

MCB 1201 Virus Hunting: Applied Bioinformatics

Semester: Spring 2021



M/W 1:30-4:30pm <https://uconn-cmr.webex.com/join/jpg02006>

open lab times by arrangement during M/W/F 9am-1:30pm F 1.30-3pm

Instructors

Dr. Johann Peter Gogarten; Office BPB 404, 486-4061; gogarten@uconn.edu

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Audience

Recommended for freshmen and sophomores; science and non-science students welcome!

This course fulfills the GenEd CA3 Science and Technology Lab Course Requirement.

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. **MCB 1200 and 1201 can be taken independently.** 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 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 the University of Pittsburgh, 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.

Requirements

The is open to all UConn students. Students need to have access to a computer running either MacOSX or Microsoft Windows with access to a camera and a microphone that allows the use webex. An official UConn email address and netID is necessary to access the class-notebook.

Grading: Grades will be based on the following:

Electronic notebook of gene annotations and evidence	20%
Midterm Exam	20%
Research project	20%
Poster / Final Presentation	20%
In-class presentations of work ("Group meetings")	20%

Grading Scale:

Letter Grade	If your overall percentage is greater than or equal to this	and your overall percentage is less than this
A	93	—
A-	90	93
B+	87	90
B	83	87
B-	80	83
C+	77	80
C	73	77
C-	70	73
D+	67	70
D	63	67
D-	60	63
F	0	60

Oral Presentations

Brief oral presentations will be delivered by each student on the phage genome they have characterized and on their research project.

Poster/Final Presentation

At the end of the semester, each student in MCB 1201 will present their work in a public poster or powerpoint presentation. You will each present on the rationale, experimental design, results, and conclusions from your analyses of one or several phage genomes. This will be your opportunity to share your discoveries with the community of scientists in the MCB Department. One or two students will have the opportunity to present their poster(s) at the 11th annual SEA Symposium at Howard Hughes Medical Institute's Janelia Research Campus in Northern Virginia, expenses paid.

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 not related to the class, or email.

Computer Use: While we understand that students have to use computers/tablets during the class, during class computer use should be limited to class materials.

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: <https://community.uconn.edu/the-student-code-appendix-a/>

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. <https://csd.uconn.edu/request-accommodations/>

Very preliminary 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. Introduction to viruses <i>Assemble a PowerPoint slide on your favorite virus</i>
2	1	Introduction to Phage Biology and genes in bacteriophage <i>Presentations on viruses</i> Introduction to the genomic analysis workflow
2	2	The strange personalities that discovered viruses that “eat” bacteria, Joseph Stalin and the Eliava Institute. <i>Introduction to annotation software</i>
3	1	Sequencing and assembly, multiplexing using barcoding primers Gene structure and regulation in bacteria and viruses <i>Annotation: Phamerator exercises</i>
3	2	Molecular biology basics <i>Annotation: introduction to DNA Master</i>
4	1	Genome annotation <i>Gene calling using genemark/glimmer</i>
4	2	BLAST and database searches <i>Annotation: BLAST exercises</i>
5	1	Error types in databank searches <i>Exercises illustrating factors impacting expectation (significance) values</i>
5	2	Proteins structure data banks and Position Specific Iterated blast searches <i>Identifying protein domains</i>
6	1	Lecture <i>Annotation</i>
6	2	Lecture <i>Annotation</i>
7	1	Discussion of post annotation analyses <i>Students discuss finish annotations.</i>
7	2	Midterm Exam
8	1	Intro to phylogenetic reconstruction <i>Introduction to R.</i> <i>Phylogenetic comparisons of genes & genomes of interest</i>
8	2	Phylogenetic reconstruction part 2 and horizontal gene transfer <i>Introduction to Data visualization</i>
9	1	Levels of selection and Gene Transfer Agents <i>Introduction to Poster Design</i> <i>Post-annotation analyses</i>
9	2	Phages as a second adaptive immune system / phage therapy <i>Post-annotation analyses</i>
10	1	How many phages are there? How do we know? <i>Post-annotation analyses</i>

10	2	Lecture <i>Post-annotation analyses</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>Intro to protein visualization software (chimera)</i>
12	1	<i>Group presentations and discussions</i>
12	2	<i>Group presentations and discussions</i>
13	1	<i>Writing abstracts / prepare posters / presentations</i>
13	2	<i>Critique and edit poster/presentaion 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>

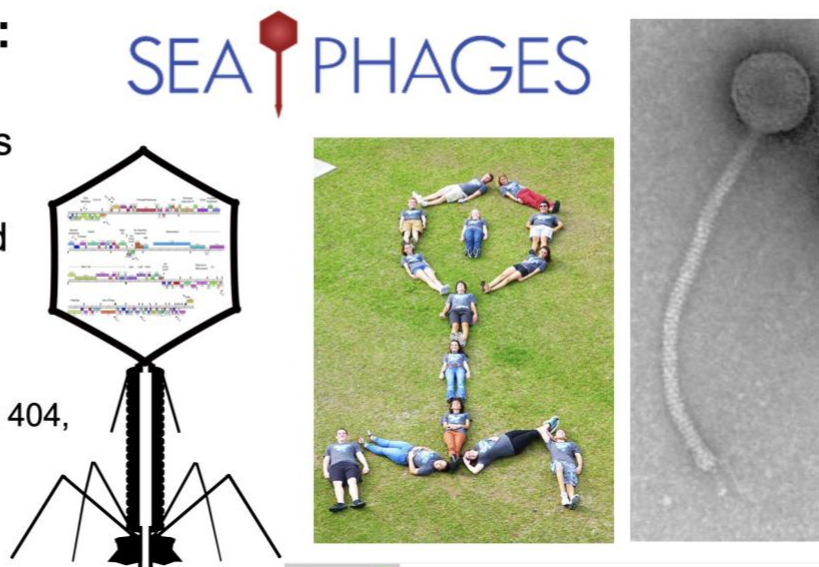
Class meetings will be on M/W 1:30-4:30. These include lectures, demonstrations, group discussions, and computer-lab exercises. Most exercises during the class periods will use examples provided by the instructors to familiarize students with concepts, analyses, and programs. The open lab times (M/W 9-1:30, F 1.30-3pm) 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 on instructor will be available via webex during the open lab times.

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Spring Semester 2021, 4 credits
M/W 1:30-4:30 via webex,
open lab times M/W 9-1:30, and
most Fridays

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Join Phage Hunters to Advance Genomics and Evolutionary science. Contribute to science and discovery through annotating a previously uncharacterized bacteriophage genome.

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Approved for the GenEd CA3 Science and
Technology Lab Course Requirement



Type phage name

Search

Recently Added Phages

- Schroedinger
- MalusLutum
- Elera
- Nadie20
- PuffCorn

Recently Modified Phages

- HarmonyHill
- Rudtzsky
- Bleien
- Bla
- LowAndGut

Recently Finished Phages

- None (0/0)
- SuperKase (0/0)
- Cheslet (0/0)
- SalleyBla (None)
- Kenzers (0/0)

Connect to Social Account

Sign out

Microbacterium phage Lovelyunicorn

Locally BLAST this genome

Run GeneMarkS

Run GeneMark (M. folio B-24224)

Know something about this phage that we don't? Modify its data.

Detailed Information for Phage Lovelyunicorn

Discovery Information	
Isolation Host	<i>Microbacterium fallorum</i> NBRL B-24224
Former names	lovelyunicorn
Found By	Xiaoxue Li
Year Found	2019
Location Found	Storrs, CT USA
Finding Institution	University of Connecticut
Program	Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science
From enriched soil sample?	Yes
Isolation Temperature	20°C
GPS Coordinates	41.809167 N, 72.25 W Map
Discovery Notes	I took the soil sample around the lake in my school where is really beautiful.
Naming Notes	because the unicorn is very lovely, and I think my phages are lovely too.