

MCB 1200/1201, Virus Hunting: Join an international science program (Howard Hughes Medical Institutes (HHMI) Science Education Alliance (SEA) Phage Research Program) that seeks to identify new therapies for diseases. In a real research project, students will isolate viruses that infect non-pathogenic bacteria that are related to disease-causing strains. There are more of these viruses, known as bacteriophages or phages, than any other group of organisms on Earth--but relatively few of them have been isolated or characterized. Phage therapy is a way to treat bacterial infections without using antibiotics, so the phages isolated in the class could have real therapeutic uses.

Applied Bioinformatics (MCB 1201): The goal of the course is for every single student to characterize a bacteriophage genome. This involves finding genes and annotating them, comparing the gene content of this phage to other known phages, and using sequence analysis to infer evolutionary relationships. Grading is based on: electronic notebook of gene annotations and evidence (20%), exams (30%), research paper (25%), poster (15%), and in-class presentations ("group meetings", 10%).

MCB 1201 Virus Hunting: Applied Bioinformatics

Semester: Spring

M/W 1:30-4:30 Beach Hall,

open lab times M/W 9-1:30, most Fridays



Instructors:

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Course description and rationale

This course is a unique classroom-based undergraduate research experience that is part of the Howard Hughes Medical Institutes Science Education Alliance Phage Research Program. It spans two terms (with MCB 1200, Phage Hunters) and culminates in a research symposium held at HHMI's Janelia campus. Throughout this semester, you will learn about the biology of bacterial viruses by identifying a new one from the environment. Your work will be connected to a larger community of undergraduate and graduate level research scientists that are exploring the biology and evolution of bacteriophages. This course is a part of a Phage Hunters Advancing Genomics and Evolutionary Science (PHAGES) educational program sponsored by the Howard Hughes Medical Institute (HHMI) and one of its divisions called the Science Education Alliance (SEA).

Course objectives:

Goal of the course is for every single student to characterize a bacteriophage genome. This involves finding genes and annotating them, comparing the gene content of this phage to other known phages, and using sequence analysis to infer evolutionary relationships. The genomic sequences will then be submitted to Dr. Graham Hatful at U.Pitt, and eventually to the National Center for Biotechnology Information (NCBI's) GenBank database for publication. Your phage data will also be entered into the PhagesDB database.

Learning objectives: By the end of the semester students will be able to

1. Use annotation software to predict genes from DNA sequence.
2. Refine computer-generated gene predictions using evidence and informed judgment.
3. Show proficiency with DNA Master, Blast, Phamerator, HHPred, Aragorn and other programs used to analyze DNA and protein sequences.
4. Describe the biology of bacteriophage in general, and mycobacteriophage in particular.
5. Design and execute a research project related to mycobacteriophage genomics.
6. Write a scientific abstract and a scientific paper reporting the results of the research project.
7. Construct a poster reporting on the research project.
8. Keep clear and informative electronic records of gene annotations and associated evidence.
9. Present data orally.

Grading: Grades will be based on the following:

Electronic notebook of gene annotations and evidence	20%
Exams	30%
Research paper	25%
Poster	15%
In-class presentations of work ("Group meetings")	<u>10%</u>

Oral Presentations

A brief oral presentation will be made by each student on the phage genome they have characterized.

Poster

At the end of the semester, each student in MCB 1201 will present their work in a public poster session with details to follow. You will each present a poster on the rationale, experimental design, results, and conclusions from your analysis of a phage genome. This will be your opportunity to share your discoveries with the community of scientists in the MCB Department.

Participation

Engagement with instructors and classmates is an integral part of this course. Thus, participating in all class activities will be required. Class absences will be excused only with documentation and will require make-up labs to complete the necessary laboratory experiments. A failure to make-up the laboratory experiments will result in a grade deduction.

Classroom Etiquette

Cell Phones: Cell phone use is only permitted during the lab portion of class for data recording (pictures, notes, etc) and is never permitted for texting, calls, apps, or email. If a student is observed using the phone inappropriately he/she will be asked to turn in their phone and may lose privileges for the remainder of the semester.

Computer Use: While we understand that students will be using computers/tablets for note-taking during the class, if a student is observed using the computer for anything other than lecture materials (email, facebook, youtube, etc...) the same policy as outlined for cell phone use will apply.

Our Philosophy

We believe in having a dynamic classroom, open to discussion, participation, and inquiry from all members of the class. We strive to establish a fair and balanced classroom where all students can participate.

Academic Honesty

Academic misconduct is dishonest or unethical academic behavior that includes, but is not limited to: misrepresenting mastery in an academic area (e.g., cheating), intentionally or knowingly failing to properly credit information, research or ideas to their rightful originators or representing such information, research or ideas as your own (e.g., plagiarism). Examples of misconduct in this class include, but are not limited to: cheating on exams, plagiarism, turning in questions for fellow students, impersonating another student, falsifying data, copying, fabricating or stealing data. For more details on the University of Connecticut's policy on academic integrity, including the instructor's role and procedures you are referred to the following page and references therein: http://www.community.uconn.edu/student_code_appendixa.html

Disabilities:

It is the policy of the University of Connecticut that no qualified person be excluded from participating in any University program or activity or otherwise be subjected to discrimination with regard to any University program or activity. This policy derives from the commitment to non-discrimination for all persons in employment, access to facilities, student programs, activities and services. If you have a disability and need assistance please contact me as soon as possible so that appropriate arrangements can be made. Also refer to Center for Students with Disabilities for guidelines to request accommodations or any other assistance you may require. http://www.csd.uconn.edu/accommodation_services.html

Draft Schedule

(lecture topics are in normal font, *exercises and group activities in italics*)

(Course materials that include a guide to most of the programs used in the exercises is available at <https://seaphagesbioinformatics.helpdocsonline.com/home>)

Week	Class Day	Topic
1	1	Introduction to course. Next generation sequencing technologies. <i>Using the Linux/Ubuntu OS</i>
2	1	Introduction to Phage Biology and genes in bacteriophage <i>Introduction to the genomic analysis workflow</i>
	2	Sequencing and assembly, multiplexing using barcoding primers <i>Fasta and fastq files, sequence assembly exercise</i>
3	1	Databank search and annotation software: Blastn and Blastp <i>Blastn and Blastp databank searches</i>

	2	Introduction to 'Starterator' & Genome assignment <i>ORF finder, Gene calling software</i>
4	1	Gene structure and regulation in bacteria and viruses <i>Annotation software: Gene Mark, Glimmer</i>
	2	Introduction to 'Phamerator' <i>Blast genome to determine cluster membership</i>
5	1	Annotation software: DNA Master <i>DNA Master exercises</i>
	2	Cross-molecular searches: BLASTX & TBLASTN <i>Comparison of blastn and blastx and tblastn searches</i>
6	1	Global versus local sequence alignment <i>Exercises illustrating dot matrix representations of pairwise sequence alignments</i>
6	2	Multiple sequence alignments <i>Exercises exploring the impact of scoring matrices and gap penalties on the placement of insertions and deletions.</i>
7	1	Error types in databank searches <i>Exercises illustrating factors impacting expectation (significance) values</i>
7	2	Proteins structure data banks and Position Specific Iterated blast searches <i>Identifying protein domains</i>
8	1	Discussion of post annotation analyses <i>Students discuss and work on annotation of their assigned genome</i>
8	2	Annotation artifacts in existing databanks <i>Students work on annotation of their assigned genome</i>
9	1	Intro to phylogenetic reconstruction <i>Groups of students discuss and plan post-annotation analyses Phylogenetic comparisons of genes & genomes of interest</i>
9	2	Phylogenetic reconstruction part 2 and horizontal gene transfer <i>Students complete annotation of the genome</i>
10	1	Levels of selection and Gene Transfer Agents <i>Students pursue post-annotation experimentation on their phages.</i>
10	2	Phages as a second adaptive immune system / phage therapy <i>Students complete post-annotation experimentation on their phages and discuss obtained results in small groups</i>
11	1	The role of phages in the global carbon cycle <i>Students discuss and plan group presentations and refine post-annotation experimentation</i>
11	2	<i>Group presentations #1</i>
12	1	<i>Group presentations #2</i>
12	2	<i>Group presentations #3</i>
13	1	<i>Writing abstracts / prepare posters</i>
13	2	<i>Critique and edit poster drafts</i>
14	1	<i>Student-annotated files are merged, finalized, and reviewed by the Hatfull Laboratory for submission to GenBank. Complete Posters</i>
14	2	<i>Poster presentations and class wrap-up</i>

Class meeting will be on M/W 1:30-4:30. These include lectures, demonstrations, group discussions, and computer-lab exercises. Most exercises during the class periods will use examples provided by the instructors to familiarize students with concepts, analyses, and programs. The open lab times (M/W 9-1:30, most Fridays) are for students to apply the learned approaches and programs to the phage genome assigned to each student, and to explore additional comparative analyses on their genomes. The open lab times are an integral part of the course during which students pursue their own research projects. At least one instructor will be presents during the open lab times.