

Preliminary Syllabus for Fall 2013

MCB 3421: Introduction to Molecular Evolution and Bioinformatics

http://gogarten.uconn.edu/mcb3421_2013

Instructor:

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Office hours

MW noon-1pm or after arrangement: for fast response send an [email!](#)

For questions of general interest, use the bulletin board on WebCT.

Teaching Assistant: Amanda Dick <amanda.dick@uconn.edu>

Basis for grading:

Participation (webct discussion board, in class discussions),

Assignments from the computer labs,

Take-home quizzes and questions,

Midterm,

Final.

Weights:

Final: 30%,

Midterm: 25%,

Participation, bulletin board postings, and in-class assignments: 10%

Take-home assignments, quizzes, and presentations: 35%

(You can drop the worst 4 grades from the Take Home Assignments).

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 counted towards the final grade.

Exam policy: When students are forced to miss a final examination due to illness, accident, death in the family or other unavoidable reasons they can come to the Office of Student Services & Advocacy to receive approval to arrange another exam time with their instructor. 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, religious obligation, legal/medical appointments...) MUST seek permission to reschedule their assessment NO LATER THAN November 30th.

With other exams and assignments, which are required during the semester students bring their documentation of extenuating circumstances directly to their instructors. There are no make-up exams for the take-home exam. If you need to reschedule your final, please let your instructor know ASAP.

Preliminary Schedule

red: computer lab exercises in T115 (F 10.10 -11.40 or 13.25-14.55);

blue: lectures, demonstrations and discussions in CB110 (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 Deep View

Class 4: Why is an evolutionary perspective important?

Class 5: Aligning protein pdb files in deep view

Class 6: Aligning pdb file in Deep 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, and exon shuffling (broken projection equipment)

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