TO: The Faculty of the College of Engineering

FROM: School of Agricultural and Biological Engineering

RE: New Undergraduate Course, ABE 22700 Biotechnology Lab II

The faculty of the School of Agricultural and Biological Engineering have approved the following new course. This action is now submitted to the Engineering Faculty with a recommendation for approval.

Course no. **ABE 22700 Biotechnology Lab I**
Terms offered – Fall, Lab 4, Cr. 2
Requisites, Restrictions, and Attributes: ABE 22600 Minimum Grade D-

Description: The second laboratory course should use the cloned material to produce a protein. This protein should be purified, utilized immunologically, checked for purity by Edman degradation, and in some kind of bio assay. ABE 22700 content is primarily based on biological sciences, not engineering. Prerequisites: ABE 22600 Minimum Grade of D-

Reason: ABE is creating ABE 22700 for the purpose of cross-listing with the existing IT 22700. This is to reflect increased involvement of ABE instructors and students as well as ABE's significant resource support for this course. In Spring 2017, IT 22700 was taught by a faculty member with a 50% appointment in ABE, and 34 out of 45 (76%) of registered students were ABE. The ABE 22700 Form 40 will be routed through Agriculture. The course descriptions are identical excepting the final statement which is included for ABET purposes.

Bernard Engel, Head
School of Agricultural and Biological Engineering

Example Syllabus – ABE/IT 22700

SYLLABUS ABE22700
Spring 2016

BIOTECHNOLOGY LAB II

Instructor: Dr. Kari Clase

Office: Young 367

Office Phone: 494-4649

Email: kclase@purdue.edu

Teaching Assistants: Yi Li (li949@purdue.edu)

Class Time: Lab (Section I) 9:30-11:20 W/F (DLRC228C)

Lab (Section II) 3:30-5:20 W/F (DLRC228C)

Office Hours: Available by appointment

Course Description

The course is a Course Undergraduate Research Experience (CURE), more specifically, a part of the Howard Hughes Medical Institute's (HHMI) (http://www.hhmi.org/grants/sea/) Science Education Alliance and is an authentic research experience. Students engage in hands-on discovery as scientists with the ultimate objective of contributing new mycobacteriophage genomes to the scientific literature and public databases (http://www.hhmi.org/news/pdf/hatfulljacobs.pdf and www.phagesdb.org).

Welcome BACK to the SEA

In a prior course (ABE 22600, Biotechnology Lab I) students isolated bacteriophage from soil samples, purified them, performed electron microscopy, and isolated the viruses' DNA. Phage genomes were sequenced at the Purdue sequencing center. In this course, students will translate the

As, Ts, Gs, and Cs of the phage genome into biological information. Like the *In Situ* phase last semester, the In Silico portion, is divided into three sections: ***Analyze, Discover***, and ***Share***. In analyze, the student will be introduced to genomes and genes. Additionally, the student will be given information to help them examine the DNA sequence and identify potential genes. Students will download their sequence information from the Internet, annotate their selected phage genome (that is, identify the genes and other structures present), and compare their genome to other phage genomes. The student will use a variety of bioinformatics tools to *discover* genomic organization by mapping gene locations, identifying potential gene products, and placing genes into families with the use of several different types of databases. Finally, the student will have the opportunity to share their discoveries with others within the Alliance and with the scientific and general population communities. While the object of In Situ was to obtain a novel phage, the object of In Silico is to analyze the **genome** and discover its novelties. These unique features will be found in the form of DNA **sequence** information, i.e., the ordering of its building blocks (nucleotides). The sequence information encodes the organism's **genes**, the characteristics that make an **organism** what it is. (*From the HHMI--SEA Lab manual*).

All participants will share their discoveries, ideas, and challenges via the HHMI Science Education Alliance wiki (http://www.hhmi.org/seawiki/dashboard.action). It is expected that all students who contribute data and intellectual information to the genome will become authors on the published genome announcement.

Course Goals

A. The student will analyze the genetic code of a unique phage in order to determine potential genes
B. The student will discover the genomic organization of their unique phage
C. The student will use algorithms to define potential genes, assign putative functions to them, and determine the order in which they appear in the genome.
D. The student will read and discuss scientific literature related to their research project
E. The student will share the information gathered with others in the scientific community

Learning Objectives

CURE learning outcome 1: Students will be involved in the use of scientific practices.

- The student will gain literacy in the basic methods and applications of bioinformatics, including quantitative literacy.
    - The student will be able to explain the experimental basis of techniques used, indicating the significance of the work, presenting, calculating, and discussing the data, and drawing conclusions.
    - The student will describe the theory and application of computational approaches that are used to analyze biological data.

- The student will use algorithms to define potential genes, assign putative functions to them, and determine the order in which they appear in the genome.
- The student will identify genomic features that can define genes: elements important for transcription, elements important for translation, elements that indicate a non-protein-coding gene

CURE learning outcome 2: Students will be involved in the process of discovery.

- The student will gain experience in dissecting and extracting pertinent information from scientific journal articles.
- The student will be able to navigate uncertainty

CURE learning outcome 3: Students will be involved in broadly relevant or important work.

- The student will compare the structure and organization of the genome to other genomes
- The student will share the information gathered with others in the scientific community

CURE learning outcome 4: Students will be involved in collaboration.

- The student will work on a team and communicate their results

CURE learning outcome 5: Students will be involved in iteration.

- The student will design and conduct a research project to contribute new knowledge about the unique phage.

Course Requirements & Grading

Computer requirements: Students will need to own or have ready access to a computer and broadband Internet. The computer can use Mac, Windows or Linux operating systems. Each student group will need a computer with Windows. You must also have administrative privileges for the computer as you will be installing provided analytical software for genomic research. Though a laptop computer is preferred it is not required.

The final grades for the course will be determined by a total accumulation of points from all activities and assignments. Individual progress toward course objectives and final grades will be computed based on the following weights:

Assignments	**Percentage of Final Grade**
Annotation Quality	15
Lab Notebooks	20
Reflections	15
Laboratory Participation and Performance	10

Final Presentation	20
Final Research Report	20
Total	100

***We will use an electronic tool to objectively evaluate your individual contribution and group participation. Your grade for the highlighted rows above (Annotation Quality, Lab Notebooks, Lab Participation and Performance, and Final Presentation) will be weighted from the peer group score in CATME* (www.catme.org).**

Annotation Quality

As a class, we will be annotating genomes. It is important that your data is submitted on time and in the format requested and that all annotation activity be completed by the end of the semester.

The quality of your data, including quality and clarity of the annotation is critical and will account for 10% of the 15% total. Timeliness will account for the remaining 5%. A format for annotation will be provided and must be strictly adhered. Deadlines for submission will be determined from the date that the data becomes available from the sequencing facility (currently expected by the 2nd week of the semester). Once a timetable is established it is expected that you will follow it closely.

You should review the class schedule and lab activities for each week in Blackboard. Progress will be assessed weekly, with preliminary evaluation and a time to address questions and problems that have arisen during class presentations and discussion.

Lab Notebooks.

Because your work in this course is real research, the output of your assignments and your work will be used by the broader scientific community for years to come. For this reason, documentation of your work and the data you collect is critical. You will maintain an electronic laboratory notebook using Evernote (http://evernote.com/). The free version of Evernote is sufficient. You will create a shared (i.e. viewable by your instructors and peers) notebook. You will be graded on the completeness, organization, accuracy, ease of use by outside readers, and adherence to our research documentation protocols (to be distributed and discussed in class). Your electronic lab notebooks will be graded at periodic checkpoints during the semester and again at the end of the semester.

Reflections.

Reflections will be completed weekly and submitted electronically to provide updates of laboratory progress, troubles encountered, and laboratory plans for the upcoming week.

Laboratory performance.

A portion of your grade (10%) will also depend on laboratory performance including, but not limited to, any of the following:

• Arriving late to class

• Being unprepared for the exercise and lab meetings

• Leaving the laboratory before completing the exercise

• Conducting yourself unprofessionally

• Any activity that is considered to violate academic integrity and research ethics standards

Your laboratory performance will also be impacted by your CATME group peer review feedback and lab participation:

- The class meets twice a week for 2 hours. You are expected to attend each class, prepared to learn the computational repertoire needed for the course, to update the class on the status of your analysis, discuss both the implication of your own and your peer's work, and discuss strategies for the next steps.
- Grading of participation will be assessed based on in-class participation (includes active participation in discussion, preparation for class, active role in data assessment and analysis).
- During class time you should be on task. Do not browse the Internet, check your social sites, email, or chat. Internet should be used for class purposes.

Assigned Readings.
Weekly readings will be assigned to provide more information and background on the concepts applied in the research laboratory. There will be oral discussions over the readings and occasional writing activities. Oral participation will count toward your Laboratory Performance grade. Discussion questions may be included in your weekly reflections.

Final Presentation and Final Report.
A final presentation and report will be completed to both summarize research findings from the semester and outline potential future areas of research. The final report will follow a rubric given in class and will take the form of a research proposal. The data that you collect throughout the semester will be summarized in the proposal and presented as preliminary data that justifies your proposed future experiments. The final presentation will be prepared using tools available online. The presentation will be shared virtually with your peers to summarize your research findings for the semester. You will also have the option to share your presentation publicly with other scientists.

Required Texts & Reading

1. A User Guide to DNA Master; Jacobs-Sera D, Pope WH, Russell DA, Cresawn SG, and Hatfull GF; University of Pittsburgh, Pittsburgh, PA; 2012. (available at seaphages.org http://seaphages.org/media/docs/Annotation_Guide_12.08.2015.pdf)

2. Selected journal articles including:

- "Mycobacteriophages: Genes & Genomes" G. Hatfull. 2010 Annual Reviews of Microbiology. Vol 64. Pg 331 – 356. *Available at the Phage Database (www.phagesdb.org), on the HHMI SEA wiki, and via Purdue University Libraries*

- Hatfull et al. 2010. "Comparative genomic analysis of 60 Mycobacteriophage genomes: genome clustering, gene acquisition, and gene size." Journal of Molecular Biology. Vol 397, Issue 1, Pages 119-43, 2010. *Available at the Phage Database (www.phagesdb.org), on the HHMI SEA wiki, and via Purdue University Libraries*

- Pearson, Helen. "*What is a Gene?*". Nature. 2006. Vol. 441. Pg. 399 *Available on Nature's Website Via Purdue Subscription. http://www.nature.com/nature/journal/v441/n7092/full/441398a.html*

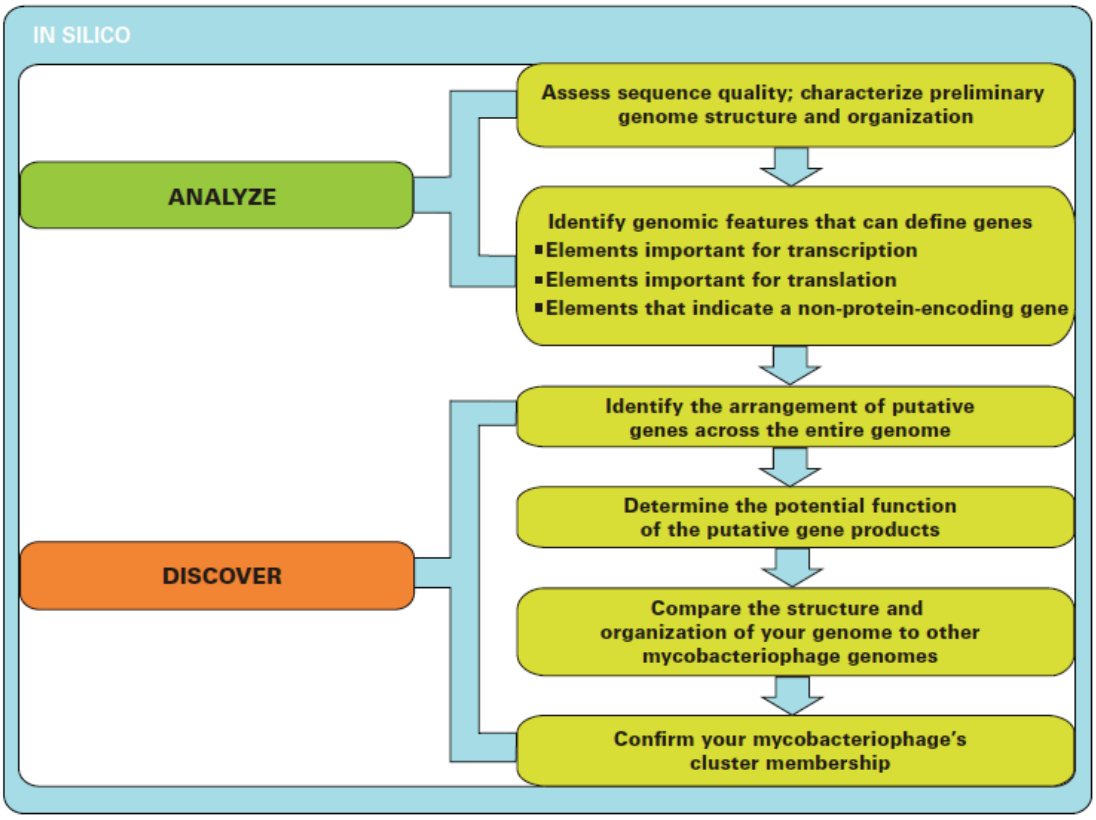
Other readings as assigned

Optional References

1. Current Protocols in Bioinformatics. Copyright (©) 2009 John Wiley & Sons, Ltd.. Online ISBN: 9780471250951. *Available On-line via the Purdue University Libraries. http://cda.currentprotocols.com/WileyCDA/CPTitle/isbn-0471250937.html*
2. Baxevanis A.D. and Ouellette, B.F. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins**.** (2005) Third Edition. Wiley-Liss. (optional)
3. Writing Reference: The Elements of Style. Fourth Edition. By Strunk & White. Allyn & Bacon Publishing. 2000.

Class Schedule –see attached document

Our timeline will follow the Research Workflow presented in the SEA In Silico Laboratory Manual:



Note that GenBank submissions and the submission of the genome announcement publication may take place AFTER the 14th week and will be handled by course faculty and TAs.

The selection of Purdue's representative to the SEA-PHAGES Symposium in June will be done in collaboration with input from the class. One presenter and an alternate will be selected. Preparation for the symposium will require some additional time after the end of classes to prepare slides and practice the oral or poster presentation at the Annual SEA-PHAGES Symposium in June 2016.

MODULE 1: ANALYZE—Introduction to Genomes and Gene Identification				
Wk	Date	Topics	Reading	Lab Assignment
1	W Jan 13	Introduction to Course and the In Silico Portion of the HHMI Science Education Alliance mycobacteriophage research project	Annotation and Bioinformatic Analysis of Bacteriophage Genomes "A User Guide to DNA Master" • Chapter 1: Introduction to DNA Master • Chapter 2: Provisional Cluster Assignment of Your Phage • Chapter 3: Importing Your Phage Genome Sequence into DNA Master • Chapter 4: Performing and Viewing a Rapid Automated Annotation of Your Genome	• DNA Master Software Installation and Introduction • Genome Assignment (EricMillard and Mesh1) • DNAMaster preferences, importing genome and auto-annotation with Blast of all genes
	F Jan 15			
2	W Jan 20	Introduction to Genes and Genomes; Beginning Genome Annotation & Documentation	Annotation and Bioinformatic Analysis of Bacteriophage Genomes "A User Guide to DNA Master" • Chapter 5: Gathering Additional Information for Refining Your Annotation • Chapter 6: Phamerator and Other Tools to Assist with Annotation • Chapter 7: Guiding Principles of Bacteriophage Genome Annotation • Analyze. Section I.A "Introduction to Genomes" • Analyze. Section II.A. "Intro to Genes" • "What is a Gene?" Nature 2006 • 60 phage paper: Hatfull. 2010. J. Mol. Biol. Vol 397, Issue 1, Pages 119-43, 2010.	• Set up lab notebook in Evernote and share • Phamerator and Virtual Box Software Installation and Introduction • Genome assignments for each group • Begin Gene Calls
	F Jan 22			

			• iBioseminar: "Part II: Bacteriophages: Genomic Insights" http://www.ibiology.org/ibioseminars/microbiology/graham-hatfull-part-2.html	
3	W Jan 27	• Evidence Based Gene Calling • Coding Potential • Differences between Glimmer & GeneMark • Sequencing Technology • Sequencing Quality Control & Finishing • Sequence Alignment, Identity, & Homology with BLAST	Annotation and Bioinformatic Analysis of Bacteriophage Genomes "A User Guide to DNA Master" • Chapter 8: Gene by Gene: Evaluating and Improving Your Draft Annotation • Chapter 9: The Mechanics of Making Changes to Your Annotation	Gene Annotation—CURE Learning Outcome 1 & 2
	F Jan 29			
4	W Feb 3	***Group presentations: Gene call progress update and discussion in class and on Mixable—CURE Learning Outcome 4***	"Mycobacteriophages:Genes & Genomes" Hatfull. 2010 Ann. Rev. Microbiol.	Gene Annotation—CURE Learning Outcome 1 & 2 CATME Notebook and Lab Participation Evaluation—CURE Learning Outcome 4
	F Feb 5			
5	W Feb 10	***Group presentations: Gene call progress***		Gene Annotation—

		update and discussion in class and on Mixable—CURE Learning Outcome 4		CURE Learning Outcome 1 & 2
	F Feb 12	Module 1 Journal Club–CURE Learning Outcome 2 • 60 phage paper: Hatfull. 2010. J. Mol. Biol. Vol 397, Issue 1, Pages 119-43, 2010.		
6	W Feb 17	***Group presentations: Gene call progress update and discussion in class and on Mixable—CURE Learning Outcome 4***		Gene Annotation—CURE Learning Outcome 1 & 2
	F Feb 19			
7	W Feb 24	***Group presentation of draft genome annotation; submit draft annotation—CURE Learning Outcome 4***		Gene Annotation—CURE Learning Outcome 1 & 2
	F Feb 26			CATME Annotation Evaluation—

				CURE Learning Outcome 4
MODULE 2: DISCOVER—Use of Bioinformatics Databases to Explore Gene Function and Genomic Organization				
8	W Mar 2	• Annotation of gene functions • Phage Anatomy & Biophysics • Functions of Genes/Proteins we expect to find in phage	Annotation and Bioinformatic Analysis of Bacteriophage Genomes "A User Guide to DNA Master" • Chapter 10: Assigning Gene Functions	Gene Function Annotation—CURE Learning Outcome 1 & 2
	F Mar 4			
9	W Mar 9	***Group presentations: Gene function progress update and discussion in class and on Mixable—CURE Learning Outcome 4*** Begin Comparative Genomics group research project (CURE Learning Outcome 3 & 5) Phage genome comparisons; evolution of phage genomes		Gene Function Annotation Comparative Genome Analysis—CURE Learning Outcome 1, 2, and 3
	F Mar 11			
10	**Mar 14—19**	**Spring Break**		

11	W Mar 23	Comparative Genomics project—CURE Learning Outcome 3 & 5		Gene Function Annotation Comparative Genome Analysis—CURE Learning Outcome 1, 2, and 3 CATME Notebook and Lab Participation Evaluation—CURE Learning Outcome 4
	F Mar 25			
12	W Mar 30	Comparative Genomics project—CURE Learning Outcome 3 & 5		Gene Function Annotation Comparative Genome Analysis—CURE Learning Outcome 1, 2, and 3
	F Apr 1	***Group presentations: Gene function progress update and discussion in class and on Mixable—CURE Learning Outcome 4***		

13	W Apr 6	Module 2 Journal Club –CURE Learning Outcome 2		
	F Apr 8			
14	W Apr 13	• Group discussion of draft genome • Submit draft annotation with functions • Merger & Checking	Annotation and Bioinformatic Analysis of Bacteriophage Genomes "A User Guide to DNA Master" • Chapter 11: Merging and Checking Annotations	Prepare File for GenBank Submission and Genome Announcement—CURE Learning Outcome 3 CATME Annotation Evaluation —CURE Learning Outcome 4
	F Apr 15			
MODULE 3: SHARE—Presentation of Research Discoveries and Findings				
15	W Apr 20	***Final Group Presentation of Genome Annotation and Comparative Genome Analysis—CURE Learning Outcome 4***		
	F Apr 22			
16	W Apr 27	***Final Group Presentation of Genome Annotation and Comparative Genome Analysis—CURE Learning Outcome 4***		
	F Apr 29	CATME Group Presentation Evaluation—CURE Learning Outcome 4		

	Finals Week—Final Research Paper Due (Individual)