UMBC
AN HONORS UNIVERSITY IN MARYLAND

Dept. of Biological Sciences
The Honors College

eBiology I & II – Hunting Phages at UMBC


eBIOLOGY I, Fall 2008


eBIOLOGY II, Spring 2009

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Abstract

The UMBC version of the National Genomics Research Initiative course (eBiology) was offered over two fourteen-week semesters to a total of 26 students. All but five of the participating students were non-STEM majors. Each student was able to isolate a phage using either the standard isolation or enrichment procedure and obtain an electron micrograph of their phage. Nearly every student was able to produce a DNA sample of their bacteriophages, and several were able to produce quantities that made their phage candidates for sequencing by the Joint Genome Institute (JGI). The selected bacteriophage was successfully sequenced by JGI, and annotated by students in the second semester. Students were successfully introduced to the scientific method, biological concepts, and experienced hands-on use of *in vitro* and *in silico* research tools.

Introduction

At the University of Maryland Baltimore County (UMBC), we interpreted the mission of the National Genomics Research Initiative program to be to increase science literacy among students with no science background or apparent interest. To accomplish this, we chose to limit the enrolment at our institution to predominantly freshman and non-science majors. Our goal was that this course will, at best, influence a student into considering Biology or another science as a major. More likely, though, is that while a student may not change her major, her opinion of science and scientific research may very well change. Ultimately, our goal was to offer a course that provides participants with a better understanding of what science is and what research really consists of. Those students, who will vote on our funding one day, will hopefully place a much higher value on research than students who have had no science research experience during their college career. We also recognize that participating students will undoubtedly share some of the insights gained to their fellow students (and faculty) in other courses throughout their academic career.

To attract non-science majors, we designed eBiology to satisfy the requirement that all graduates must complete a science course having a lab component. We also stipulated that the course not satisfy any requirement for Biology/Biochemistry majors. Additionally, to assist in its marketing the course was offered through the UMBC Honors College as well as through the Biology department.

Objectives

The overriding objective of eBiology I & II is to increase students' knowledge and appreciation of the process of science.
To do this we developed several sub-objectives inherent to the program.

Theoretical:
- To learn basic phage and bacterial biology.
- To learn the central dogma of genetics.
- To learn the theory of the bioinformatics tools used.

Technological:
- To learn microbiological lab techniques
  - Aseptic technique
  - Plaque assays
  - Electron Microscopy
  - DNA extraction and characterization
- To learn use of data mining software
  - GeneMark and Glimmer
  - Apollo
  - BLAST
  - PhiGo
  - Phamerator

Learning Objectives

Objective	Assessment	Success?
Basic Biology	Quizzes, Midterm Exam, Presentation	Yes
Central Dogma	Quizzes, Midterm Exam, Presentation	Yes
Bioinformatics Theory	Quizzes, Midterm Exam, Presentation	Yes
Lab Techniques	Experimental Success	Yes
Software	Experimental Success	Yes
Increase Knowledge and/or Appreciation of Science	Conversation, Course Evaluations, Presentations	To be determined by NGRI assessment*

Selected Student Comments

"…Getting to do real research (my phage is archived!)"

"…doing experiments some bio majors cannot do yet was fun."

"The best part about this course was the opportunity to be a part of a real experiment…and for someone who had never used a Bunsen burner before, this was AMAZING."

"This class was awesome. Makes me hate biology a lot less."

"I only took this class to fulfill an honors requirement, but it ended up being my favorite class…It is really cool to know that this research actually matters in some way".

"It gave me insight and sparked an interest in a field I was previously indifferent to and did not enjoy".

"Best part: Analyzing DNA using computer programs – just like a real researcher!"

"Great course for non-majors, and I think its success is based in being offered to non-majors".

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Delivery

Semester I

Students met formally on Tuesdays and Thursdays for three hours. The lab was open and supervised for two hours on Wednesdays and Fridays, as well as by appointment. During the open lab the students collected data and/or performed the next step in their experiment.

We started each week with a lecture covering the theory behind what the students were going to do next as well as a description and demonstration of the techniques they would be using. The Thursday lab started with a formal lab meeting during which each student described his/her progress (e.g. titrations, plaque descriptions, gel pictures, EM micrographs etc.). Any problems encountered were described, and students suggested solutions with some guidance from the instructors.

The semester started with having each student collect and analyze four or five soil samples. Those who had no plaques collected four to six more samples for primary isolation. Two students obtained plaques from their primary isolates, nine from enrichments, and two worked on a contaminant that was isolated from the lab. One student was allowed to harvest plaques from another student who had more than one plaque morphology on his plates.

The students then performed titrations until uniform plaques were apparent. One student could not attain this goal; though we believe he had a pure culture of a phage that produced variable plaque morphologies.

Once a pure phage suspension was attained, each student harvested high-titer lysates. We started with 10-plate harvests, but by the end of the semester used 20-plate harvests to garner enough DNA.

In the EM suite, the students prepared negative-stained EM grids from the high-titer lysates. Our EM tech assisted the students in finding phage. If none was found after a short search, the student came back to the lab and the EM tech continued to search. All of the students were able to obtain micrographs of their phage.

DNA extractions were performed with greater or lesser success. Every student extracted some DNA, with all but one obtaining enough to run a gel and two producing enough to send to JGI by the deadline. Extraction was problematic and required a lot of tweaking.

At the end of the semester, the students developed a group poster describing the entire research project. The students were left to determine the division of labor themselves with only suggestions from the instructors and occasional reminders of approaching deadlines. Finally, each student pair gave a PowerPoint presentation of their work in particular and how it fit with the rest of the annotated phage genome and with other genomes.

Semester II

The students met in a computer lab on Mondays, Wednesdays and Fridays for 50 minutes. We started the semester with a review of the first semester to bring new students up to speed and reinforce basic concepts in the returning students, as well as a description of the scientific goals for the second half of the course. Assessment in the second semester consisted of a midterm, unannounced quizzes, writing assignments, a final presentation, and class participation.

Students started with a writing assignment on plagiarism (*Plagiarism in the News*) and then were assigned a section of the genome to analyze. Two students analyzed each section to allow for redundancy in coverage. Students submitted periodic progress reports on their section, which grew as the data accumulated, culminating in a final progress report which discussed the whole annotated genome.

As the semester progressed, the students were given the required background information through lecture and the supplied lab manual. Lectures were given as the topic became appropriate with the steps the students were performing, and included general concepts such as the central dogma, gene structure, and sequencing early in the semester. More procedure oriented lectures based on use of the software were given immediately prior to starting a new technique.

After the students called genes in their section of the genome, they presented their calls to the rest of the class. Most gene calls found complete agreement with the class, but sometimes discussion arose concerning size of the gene, overlap, start codons, or discrepancies between GeneMark and Glimmer. These were resolved by consensus with varying levels of input from the instructors.

The students then incorporated BLAST (blastn to find homologies; blastx to identify proteins) to annotate the ORF's in their section of the genome and presented these to the class. The discussions of the annotations included value of the BLAST score and e-value, as well as a description of the gene's function.

At the end of the semester, each student pair gave a PowerPoint presentation of their work in particular and how it fit with the rest of the annotated phage genome and with other genomes.

Discussion

Our desire when designing eBiology was to have all the students who took the first semester stay and complete the second semester. As UMBC has no measures to enforce that outcome without being excessively onerous (i.e. refusing a grade for the first semester without completion of the second semester), which would likely have resulted in lower enrolment, we had to rely on student interest, our enthusiasm and ability to excite students, and some luck. Ultimately, we found some students had schedules that precluded the second semester, two graduated, two received unacceptable grades, and a couple weren't interested, resulting in only seven of the original of sixteen students returning for the second semester. To this were added nine new students for the second half, a course of action we did not originally anticipate or intend. Because the two semesters had somewhat different populations of students, it is appropriate to discuss them separately as well as the course as a whole.

Semester I

The first semester worked extremely well. All of the students had a phage to investigate, all obtained electron micrographs, and all but one were able to produce DNA for "uniqueness" identification purposes.

We found that we underestimated the commitment of these students. We originally anticipated difficulty in getting the students used to working on their own time. However, the students were for the most part very enthusiastic, with at least one complaining that the lab should be open more hours for independent work. We were probably overly cautious about giving quizzes and assignments as well as requiring them to return to the lab on their own time, but the students absorbed all assignments and were downright aggressive about coming in. With only a few exceptions, students who had other commitments during the scheduled open labs tracked down an instructor to let them at the work.

To improve the experience for the students we plan to add more attention to the notebooks and administering more quizzes. We intend to ask more theoretical questions during the lab meetings and attempt to elicit more class discussion as might be found in a genuine research lab's meeting.

Technically, a few modification need to be made as well. We will have them acquire and titrate the phage isolates more quickly to get them engaged in the experiment faster. We will also harvest more plates for the high-titer-lysates. We found twenty plate harvests to give good results. We also found multiple additional steps are necessary in the DNA purification procedure. It is also our intention to get the students into the EM suite as quickly as possible. We found that obtaining an electron micrograph was by far one of the highlights of many of the students' semesters, and can inject some energy in a semester that can become tedious after scores of titration plates

Semester II

We found that students generally acquired the theoretical background necessary to understand the landmarks of data mining without much difficulty whether they had taken the first semester or not. Students mastered the ORF analysis software without difficulty, and discussions of whether to call a gene or how to annotate it were lively and insightful. The marvel at seeing plaques and micrographs of *my* virus was not as strong when the data was shared, but there was nevertheless pride in the annotations. We were generally happier with the assessment techniques used in the second semester, though some reevaluation of what will be required on the progress report at different stages is in order. We were particularly pleased with the inclusion of the production of a poster. We found that the students, with only a few exceptions, worked very well as a group to produce a strong final product with which they were justifiably proud.

There were some serious technical problems, some of which were avoidable and some not. The avoidable problems can be attributed to placing too much confidence in the robustness of the software as installed on our network. We spent too much class time downloading data and installing software on the lab computers where the few expected minutes of downloads turned into many. We also had significant problems with the Phamerator software on lab computers, which made it problematic for students. We believe a more thorough advance preparation and testing of the software on the lab computers should eliminate this problem in the future.