Building a cohesive bioinformatics classroom: implementation of wireless sharing technology in a large scale-up of SEA-PHAGES introductory biology lab

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Biological Sciences
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The SEA-PHAGES Program

SEA-PHAGES (Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science) is a two-semester, discovery-based undergraduate research course that begins with simple digging in the soil to find new viruses, but progresses through a variety of microbiology techniques and eventually to complex genome annotation and bioinformatic analyses.

The program aims to increase undergraduate interest and retention in the biological sciences through immediate immersion in authentic, valuable, yet accessible research. By finding and naming their own bacteriophages, students develop a sense of project ownership and have a ready-made personal research project at a fraction of the cost of traditional apprentice-based research programs. Some of the positive effects of the SEA-PHAGES program have been reported here.

SEA-PHAGES is jointly administered by Graham Hatfull's group at the University of Pittsburgh and the Howard Hughes Medical Institute's Science Education division.

Message in a Bottle, Issue 4
Written by Welkin Pope on June 17, 2015 in Message in a Bottle.

Message in a Bottle, Issue 4, is now available. Download it here for a snapshot of what was covered in the Symposium faculty meeting.
Brussow and Hendrix, 2002
Welcome to the Actinobacteriophage Database at PhagesDB.org, an interactive site that collects and shares information related to the discovery, characterization, and genomics of phages that infect bacterial hosts within the phylum Actinobacteria.

A paper describing the scientific and educational success of the HHMI SEA-PHAGES program has been published in mBio.
Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity

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University of Pittsburgh, United States; Howard Hughes Medical Institute, United States; James Madison University, United States; Albert Einstein College of Medicine, United States

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Abstract

The bacteriophage population is large, dynamic, ancient, and genetically diverse. Limited genomic information shows that phage genomes are mosaic, and the genetic architecture of phage populations remains ill-defined. To understand the population structure of phages infecting a single host strain, we analyzed the genomes of phages infecting Mycobacterium tuberculosis H37Rv, and present a panoramic view of the distribution of genomic diversity in the phage population.
Fall semester: Phage Discovery
Find phage—purify—amplify—extract DNA—characterize
(2x per week, 2 hour classes)

- Design an experiment with hypothesis, controls, etc
- Keep lab notebooks
- Scientific notation
- Serial dilutions
- Use micropipettors
- Sterile technique
- Scientific presentation (Poster, Figures)
• Spring semester: Bioinformatics
• Annotate genome—comparative genomics—further explorations
(2x per week, 2 hour classes)

– Design experiments in bioinformatics (computer programs as experiments)
– Keep electronic lab notebook
– Further develop presentation skills
– Read and write primary literature (genome announcements)
– Generate, plan and execute multi-experiment project in phage biology using what they have learned.
• Anaya Complete Sequence, 60835 bp, including 11 bp 3' overhang (CTCGTAGGCAT), Cluster K1
  • AGGCCACCTTTCTCTCCCCAGCATTTTTTTAAAAGGCGATTCAGCCTTTTT
  • CCAAGCCTGACAGACAGGACAAGATCGAATGCAGACTGACCAGAATCCGAAC
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  • GAGCAATCAATGACATCGGCTTTGAAAGCCGAGGACATCGTGCTTCTCGG
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  • GTTCATTACCAGTCTTACGGCACGCCGCGGCGAGCACCTGCCTGCAGCC
  • CCGCGCCGCGGTGCTGACCCTGAGCTGTGACCCCGACTGTCGGCCGATC
Inaugural SEA-PHAGES class at Pitt, 2012-2013
Challenges: Multi-year large scale-up from 1 section to 15(?)

- Maintain the quality of the student experience and the scientific research with non-expert instructors and many many MANY more students!
- Maintain the sense of community in the course
- Logistics: how do we fit all those lab sections into the space available?
Last year’s solutions
(increased from 1 to 5 sections)

• Added 1 lecture per week, all students attend.

• Increased number of UTAs (used alumni)

• Decreased length of lab classes (1hr 20min each; still 2x per week)

• Students used own laptops for bioinformatics
Bioinformatics Challenges

Students work in groups to annotate different bacteriophage genomes.

• Concepts are more abstract than in fall semester
• More room for interpretation in making final decisions
• Genomes are all different
  – May or may not be similar to previously annotated genomes
  – May or may not be similar to others in class
Annotation requires application of “guiding principles” of bacteriophage annotation and careful analysis of (sometimes conflicting) data from multiple computer programs: DNA Master, Phamerator, Starterator, GeneMark, Glimmer, BLAST, HHPre, and others.
Goals for Course Transformation:
* Decrease amount of course time spent doing annotations
* Expose more students to genomes and genome features
* Build sense of cross-section community

Problem: How to share data live during class for discussion/demonstration?

Tried: Box, Power Point, Google Slides, email....
All of these require either forethought or wasting class time for file transfers.
• Solution:
  ClickShares!
  – Wireless receiver connected to projector; can connect any computer via USB; or can connect tablet/smart phone
  – Can show up to four screens at once.
Assessment

- Pre- and post- survey
- Student interviews during implementation
- Pre- and post- measurement of time on task
- Survey designed with the assistance of Dr David Hanuaer, IUP, and lead SEA-PHAGES assessment coordinator; uses validated tools.
Pre-survey

• Administered spring 2015, voluntary
• 38 out of 82 students answered
• Three questions:
  – Where did students get help/feedback on annotations?
  – How familiar did they feel with other groups’ annotations?
  – How comfortable were they with the annotation process, including genome features that were not present in all genomes?
1. To what degree did you receive feedback on your annotations from:

<table>
<thead>
<tr>
<th>#</th>
<th>Question</th>
<th>Not At All</th>
<th>Occasionally</th>
<th>Frequently</th>
<th>Total Responses</th>
<th>Mean</th>
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<td>Your course instructor</td>
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<td>16</td>
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<td>Students in your group</td>
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<td>25</td>
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<tr>
<td>4</td>
<td>Other students in your lab section</td>
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<td>19</td>
<td>4</td>
<td>38</td>
<td>1.71</td>
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<tr>
<td>5</td>
<td>Students that are in the SEA-PHAGES but not in your lab section</td>
<td>23</td>
<td>13</td>
<td>2</td>
<td>38</td>
<td>1.45</td>
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1. To what degree did you receive feedback on your annotations from:

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Your course instructor</th>
<th>Your TAs</th>
<th>Students in your group</th>
<th>Other students in your lab section</th>
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<tr>
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<td>2.58</td>
<td>1.71</td>
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</table>
2. Please rate your familiarity with other student groups annotations

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<tr>
<th>#</th>
<th>Question</th>
<th>I know nothing about the annotations of other students</th>
<th>I have seen some of the annotations but I am not familiar with them</th>
<th>I have seen some of the annotations but I am not really sure I am familiar with them</th>
<th>I have seen the annotations of other students and have some familiarity with them</th>
<th>I am completely familiar with other students annotations</th>
<th>Total Responses</th>
<th>Mean</th>
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<tbody>
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<td>To what degree are you familiar with the annotations of other groups of students</td>
<td>1</td>
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<td>13</td>
<td>16</td>
<td>1</td>
<td>38</td>
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</table>
2. Please rate your familiarity with other student groups annotations

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To what degree are you familiar with the annotations of other groups of students
3. Rate the degree to which you agree or disagree with the following statements

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<thead>
<tr>
<th>Question</th>
<th>Strongly Disagree</th>
<th>Disagree</th>
<th>Neither Agree nor Disagree</th>
<th>Agree</th>
<th>Strongly Agree</th>
<th>Total Responses</th>
<th>Mean</th>
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<tbody>
<tr>
<td>I feel confident that I know how to apply the guiding principles to my phage genome annotation</td>
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<td>1</td>
<td>1</td>
<td>22</td>
<td>14</td>
<td>38</td>
<td>4.29</td>
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<tr>
<td>I feel comfortable assigning functions to phage genes</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>23</td>
<td>11</td>
<td>38</td>
<td>4.18</td>
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<tr>
<td>I feel comfortable annotating a tRNA</td>
<td>6</td>
<td>12</td>
<td>12</td>
<td>6</td>
<td>2</td>
<td>38</td>
<td>2.63</td>
</tr>
<tr>
<td>I feel comfortable annotating a programmed translational frame shift</td>
<td>7</td>
<td>10</td>
<td>8</td>
<td>11</td>
<td>2</td>
<td>38</td>
<td>2.76</td>
</tr>
<tr>
<td>I can easily describe what is specific about my phage genome that isn't found in other phage genomes in this course</td>
<td>0</td>
<td>4</td>
<td>2</td>
<td>20</td>
<td>12</td>
<td>38</td>
<td>4.05</td>
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</table>
3. Rate the degree to which you agree or disagree with the following statements

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<th>I feel comfortable assigning functions to phage genes</th>
<th>I feel comfortable annotating a tRNA</th>
<th>I feel comfortable annotating a programmed translational frame shift</th>
<th>I can easily describe what is specific about my phage genome that isn't found in other phage genomes in this course</th>
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<td>Mean</td>
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Additional thoughts?

- Incorporate grades?
- Adjunct instructors and “expert” UTAs
- Replace lecture with online modules?
- Open lab hours?