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Flipping Virtual Labs into Team-Based Learning Tools

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Support is growing for ‘flipped classrooms’, wherein the majority of instruction occurs via inquiry-based team activities with very little lecture content, as an effective way to promote student learning. We demonstrate how interactive simulations in virtual labs can be incorporated into the Team-Based Learning (TBL) flipped classroom framework. We adapted three SimBio Virtual Labs for use in a 300-level TBL course. Students complete structured portions of the labs on their own and an open-ended inquiry in class as part of a team activity. Our approach could be implemented across undergraduate course levels.

Keywords: flipped classroom, team-based learning, virtual lab, evolution, conservation

Introduction

Team-Based Learning (TBL) is one form of ‘flipped classroom’ wherein the majority of instruction occurs via inquiry-based team activities with very little lecture content (Michaelsen and Sweet, 2011). Support is growing for TBL as an effective way to promote student learning and engagement with material (Hake, 1998; Whiteside *et al.* 2010). TBL courses are structured into content-based units. Each unit begins with a Readiness Assurance Test (RAT) taken by students individually (iRAT) and as teams (tRAT). RATs are based on background reading that students conduct outside of class. The remainder of each unit consists of team-based activities conducted in class. Grading is divided between individual and team points. Peer evaluations are often used as a tool to enhance team performance and to weight team points allocated to each individual. Variation in implementation occurs among other aspects of TBL courses. For example, some instructors use unit-ending quizzes to test comprehension and final team projects are often used at the end of the course. For more background information on TBL, we have developed a PowerPoint presentation that provides information about the structure of TBL courses and further explains our motivation for using SimBio Virtual Labs in a TBL course (available by email to active-learning@simbio.com).

Here, we demonstrate how interactive simulations in virtual labs can be incorporated into the TBL framework as part of the team activity portion of a course. We use as an example three SimBio Virtual Labs (*Darwinian Snails*, *Mendelian Pigs*, and *Genetic Drift & Bottlenecked Ferrets*) that one of the authors has adapted to use in a TBL Conservation Genetics course at the University of Massachusetts Amherst. The three labs chosen for demonstration are aimed at student comprehension of aspects of mechanisms of evolutionary change in populations. *Mendelian Pigs* focuses on Mendelian inheritance, modes of gene action, and natural selection. *Genetic Drift & Bottlenecked Ferrets* focuses on genetic drift and the conservation relevance of this evolutionary mechanism. *Darwinian Snails* focuses on common misunderstandings of the central tenants of evolution by natural selection. These concepts are first introduced to the students in the text: Evolution, Making Sense of Life by Carl Zimmer and Douglas Emlen. We demonstrate the use of these modules in a 300-level course, but the same labs are commonly used in introductory Biology courses.

For each lab, students complete a set of preliminary exercises on their own outside of class. Students are graded individually on this portion of the lab. Students then complete an open-ended exercise in class as part of a team project, for which they earn team points. After all exercises have been completed, each student individually answers a set of final questions that are integrated into the SimBio lab. The SimBio labs provide a mix of structured and open-ended inquiry, which facilitates this approach. Here, we provide notes for the instructor and a student handout for the open-ended exercise for each of the three example labs (Appendix A-D).

For implementation in the ABLE workshop, participants were divided into teams of three or four. Each team had access to one computer. Each participant received a USB flash drive containing evaluation copies of SimBio Virtual Labs, including the modules used in the workshop. We began with an overview of TBL and how the lead author has implemented TBL at University of Massachusetts Amherst for a 300-level class. This involved a general discussion of TBL activities that work and do not work. It also included a discussion of rules of thumb for using simulations in a TBL course and additional extensions others have implemented, such as independent student projects where students use virtual labs to ask their own novel scientific questions. The remainder of the workshop was a demonstration of how the three SimBio Virtual Labs are used (*Genetic Drift and Bottlenecked Ferrets, Mendelian Pigs,* and *Darwinian Snails).*

Student Outline

Lab 1: Genetic Drift & Bottlenecked Ferrets
Topics: Genetic drift, effective population size, and conservation genetics.
See Appendix A for Student handout.

Lab 2: Mendelian Pigs
Topics: Mendelian inheritance, dominant vs. recessive alleles, natural selection on dominant and recessive alleles.
See Appendix C for Student handout.

Lab 3: Darwinian Snails
Topics: Natural selection, experimental design.
See Appendix D for Student handout.

Materials

All three labs require:

- One laptop per team
- SimBio lab loaded on the laptop
- Note: students purchase and use their own copy of the software, which can be loaded on a public computer via USB drive if necessary

In addition, Lab 1 requires an instructor laptop with SimBio, Excel for data recording, and software to produce a graph (R demonstrated in Appendix B).

Notes for the Instructor

See Simbio (http://simbio.com/products-college/EvoBeaker) to request an evaluation copy of described lab simulations.

Lab 1: Genetic Drift & Bottlenecked Ferrets

Background

The goal of this lab is to increase student understanding of genetic drift and its relevance for conservation problems. The students are introduced to conservation problems facing black-footed ferrets in Exercises 1 through 4 of the lab. Students are required to complete these exercises on their own outside of class. The final open-ended team activity requires the students to test various reserve designs that differ in the amount of habitat available for each subpopulation and the degree of connectivity among subpopulations. The students are manipulating subpopulation size (and hence strength of genetic drift) and gene flow (connectivity) with their simulations. Students are asked a series of questions aimed to get them to realize that intermediate-sized populations that are connected are the best conservation option for maintaining genetic diversity. This is clearly a better option than small and isolated populations because each of the isolated population loses genetic diversity quickly (because of genetic drift). Students find the difference between a single large population and three smaller but connected populations more challenging to understand. The challenge is overcome if they realize that genetic drift and gene flow counteract one another in the intermediate population size with connectivity scenario in a way that is not possible when genetic drift alone acts on a single large population.

Instructor Notes

Genetic drift is a random process. Students are likely to find that intermediately sized populations with some connectivity (scenario b, Figure 1 of Appendix A) maintain the most genetic diversity. With many replicates run by the entire class, this pattern should emerge. However, it is possible that some of the scenario (a) simulations will perform well (in terms of maintenance of genetic diversity). Scenario (c) should lose the most genetic diversity. Standardization of the length of simulations (400 generations) and number of starting animals (all available) should help to yield clear patterns. These results have important conservation implications. Many species are being forced to have population structures that resemble scenario c (small, isolated populations). Often management plans aim to either maintain scenario b (intermediately sized populations with connectivity), or try to manage to restore this scenario. This lab allows students to simulate data that demonstrate why we take these conservation and management approaches.

Preparation Instructions

The instructor must be familiar with the SimBio lab. Appendix A diverges from the lab manual in several ways, meant to add conservation relevance to the activity. Students must have access to at least one laptop per team and have the SimBio lab loaded onto that machine. As implemented, the students write their results on a white board. The instructor records these results onto a spreadsheet, visible to the class. The instructor then quickly produces a graph that summarizes results (see Figure 1). R code has been provided to generate the graph shown in Figure 1 (Appendix B).

Lab 2: Mendelian Pigs

Background

This lab requires students to combine knowledge of inheritance of Mendelian traits with natural selection. Students must apply the knowledge they gain from a series of simulations with pigs and their coloration to an open-ended exercise about hair color in humans and whether a recessive trait (blond hair color) is likely to be lost through evolution solely due to its recessive nature. The students conduct a series of breeding experiments to gain understanding of Punnett squares and Hardy-Weinberg proportions in the first set of exercises (completed on their own). They also learn the mechanistic details of the genes underlying coat color variation in pigs, which also applies to coat color variation in many other taxa. Finally, the students explore models of genetic drift and natural selection acting on single loci and gain understanding of how dominance and recessiveness of alleles affect drift and selection.

Instructor Notes

The instructor should be familiar with Mendelian inheritance, become familiar with the example used in this study related to genes that underlie coat color variation, and understand single-allele models of evolution acting on dominant vs. recessive alleles. The final activity is predicated upon an incorrect news story that claimed blond hair color in humans would soon disappear, so the instructor should also understand that hair color genetics in pigs and humans is quite similar, though not identical.

Students use model pigs that vary in coat color to simulate the potential loss of a recessive human trait (blond hair color). The trick is for students to realize that they can simulate the recessive human allele by using a recessive pig allele. They should use a dominant phenotype in the pigs to represent black/brown hair in humans and a recessive phenotype in the pigs [brown (recessive to black) or red (recessive to brown and black)] to represent blond hair in humans. The TBL activity here focuses on the interplay of selection with recessiveness.

Students should examine what happens to the recessive trait in pigs as a surrogate for what might happen to blond hair in people. They will have already seen in the lab that without selection, recessive / dominance doesn't matter. In the exercise in Appendix C they select against the recessive trait and see if the recessive allele goes to zero frequency. It should not, because the population is large. The students should conclude that the loss of blond hair in human populations is unlikely because human populations are very large and therefore genetic drift will be minimal. Even if non-blonds were favored to blonds, the recessive blond allele will remain in the population and occasional recessive homozygote phenotypes will appear.

This lab in general provides an opportunity to discuss the *MC1R* (melanocortin 1 receptor) gene, which underlies color variation in many taxa ranging from reptiles to mammals. Because the example draws from an incorrect news story on a widely broadcast news source (BBC), the lab also sets up an opportunity to discuss media miscommunications about science.

Preparation Instructions

The instructor must be familiar with the SimBio lab. Appendix C diverges from the lab manual in several ways. Students must have access to at least one laptop per team and have the SimBio lab loaded onto that machine.

Lab 3: Darwinian Snails

Background

Evolution by natural selection has three requirements. First, a population must contain variation for a trait. Second, that variation must be heritable, that is, differences among individuals must at least be partly due to differences in the genes that individuals have inherited from their parents. Third, certain trait values must confer higher survival or reproductive rates to the individuals that posses those trait values. If these three conditions are met, evolution by natural selection will cause the distribution of that trait in the population to change over time. This lab allows students to investigate and experimentally "discover" each of the three requirements of natural selection. Along the way, students also explore concepts related to experimental design.

Instructor Notes

This lab combines two concepts that students tend to think they understand, but for which they often have misconceptions or confusions. The first is evolution by natural selection, the second is experimental design. This lab allows students to increase understanding of both. In the open-ended exercise, they are asked to test one component of natural selection related to differential survival as a function of a trait of interest (in this case snail shell thickness). Students tend to make their experimental tests overly complicated and they tend to not directly test for differences in survival as a function of shell thickness. This lab provides an opportunity to review experimental design. After teams completed the lab, teams are randomly called on to explain their experimental design and results. The instructor must be familiar with the requirements for evolution by natural selection. There is an additional component of this lab that requires familiarity with phenotypic plasticity, which occurs when a trait is sensitive (changes value) to environmental conditions. In this case, the presence of crabs, independent of direct predation, causes a small change in snail shell thickness, probably due to the ability of the snails to detect the scent of this predator.

Preparation Instructions

The instructor must be familiar with the SimBio lab. Appendix D diverges from the lab manual in several ways. Students must have access to at least one laptop per team and have the SimBio lab loaded onto that machine.

Literature Cited

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SimBio labs discussed here, including most directly Jon Herron, Susan Maruca, and Jennifer Wallner, along with many others who develop the underlying software infrastructure, test, and support labs at SimBio

About the Authors

Andrew Whiteley is an Assistant Professor at the University of Montana. He relocated from UMass Amherst in 2016. Andrew directs the Montana Conservation Genomics Lab, where he addresses questions in conservation genomics as well as evolutionary biology and ecology. Andrew teaches undergraduate and graduate courses for the Wildlife Biology Program at the University of Montana.

Ellie Steinberg and Eli Meir run SimBio, a leading developer of discovery-based biology education software, and help author many of the SimBio Virtual Labs.

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Appendix A
Lab 1: Genetic Drift and Bottlenecked Ferrets

Exercise 5 – Save the Ferrets – Team Activity
Team: ________________________
Team Members Present: ____

Follow the instructions in Exercise 5 – Save the Ferrets from the SimBio lab ‘Genetic Drift and Bottlenecked Ferrets’.

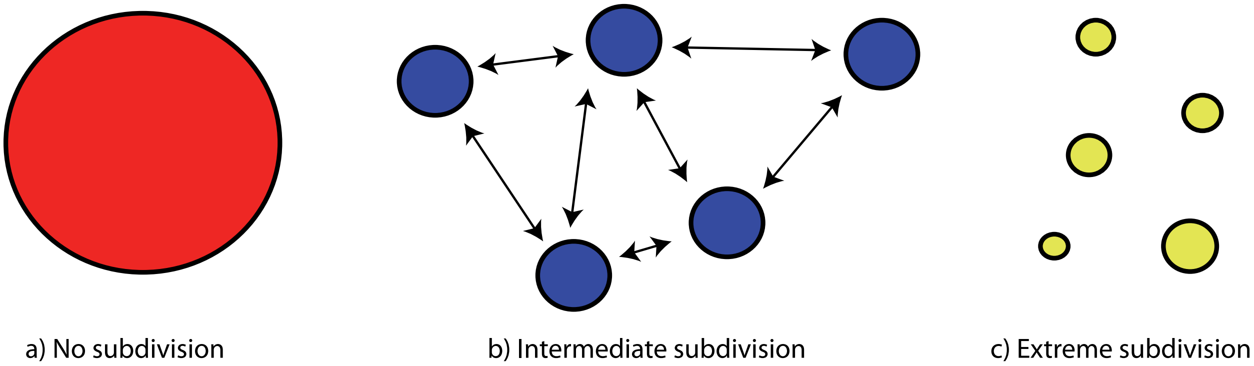
Follow steps 1 through 5 in the laboratory PDF provided by SimBio.

1) [6 from PDF] Provide answer for “Test Your Understanding” ________________

2) [similar to 7.1 from PDF] As a warm-up, come up with two reserve designs. Sketch your two designs here. Remember you want to maintain **allelic** diversity (both the *S* and *C* alleles) in the total ferret population AND you want to maintain as many **heterozygous** ferrets as possible.

3) We will now diverge from the PDF provided with the lab. Which design maintained greater allelic diversity and greater heterozygosity?

4) Examine Figure 1 below. There are three scenarios: a) a single large population, b) several intermediate-sized populations connected by migration (also called gene flow), and c) several small and completely isolated populations.


a) No subdivision
b) Intermediate subdivision
c) Extreme subdivision

Lab 1, Figure 1

You will run simulations that replicate the scenarios from Figure 1. If you team is an even number, you will run scenarios (a) and (b). If your team is an odd number, you will run scenarios (b) and (c). For scenario (b) use 3 subpopulations (each fragment is considered a subpopulation) and for scenario (c) use 6 subpopulations but use a total of approximately 100km^2 of reserve habitat for all scenarios. Run your scenarios for 400 generations and use all of the ‘zoo’ animals, partitioned the way you choose. Run 3 replicate simulations of each of your team’s two designs and fill in the table below.

Write the letter of the scenario on the line after is says 'Scenario _____'. Your goal is to evaluate each reserve design's performance in terms of preserving alleles and maintaining heterozygotes. Number of subpopulations for (a) is 1, (b) is 3, and (c) is 6. Connectivity is 'n' for scenarios (a) and (c) and 'y' for scenario (b). We will also have you add your team's results to a combined class tally on the white board.

Scenario from Figure 1	Number of subpopulations	Connectivity (Y/N)?	Total number of alleles remaining in all subpopulations	Avg. heterozygosity from all subpopulations
Scenario______				
Replicate 1				
Replicate 2				
Replicate 3				
Scenario______				
Replicate 1				
Replicate 2				
Replicate 3				

5) Based on the combined class data, which scenario performs best in terms of preserving alleles and maintaining heterozygotes in the entire population? Why do you think this is? For which scenario do we have the biggest concern about inbreeding? Why? Which scenario has the largest effective population size? Why? Which scenario do you think will maintain the most adaptive potential? Why? (4pts)

Note: You do **not** need to prepare a one page formal report.

Appendix B
Graphing Instructions for Lab 1, Genetic Drift & Ferrets

R code used to create graph during class period:

```
library(ggplot2)
graph <- ggplot(data = ferret, aes(x = scenario, y = Avg.Heterozygosity)) +
    geom_boxplot(aes(fill = factor(connectivity))) +
    scale_y_continuous("Heterozygosity") +
    scale_x_discrete("Scenario from Fig. 1") +
    scale_fill_discrete(name = "Connectivity") +
    theme_bw(base_size=20)
```

Table B1. Example data set collected from a class. Students write data on the whiteboard. Scenario corresponds to Appendix A, Figure 1. Number of subpopulations for each scenario is (a) = 1, (b) = 3, (c) = 6. Connectivity is present (yes) in scenario (b), absent (no) in scenarios (a) and (c). Number.alleles is the number of alleles present after 400 simulated generations in the entire collection of ferrets in reserves. Avg. Heterozygosity is the heterozygosity of the entire collection of ferrets in reserves and is plotted on the *y*-axis in Figure B1.

scenario	numb.subpop	connectivity	Number.alleles	Avg.Heterozygosity
a	1	no	2	0.17
a	1	no	1	0
a	1	no	2	0.2
a	1	no	1	0

Figure produced:

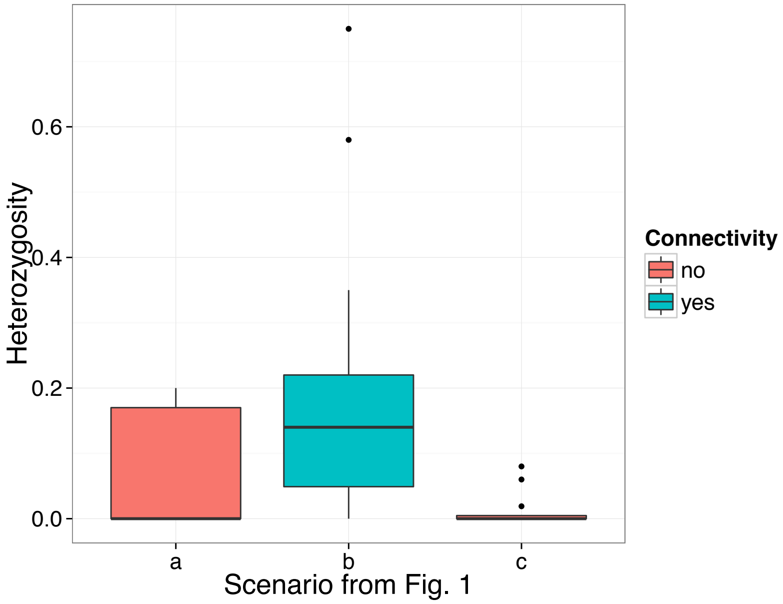


Figure B1. Results from Exercise 5 of Ferret Lab as performed in a 300-level Evolution course at UMass Amherst. The *y*-axis shows average heterozygosity. The *x*-axis shows the scenarios (a, b, and c) from Lab 1, Figure 1. Scenario (a) consists of one large population. Scenario (b) consists of three intermediate-sized populations with connectivity. Scenario (c) consists of six small and isolated populations. Treatments are further classified by the presence or absence of connectivity (scenario (a) and (c) = no connectivity; scenario (b) = connectivity).

These results support evolutionary theory and predictions. Most prominently, six subpopulations with no connectivity lost the most genetic diversity because they experience the most genetic drift. This demonstrates the importance of connectivity (gene flow) for maintaining genetic diversity. The most genetic diversity occurs with three subpopulations with connectivity, which is also what is expected. An intermediate level of drift within subpopulations combined with connectivity that spreads alleles among the subpopulations should maintain more genetic diversity than a single large population. This has very important implications for the conservation of natural populations of many different species. This activity provides a nice lead-in to discuss these conservation issues.

Appendix C
Lab 2: Mendelian Pigs

Section 3: Going Hog Wild – Team Activity

Team: ______________
Team Members Present: ____

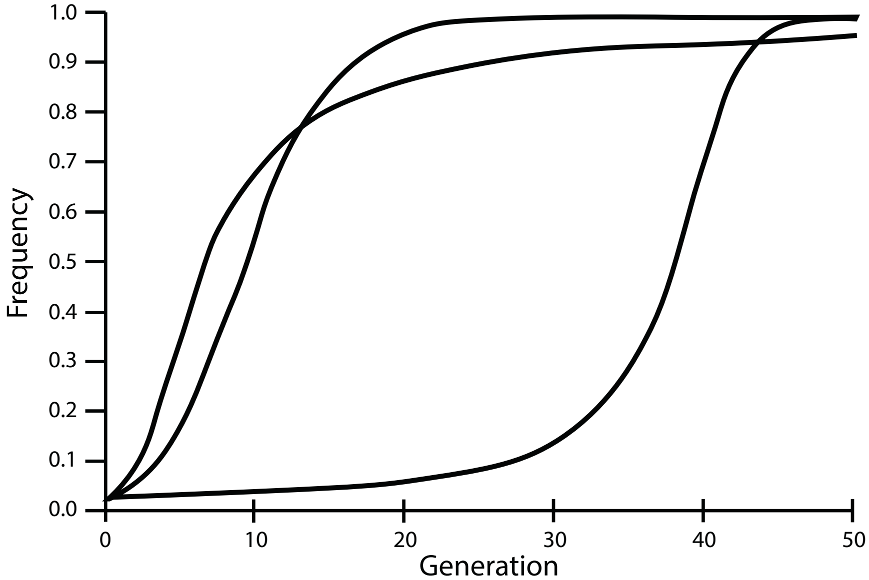
Today you are going to finish the Mendelian Pigs SimBio lab as a Team. Follow the instructions on the handout and provide your answers here. You will turn in one hard copy per team.

A) Start on **SECTION 3**. Going Hog Wild **10/13** Hungry Wolves. In the previous simulations from section 3, you should have noticed that recessive alleles don't disappear from a population just because they are recessive. In the Hungry Wolves simulation, you will add selection to the mix.

Follow the instructions on page **10 (of 13)** in Section 3. **Note** that the simulated pig populations are very large, so that genetic drift plays little role in this activity. Also, it will be helpful to switch between histograms showing phenotypes, genotypes, and alleles and it might be helpful to look at the frequency of the dominant and recessive alleles over time.

1. Answer Q46. What happened to the frequency of the dominant allele? Write out your answer here:

2. Answer Q47: Approximately how long did it take for the frequency of the dominant allele to fall to half its starting value? __________



Lab 2, Figure 1. Change in allele frequency under directional selection. In each case, the relative fitness of homozygote for the favored allele is 1.00 and the relative fitness for the alternate allele is 0.50. The heterozygote has the same fitness as the favored allele (1.00, dominant), intermediate fitness (0.75, intermediate, or the same fitness as the unflavored allele (0.50, recessive). The favored allele has an initial allele frequency of 0.03.

3. Which of the three lines in Figure 1 are being depicted by this simulation? (please circle)
A. Recessive
B. Additive
C. Dominant

SECTION 3. Going Hog Wild 11/13 Hungry Wolves

Follow the instructions on page **11 (of 13)** in Section 3.

4. Which of the three lines in Figure 1 is being depicted by this simulation? (please circle)
A. Recessive
B. Additive
C. Dominant

5. Answer Q48: Approximately how long did it take for the frequency of the recessive allele to decline to half its initial frequency? __________

6. Answer Q49: Which allele, dominant or recessive, declined in frequency more quickly when wolves displayed a taste for pigs with the associated phenotype? Write out your answer here:

7. Why?

B) Read through “Will Blondness Really Disappear?” on page **12 of 13**.

Design the experiment to test the hypothesis that dyed blondes have a selective advantage over natural blondes. This is a little bit tricky. Keep in mind that the pigs are serving as a model for you to test this hypothesis, but don’t take the color of the pigs too literally.

You don’t need to write a short scientific paper, but answer these questions.

8. How did you set up your experiment? Provide details about the pig phenotypes you chose and how you set up fitness values (Death Rate From Wolves)

9. What do you conclude about the extinction of blond hair in humans, even if blond hair were selected against?

Appendix D
Lab 3: Darwinian Snails

Section 6: Snail Challenge – Team Activity

Team: ______________
Team Members Present: ____

Exercise 6: Challenge

Your team will focus on the portion of Exercise 6 that starts on P. 16 of the PDF of the lab that says "The remainder of this section is slightly more advanced….". You will conduct experiments to address the two questions posed below. There are therefore two portions of the lab. For each portion of this lab, you will set up an experiment and collect data. You will write your methods, results (including supporting graphs), and conclusions and turn it in. Please keep your writing brief and to the point, I expect you to submit a bullet-pointed list. We will randomly call on a team to present their findings to the class. Think of this as a mini-presentation where the rest of the class will be able to ask you questions about your results. You may either hand-write the lab, or submit a word document via email to your instructor.

1) In the PDF from the lab, the first part of Ex. 6 focuses on whether Robin Seeley demonstrated all three requirements for evolution by natural selection in the Appledore Island snails. We will discuss that she has more or less demonstrated two of these requirements (variation in shell thickness occurs, some variants survive at higher rates than others). She has not demonstrated that there is heritable variation for shell thickness in these snails. Therefore, first focus on the following question:

Is there heritable variation for shell thickness in these snails?

Conduct an experiment to determine whether shell thickness is heritable in the snails from both populations. Hint: in Ch. 7 from the Zimmer and Emlen textbook, two ways to estimate heritability are discussed.

Extra Credit: Estimate the value of heritability of shell thickness in each pond (provide your methods).

2) Snail shell thickness could also be responding in some way to environmental cues from the presence of crabs. This would be an example of a phenotypically plastic response. Now focus on the following question:

Do snails from the East have thicker shells because of evolution by natural selection imposed by crab predation, or do they have thicker shells simply because snails can smell crabs and grow thicker shells when they need them?

Conduct an experiment to test for plasticity of snail shell thickness. Here are some related questions I want you to focus on: Are the differences between the two populations (East vs. West) due to plasticity, genetically evolved differences, or some combination of the two? If it's a combination, which factor (plasticity vs. genetically evolved difference) has the greater relative effect?