

Using technology to scale up innovative research-based introductory laboratories

Discussion leader: Dr. Welkin Pope, Biological Science

Dr. Pope discussed the design of a project for which she has received a dB-SERC Course Transformation Award. The transformation effort centers around using Wireless ClickShares to help maintain a sense of community in the face of increasing enrollments in the SEA-PHAGES introductory lab course.

The SEA-PHAGE program has been discussed at length by Dr. Graham Hatfull at a previous dB-SERC lunch on November 24, 2014. For detailed information on the program, see [Dr. Hatfull's presentation](#) and [the summary of the discussion](#).

The program has been running at University of Pittsburgh for two years. Students who take the SEA-PHAGE lab course are essentially doing research in bacteriophage discovery: in the first semester, they dig in the dirt, find a bacteriophage, they purify it and extract its DNA, after which they characterize it. In the second semester, students use bioinformatics to sequence the genome of their bacteriophage. In the SEA-PHAGE labs, students delve deeply into a topic and use it to discuss many aspects relevant for biology. The course is taken primarily by freshmen and does not have any pre-requisites. Also, it can be substituted for a “traditional” lab (the course meets once a week for three hours, just like the traditional labs).

- Academic advisors are aware of this course and they encourage students who say they are interested in getting involved in research.
- There may be some self-selection, possibly because more motivated students may be more likely to take this course.

There are an estimated 10^{31} bacteriophages on the Earth, and basically every single one discovered by students is different from any others that have been discovered before. Students get to name their own bacteriophage and post it on the [SEA-PHAGE database](#), which gives them a sense of ownership. To date, there are more than 10,000 bacteriophages found, and another 6,000 in labs of various institutions waiting to be sequenced. The goal of the program is to have 5,000 students each year take this course at various institutions. Currently, there are around 80 institutions at which this program is running and there are plans of adding another 17 in the next couple of years.

In the last 9 years, there were more than 20 publications in peer-reviewed journals related to phage discovery. There are more than 2,800 authors, the majority of them students (freshmen). Dr. Pope showed an example of a recently published article she and some of her students co-wrote. In addition, recently, two students presented their work at a research symposium and one of the posters won a blue ribbon for the quality of the work and presentation – which was very exciting, both for the student and for Dr. Pope!

The project is focused on the second term during which students primarily work on the computer and use specially designed software (primarily written by researchers for use in their own labs) to characterize the genomes of the bacteriophages they discover. Generally, there is very good retention of students from the first to the second term, in the first year, the retention rate was 100%, and in the second it was 91%. However, Dr. Pope has found that students generally have difficulty moving from the first term, in which students spend the majority of their time in the lab, to the spring term in which their work is done primarily on the computer. In the first year they implemented the program, everything worked really well, there were 4 instructors (2 faculty members and 2 TAs) working with 20 students, and therefore students got a lot of personalized attention. Students were generally very excited about the course and more than half of them came back to be TAs. After this pilot year, they added four new sections. Instead of delivering some of the content (e.g., necessary lab techniques) in the lab, 1 lecture per week was added which was attended by students from all sections (at the same time).

The real challenge comes now because they are planning to greatly increase the number of sections from the five they currently have to 15 in the next five years. In the second term, students work in groups and use computer software to annotate the genomes of their bacteriophages. This is a rather tricky process because the computer makes predictions about the genome using different algorithms and the predictions may not be correct. There are multiple ways in which the computer can get tricked and students must analyze the computer output and carefully compare different predictions. A lot of the guidance about how to use the software properly and how to interpret different outputs is done in the main lecture component which is attended by all the students. Often, students who were struggling with something, would send their output to the instructor who would project it on the screen. However, this requires forethought, students have to prepare something ahead of time and send it to the instructor. They tried different things, cloud based stuff, box (the Pitt file sharing system), google drive, etc. In searching for a solution they heard about ClickShares. This is a system which can be used to project the display of various laptops on the screen. There is a main unit, and multiple receivers which students can plug in their own laptops, and the instructor can project any of the laptops which are plugged in a receiver on the screen at any time. This allows for the instructor to use the work of different students as example, to provide guidance in real time, e.g., project the screen of one group of students, and show the whole class how to go perform a computation or how to interpret an output. Multiple screen can be projected at once.

The cost of the main unit is about \$4,000 and each additional receiver is \$250.

Using the clickshares system will hopefully help speed up the guidance process and decrease the amount of time students spend annotating their genomes. This would give them more time work on their final project which is their favorite part!

Also, using the system will help create a sense of community as different students can offer each other guidance, and, help students learn from each other. For example, some genomes have tRNA while others do not, and if a group is working on a genome which doesn't have it, they do not learn how to use the software for a genome that does have it. Using clickshares can help students learn from each other's projects.

Assessment

- Pre- and post- surveys – obtain evidence of content learning.

- Student interviews – obtain evidence of impact on student affect and attitudes about the course.
- Pre-post measurement of time on task

One of the goals of the project is to create a community among students taking the course, and one idea suggested was to use an online wiki for the course (many such platforms available for free) which allows students to post questions and discuss course material with each other. Prior studies in physics have found that giving students the option of providing feedback for the help provided by their peers (e.g., by giving a “thumbs up”) can be a great motivator to engage with one another.

Question: what is graded in the course?

- Lab notebooks
- Gene annotation
- Weekly quiz
- Final presentation
- Writing responses to other students’ papers

A big part of this course requires group work. How does the course structure ensure that there is individual accountability?

- Students are graded in multiple ways for their own work. The weekly quiz is an example. Another example is that gene annotation is done both individually and as a group. Five students have to annotate 50,000 base pairs, and each student is given 20,000 – Student 1 annotates base pairs from 0→20,000; Student 2 annotates from 10,000→20,000 etc. This has two benefits: students are individually graded for their annotations, and it also encourages collaboration between different students in coming to a consensus about the overlap in base pairs they each have to sequence.

Is there a follow up to the course (e.g., students using the skills learned in the SEA-PHAGE program in an upper level course)?

- Currently there is a phase genomics course students can take after SEA-PHAGES, but they are working on developing another course.