Syllabus for Fall 2019

MCB 3421: Introduction to Molecular Evolution and Bioinformatics
http://gogarten.uconn.edu/mcb3421_2019

Prerequisites: Recommended preparation: At least one 2000 level course in MCB.
Grading Basis: Graded
Evolution of biomolecules and application to molecular data analysis and the design of new molecules.
Topics include prebiotic chemistry, origin of cells, selfish genes, molecular innovations, data bank searches, alignment of sequence and 3-D protein structures.
Course includes lectures, discussions and computer lab exercises.

Mondays & Wednesdays 11.15AM-12.05PM, TLS 301
Fridays 10:10AM - 11:40AM or 1:25PM - 2:55PM Whetten Graduate Center 300A

Instructors:
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Office hours
MW after class - 2pm or after arrangement: for fast response send an email!
For questions of general interest, use the bulletin board on WebCT.

Basis for grading:
Participation (huskyct discussion board, in class discussions, in class pop-up quizzes),
Assignments from the computer labs, **Take-home exams**, **Midterm**, **Final**.
> **Weights:**
> Final: 30%,
> Midterm: 25%,
> Participation, bulletin board postings, pop-up quizzes, other in-class assignments: 15%
> Take-home assignments: 30%
> (You can **drop the worst 4** grades from the Take Home Assignments – at least 8 will be offered).

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 the final examination due to illness, accident, death in the family, or other unavoidable reasons they need to contact the Office of Student Services & Advocacy to receive approval to arrange another exam time. Students should present appropriate documentation to support their request. Students who have a conflict about which they have or should have had advanced notice (bunched finals, religious obligation, legal/medical appointments …) should seek permission to reschedule their assessment NO LATER THAN November 30th.
If you need to reschedule your midterm or final exam, please let your instructor know ASAP.

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

Very Preliminary Schedule

red: computer lab exercises in the Whetten Graduate Center (F 10.10 -11.40 or 13.25-14.55);
blue: lectures, demonstrations and discussions in Gentry 140 (MW 11.15-12.05)

Class 1: Overview; topics; textbook; reading materials; How will grades be calculated?
Class 2: Protein structure, protein evolution, Swiss Protein Data bank Viewer
Class 3: Using Chimera
Class 4: Why is an evolutionary perspective important?
Class 5: Aligning protein pdb files in chimera
Class 6: Aligning pdb file in chimera view, review of the homology concept
Class 7: Databanks, Entrez
Class 8: Simple Databank searches using Entrez and Web of Science
Class 9: Discussion and review
Class 10: Z scores, expectations and probabilities
Class 11: Simple homology searches
Class 12: Multiple substitutions, dot matrix representation
Class 13: Blast and the command line
Class 14: Simple blast and blastall searches
Class 15: blastall discussion, optimal pairwise alignment
Class 16: dotlet, optimal alignments, intro to trees - part 1
Class 17: dotlet, inspecting protein protein and protein DNA alignments
Class 18: dotlet, exon shuffling, chromosome rearrangements
Class 19: clustal, muscle and SATe
Class 20: clustal and jalview
Class 21: Trees, terminology and coalescence
Class 22: Tree terminology, part 1
Class 23: Finding ORFs, Gene Plots, and Synteny
midterm
Class 24: Tree terminology, part 2
Class 25: Intron/Exon detection, prediction of membrane spanning helices
Class 26: Gene duplications, types of homology
Class 27: Gene duplications continued
Class 28: TaxPlot, TaxTable and Mummer
Class 29: Genes, populations and selection
Class 30: In vitro selection, recombination and linkage between protein evolution and the encoding genes
Class 31: Trees with clustal and phylip
Class 32: Neutral Evolution
Class 33: PSI blast
Class 34: PSI blast exercises
Class 35: Building trees, support values
Class 36: Bayes and ASRV
Class 37: Distance matrix, bootstrap and parsimony analyses - long branch attraction.
Class 38: Probability mapping and detecting positive selection
Class 39: Detecting positive and purifying selection.
Class 40: MrBayes - Introductory Exercises

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 !