molecular methods. Students in both courses found the activity interesting, and would have preferred earlier and more frequent interaction with their groups to establish a defined purpose prior to beginning the project. We plan to use this project un the future, with this feedback taken into account, as well as assess learning gains in other areas through both qualitative and quantitative means.

The Genomics Education Partnership: An Opportunity for a Bioinformatics Course-based Undergraduate Research Experience for all Biology Students

Nighat P Kokan, *Cardinal Stritch University*, Vida Mingo, *Columbia College*, Christopher Shaffer, *Washington University in St. Louis*, Wilson Leung, *Washington University in St. Louis*, David Lopatto, *Grinnell College*, Sarah C.R. Elgin, *Washington University in St. Louis*

The Genomics Education Partnership (GEP) is a consortium of faculty from more than 100 colleges and universities across the United States and overseas who are including bioinformatics tools and techniques in Course-based Undergraduate Research Experiences (CUREs). The greater biological question being addressed is a comparative study of the evolution and function of the Drosophila Muller F element (dot chromosome), an unusual domain which is packaged as heterochromatin but has a normal gene density. GEP students contribute through the sequence improvement and manual gene annotation of several Drosophila species using bioinformatics tools and databases that are freely available on the Internet. Every project is undertaken by two or more different students in the consortium, working independently, and the results reconciled, allowing for quality control. Students submit their completed projects to the GEP infrastructure at Washington University where their data is pooled and complied for final analysis. Our most recent paper on the expansion of *Drosophila ananassae* F element has 31 faculty and several hundred undergraduate student co-authors who worked on sequence improvement and gene annotation for this species, which has an expanded F element. We are extending our curriculum to include teaching eukaryotic gene structure to beginning students using the genome browser, and hands-on investigations of Hidden Markov Models and Dynamic Programming.

Assessment data from faculty and students taking part, using surveys, quizzes and focus groups, seems to indicate that CUREs are most effective when faculty and students work in a collaborative effort toward the common goal. Both groups assert the importance of using human judgment when the computer output is "wrong" or needs to be further explored. Students' comments seem to indicate that they find this open-ended, independent research learning challenging but worthwhile. Nonetheless, students do not demonstrate a change in "grit" in light of this experience. In a joint effort with Galaxy, we are creating G-OnRamp, a Galaxy workflow that enables biologists with little IT know-how to create Genome Browsers with appropriate tracks (e.g., sequence similarity, gene predictions, RNA-Seq) for annotation of new and novel eukaryotic genome projects. Faculty and educators who are interested in participating in a beta-users workshop for G-OnRamp, should contact S. Elgin (selgin@wustl.edu).
Supported by NSF IUSE #1431407, NIH R25GM119157, and Washington University in St. Louis.

The importance of outreach science: Turning the tide on ocean conservation
Holly Nance, *College of Coastal Georgia*
Outreach education and the ability to speak scientifically to a non-academic audience are important skills which Biology majors need to develop as they prepare to enter their fields as scientists. Given the College of Coastal Georgia's proximity to the coast, and a local economy based on fisheries, shipping, and ecotourism, ocean conservation is an issue demanding not only community awareness, but also community activism. To that end, my BIOL 4001 Special Topics class has focused on various environmental threats to our coast as a topic to discuss with 7th graders at Glynn Middle School and students at Brunswick High, emphasizing the underlying causes of these threats to our oceans, and providing examples of how students can be active participants in ocean conservation. To assess the efficacy of their outreach education, the BIOL 4001 class has prepared pre- and post-presentation questionnaires intended to demonstrate how local students' knowledge base, opinions, and perceptions regarding specific conservation issues may have changed as a result of their outreach science efforts. These questionnaire results will provide valuable feedback on how they may improve their science communication skills.

Effect of Active Learning Exercises on Cognitive Skill Level and Student Performance in Exams
Scott M. Shreve, *Lindenwood University-Belleville*
The efficacy of the traditional lecture, the predominant mode of teaching in colleges and universities for hundreds of years, has been increasingly challenged. Active learning, as an alternative to traditional lectures, has been shown to increase student performance (Freeman et al, 2007) and decrease failure rate (Freeman et al, 2011; 2014) in introductory biology courses. I compared performance on exam questions covering the three main parts of the first biology course majors take at Lindenwood University: evolution, biodiversity, and ecology. In the fall semester, all three parts where primarily taught using a traditional lecture format. In the spring semester, I used weekly case studies during the evolution unit, weekly IF-AT review quizzes during the biodiversity unit, and both case studies and IF-AT quizzes during the ecology unit. Students in the spring semester were significantly more likely to have lower scores on exam questions from the ecology unit ($P = 0.22$, $p=0.0016$); there was no significant effect in the evolution and biodiversity units. Use of active learning in the classroom significantly increased the average Bloom level of exam questions in biodiversity unit ($p=0.034$). Overall, active learning did not increase student learning as assessed by exam questions. The disparity between these results versus the predicted effect of active learning may be due to the quality of delivery and differences in student ability between semesters.

Teaching the Current Trends in Immunology: A Layered Learning Approach
Denise L. Slayback-Barry, *Indiana University – Purdue University*
Immune intricacies are unearthed every day: identifying new mechanisms or new details about well-studied processes; demonstrating novel manipulations of immune components to treat diseases; and investigating new drugs to treat immune dysfunction. While these discoveries advance our understanding of the immune system, they also result in a minutia of detail to assess and integrate, as appropriate, into immunology education. It is imperative, as educators, to build a solid framework of understanding core concepts and basic mechanisms, and then to layer upon this framework the appropriate details for the target student audience. This concept of layered learning can be applied to any level of immunology education; within undergraduate, graduate or courses within the health professions. For example, cancer immunotherapy is an exciting field with new treatment strategies at the forefront of research and drug discovery. However, discussing the anti-PD-1 monoclonal antibody clinical trials with students who do not understand anti-tumor immunity, tumor escape mechanisms and manipulations of immune effector mechanisms, would be confusing and lead to memorization rather than understanding. It is essential that the educator first builds a functional immune system, layer-by-layer, allowing students to understand the various

mechanisms involved with overall immunity. The next layer of learning would direct students to scrutinize these effector mechanisms with respect to tumor immunity. Most importantly, the instructor must filter the emerging science and determine the most essential details to include as the final layer for that student population. The need-to-know details will depend upon the established course objectives.

Formal involvement of students in new course development provides a unique educational experience and valuable perspective for students and the instructor

Matthew M. Stern, *Winthrop University*

A common model for developing a new course is for a department or faculty member to identify the desire and/or need for a new course, develop a plan for the structure and content of course, and then implement the course. While student input may inform the decision to offer a new course, students are typically not formally involved in the actual development of a course. When I was allowed to create a new upper-level course on stem cell biology at Winthrop University, I decided to formally involve two senior undergraduate students in the development of the course. My motivation for this approach to course design was to 1) provide a unique and challenging educational experience for two advanced students, 2) better understand student perspective on the different options for course structure and content that are considered when developing a course, and 3) gain assistance with the large workload associated with developing a new course. To formalize this plan, I was able to enroll the students in a flexible three-credit-hour “special topics” course in the semester prior to the initial offering of the new stem cell biology course. Here, I describe the structure of my approach to student-assisted course design, the benefits and challenges of this approach, the feedback provided by the students who participated in the course’s design, and the feedback of the students who took the initial iteration of the course. My experience was overwhelmingly positive, and the students involved stated that they benefited in many ways from their involvement in developing the course. This approach can be used in any discipline and is a way of offering students a unique educational experience while providing faculty with valuable assistance and perspective.

The Strategic Undergraduate STEM Talent Acceleration INitiative (SUSTAIN)

Jason Wiles, *Syracuse University*

The "Strategic Undergraduate STEM Talent Acceleration Initiative" (SUSTAIN) project at Syracuse University will address the challenges of recruiting and retaining high-achieving, low-income students from diverse backgrounds into undergraduate STEM programs. The SUSTAIN program will award thirty $10,000 scholarships for up to two years, and will provide a coherent system of academic, social, and career support services strategically designed to enhance the success of biology and chemistry students during their first and second years of undergraduate study. Program goals include retaining at least 90% of the initial cohort of 30 scholars as intended or declared STEM majors following their freshman year, and to retain at least 80% of these students as declared STEM majors following their second year of participation in the SUSTAIN program. The program will establish a STEM faculty professional development workshop designed to foster the implementation of cutting-edge instructional practices that support dynamic, active learning approaches in introductory STEM courses. Scholars will be provided 360 degree wrap-around support programming that is responsive to their evolving academic, social, and career development needs as they move through the freshman and sophomore years. Research efforts will investigate the socialization experiences of scholars throughout the program to examine the efficacy of the multi-faceted series of intervention supports to assess their impact on the future STEM trajectories of students. Findings from this project will promote the identification of promising approaches, identify areas for program refinement, and result in the development of a sustainable model for providing wraparound academic and social support services to STEM majors that can be replicated on other campuses.

Bioscene: Journal of College Biology Teaching
Submission Guidelines

I. Submissions to *Bioscene*

Bioscene: Journal of College Biology Teaching is a refereed quarterly publication of the Association of College and University Biology Educators (ACUBE). Submissions should reflect the interests of the membership of ACUBE. Appropriate submissions include:

- Articles: Course and curriculum development, innovative and workable teaching strategies that include **some type of assessment** of the impact of those strategies on student learning.
- Innovations: Laboratory and field studies that work, innovative and money-saving techniques for the lab or classroom. These do not ordinarily include assessment of the techniques' effectiveness on student learning.
- Perspectives: Reflections on general topics that include philosophical discussion of biology teaching and other topical aspects of pedagogy as it relates to biology.
- Reviews: Web site, software, and book reviews
- Information: Technological advice, professional school advice, and funding sources
- Letters to the Editor: Letters should deal with pedagogical issues facing college and university biology educators

II. Preparation of Articles, Innovations and Perspectives

Submissions can vary in length, but articles should be between 1500 and 5000 words in length. This includes references and tables, but excludes figures. Authors must number all pages and lines of the document in sequence. This includes the abstract, but not figure or table legends. Concision, clarity, and originality are desirable. Topics designated as acceptable as articles are described above. The formats for all submissions are as follows:

A. Abstract: The first page of the manuscript should contain the title of the manuscript, the names of the authors and institutional addresses, a brief abstract (200 words or less) or important points in the manuscript, and keywords in that order.
B. Manuscript Text: The introduction to the manuscript begins on the second page. No subheading is needed for this section. This supply sufficient background for readers to appreciate the work without referring to previously published references dealing with the subject. Citations should be reports of credible scientific or pedagogical research.

The body follows the introduction. Articles describing some type of research should be broken into sections with appropriate subheadings including Materials and Methods, Results, and Discussion. Some flexibility is permitted here depending upon the type of article being submitted. Articles describing a laboratory or class exercise that works should be broken into sections following the introduction as procedure, assessment, and discussion.

Acknowledgment of any financial support or personal contributions should be made at the end of the body in an Acknowledgement section, with financial acknowledgements preceding personal acknowledgements. Disclaimers and endorsements (government, corporate, etc.) will be deleted by the editor.

A variety of writing styles can be used depending upon the type of article. Active voice is encouraged whenever possible. Past tense is recommended for descriptions of events that occurred in the past such as methods, observations, and data collection. Present tense can be used for your conclusions and accepted facts. Because *Bioscene* has readers from a variety of biological specialties, authors should avoid extremely technical language and define all specialized terms. Also, gimmicks such as capitalization, underlining, italics, or boldface are discouraged. All weights and measures should be recorded in the SI (metric) system.

In- text citations should be done in the following manner:

Single Author:

"… when fruit flies were reared on media of sugar, tomatoes, and grapes" (Jaenike, 1986).

Two Authors:

"…assay was performed as described previously (Roffner & Danzig, 2004).

Multiple Authors:

"…similar results have been reported previously (Baehr et al., 1999).

C. References: References cited within the text should be included alphabetically by the author's last name at the end of the manuscript text with an appropriate subheading. All listed references must be cited in the text and come from published materials in the literature or the Internet. The following examples indicate *Bioscene*'s style format for articles, books, book chapters, and web sites:

(1) Articles-

(a) Single author:
DEBURH, L.E. 1991. Using *Lemna* to study geometric population growth. *American Biology Teacher* 53(4): 229-32.

(b) Multi-authored:
GREEN, H., GOLDBERG, B., SHWARTZ, M., AND D. BROWN. 1968. The synthesis of collagen during the development of *Xenopus laevis*. *Dev. Biol*. 18: 391-400.

(2) Books-
BOSSEL, H. 1994. *Modeling and Simulation*. A.K. Peters, London. 504p.

(3) Book chapters-
GLASE, J.C., AND M. ZIMMERMAN. 1991. Population ecology: experiments with Protistans. In Beiwenger, J.M. 1993. Exper
iments to Teach Ecology. Ecological Society of America, Washington, D.C. 170p.

(4) Web sites-
MCKELVEY, S. 1995. Malthusian Growth Model. Accessed from http://www.stolaf.edu/people/mckelvey/envision.dir/malthus.html on 25 Nov 2005.

For references with more than five authors, note the first five authors followed by et al.

D. Tables
Tables should be submitted as individual electronic files in Word (2003+) or RTF format. Placement of tables should be indicated within the body of the manuscript. All tables should be accompanied by a descriptive legend using the following format:

Table 1. A comparison of student pre-test and post-test scores in a non-majors' biology class.

E. Figures
Figures should be submitted as high resolution (≥ 300dpi) individual electronic files, either TIFF or JPEG. Placement of figures should be indicated within the body of the manuscript. Figures only include graphs and/or images. Figures consisting entirely of text will not be allowed and should be submitted as fables. All figures should be accompanied by a descriptive legend using the following format:

Fig. 1. Polytene chromosomes of *Drosophila melanogaster*.

III. Letters to the Editor

Letters should be brief (400 words or less) and direct. Letters may be edited for length, clarity, and style. Authors must include institution address, contact phone number, and a signature.

IV. Other Submissions

Reviews and informational submissions may be edited for clarity, length, general interest, and timeliness. Guidelines for citations and references are the same for articles described above.

V. Manuscript Submissions

All manuscripts are to be sent to the editor electronically. *Authors must clearly designate which type of article they are submitting (see Section I) or their manuscript will not be considered for publication.* Emails should include information such as the title of the article, the number of words in the manuscript, the corresponding author's name, and all co-authors. Each author's name should be accompanied by complete postal and email

addresses, as well as telephone and FAX numbers. Email will be the primary method of communication with the editors of *Bioscene*.

Communicating authors will receive confirmation of the submission within three days. Manuscripts should be submitted either as a Microsoft Word or RTF (Rich Text File) to facilitate distribution of the manuscript to reviewers and for revisions. A single-email is required to submit electronically, as the review process is not necessarily blind unless requested by an author. If the article has a number of high resolution graphics, separate emails to the editor may be required. The editors recommend that authors complete and remit the Bioscene Author Checklist with their submission in order to expedite the review process.

VI. Editorial Review and Acceptance

For manuscripts to be sent out for review, at least one author must be a member of ACUBE. Otherwise, by submitting the manuscript without membership, the corresponding author agrees to page charges. Charges will be the membership fee at the time of submission per page. Once the authors' membership or page charge status has been cleared, the manuscripts will be sent to two anonymous reviewers as coordinated through the Editorial Board. Authors' names will be withheld from the reviewers. The associate editors will examine the article for compliance with the guidelines stated above. If the manuscript is not in compliance or the authors have not agreed to the page cost provisions stated above, manuscripts will be returned to authors until compliance is met or the page cost conditions have been met. Reviewers will examine the submission for:

- **Suitability:** The manuscript relates to teaching biology at the college and university level.
- **Coherence:** The manuscript is well-written with a minimum of typographical errors, spelling and grammatical errors, with the information presented in an organized and thoughtful manner.
- **Novelty:** The manuscript presents new information of interest for college and university biology educators or examines well-known aspects of biology and biology education, such as model organisms or experimental protocols, in a new way.

Once the article has been reviewed, the corresponding author will receive a notification of whether the article has been accepted for publication in *Bioscene*. All notices will be accompanied by suggestions and comments from the reviewers. Acknowledgement of the reviewers' comments and suggestions must be made for resubmission and acceptance. Further revisions should be made within six months if called for. Manuscripts requiring revision that are submitted after six months will be treated as a new submission. Should manuscripts requiring revision be resubmitted without corrections, the associate editors will return the article until the requested revisions have been made. Upon acceptance, the article will appear in *Bioscene* and will be posted on the ACUBE website. Time from acceptance to publication may take between twelve and eighteen months.

VII. Revision Checklist

Manuscripts will be returned to authors for failure to follow through on the following:

A. Send a copy of the revised article back to the associate editor, along with an email stating how reviewers' concerns were addressed.
B. Make sure that references are formatted appropriately.
C. Make sure that recommended changes have been made.
D. Figures and legends sent separately, but placement in manuscript should be clearly delimited.

VIII. Editorial Policy and Copyright

It is the policy of *Bioscene* that authors retain copyright of their published material.