

Syllabus for Fall 2020

MCB 3421: Introduction to Molecular Evolution and Bioinformatics

https://j.p.gogarten.uconn.edu/mcb3421_2020/

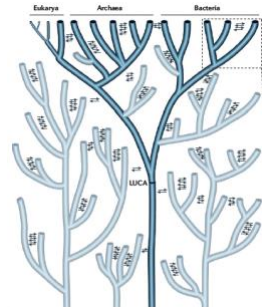
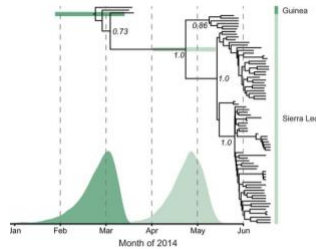
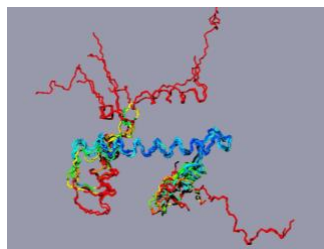
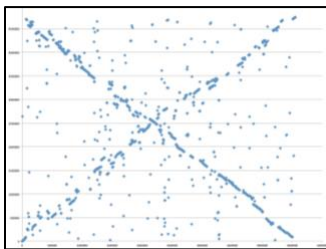
Prerequisites: Recommended preparation: At least one 2000 level course in MCB.

Grading Basis: Graded

Topics:

- Tracing the evolutionary histories of genes, organisms, and infectious diseases
- Databank searches
- Alignment of sequences and 3-D protein structures
- Comparative genomics
- Selfish genes
- Symbiotic relationships between organisms and genes
- Evolution through genetic exchange

The course includes lectures, discussions, and computer lab exercises.



Lectures:

Mondays & Wednesdays 11.15 AM-12.05 PM, (asynchronous)
online at huskyCT – lectures will be pre-recorded or recorded.
You can go through the lectures at your own time.

Computer labs and discussions:

Fridays 10:10AM - 11:40AM or 1:25PM - 2:55PM (synchronous)
online using **Webex** at <https://uconn-cmr.webex.com/meet/jpg02006>
Worksheets will be posted at https://j.p.gogarten.uconn.edu/mcb3421_2020/

Office hours, question-and-answer sessions:

Mondays & Wednesdays 12.05 PM – 12.45 PM or arranged via [email](#).
online using **Webex** at <https://uconn-cmr.webex.com/meet/jpg02006>
You can also email questions to the instructors or
for questions of general interest use the discussion board at the huskyCT course webpage.

Instructors:

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Basis for grading:

	Weight
Final project:	20%,
Midterm exam (includes multiple choice and a practical portion):	10%,
Participation in discussions, bulletin board postings:	10%
Take-home exams:	30%
(via huskyCT, open book exams on the honors system. We will have 8 of these, but you can drop the worst 4 grades).	
Completion of computer-lab assignments:	10%
Class notebook (quality and completeness of entries)	20%

Expectation: More than 4h reading/studying per week (most will do fine with about 3-6h/week).

Plagiarism and "collaborations" for writing assignments and take-home exams will not be tolerated! In case of misconduct you will receive an F for the assignment, AND the F will count towards the final grade (*i.e.*, you cannot drop an F due to academic misconduct).

Exam policy: When students are forced to miss any of exams due to illness, accident, death in the family, or other unavoidable reasons they need to contact the instructor ASAP.

The general policy for Syllabi, including links to the expected workload and class attendance is at <http://provost.uconn.edu/syllabi-references/>

The Center for Students with Disabilities (CSD) at UConn provides accommodations and services for qualified students with disabilities. If you have a documented disability for which you wish to request academic accommodations and have not contacted the CSD, please do so as soon as possible. The CSD is located in Wilbur Cross, Room 204 and can be reached at (860) 486-2020 or at csd@uconn.edu. Detailed information regarding the accommodations process is also available on their website at www.csd.uconn.edu.

If you need any additional information on this course, please send an email to gogarten@uconn.edu!

Very Preliminary Schedule

red: computer lab exercises (Fridays 10.10 -11.40 **or** 13.25-14.55 on webex);

blue: lectures and demonstrations (MW lectures on HuskyCT - asynchronous)

- [Class 01](#): Overview; topics; textbook; reading materials; How will grades be calculated?
- [Class 02](#): What has molecular evolution to do with bioinformatics? The concept of homology, combinatoric protein space, basics of protein structure,
- [Computer-lab assignment 01](#): Intro to chimera - binding pocket substrate interactions
- [Class 03](#): Overview on replication, transcription, translation; the RNA world concept; discussion of homology.
- [Computer-lab assignment 02](#): Comparing structures for ancient duplicated genes / following a structure through the catalytic cycle
- [Class 04](#): ATP binding sites and convergent evolution, natural selection and definitions of life
- [Class 05](#): Divergence of sequences, symbiotic relationships, inteins
- [Computer-lab assignment 03](#): Exploring intein structures in chimera
- [Class 06](#): The tangled tree of life.
- [Class 07](#): Mutationism and the Modern Synthesis, Mutual Aid
- [Computer-lab assignment 04](#): Literature Databanks and Entrez
- [Class 08](#): Statistics of sequence comparison
- [Class 09](#): Databanks, Blast, Unix
- [Computer-lab assignment 05](#): Statistics of Sequence Comparison
- [Class 10](#): Dayhoff and the history of bioinformatics
- [Class 11](#): Strand-bias and recombination
- [Computer-lab assignment 06](#): Blast searches using the command line
- [Class 12](#): (A) cladistics (B) early humans
- [Class 13](#): Ebola as an example for the usefulness of molecular evolution; review of endosymbiosis in eukaryotes
- [Computer-lab assignment 07](#): Creating gene plots
- [Class 14](#): Gene duplication and post mating hybridization barriers
- [Class 15](#): Recombination and strand bias in prokaryotic genomes
- [Computer-lab assignment 08](#): Gene plots, strand bias, and mummer
- [Class 16](#): split inteins as an example for constructive neutral evolution, bottlenecks
- [Class 17](#): Introns late versus introns early
- [Computerlab assignment 09](#): Dotlet and Jalview exercises on repetitive motifs, introns and sequence space.
- [Class 18](#): Intro to trees and phylogenies
- [Class 19](#): Discussion of LBA. Why can gene trees be in conflict?
- [Computerlab assignment 10](#): Phylogenies, bootstrap, model tests, LBA
- [Class 20](#): selection, deterministic models, genetic drift
- [Class 21](#): Detecting positive and purifying selection, heterogeneity and population size
- [Computerlab assignment #11](#): Simple scripts to handle genome sized data sets
- [Class 22](#): Types of selection / GTAs and purifying selection
- [Class 23](#): Intro to PSI blast.
- [Computerlab assignment #12](#): PSI blast exercises.
- [Class 24](#): Discussion of PSIBlast lab
- [Class 25](#): Discussion of student project.
- [Computerlab assignment #13](#): Bayesian analysis to determine evolutionary parameters in sequences