BIOL/GCB/CIS 536

This is a course designed for PhD level students who are seeking to pursue a major part of their dissertation projects using computational analysis and modeling. The course will be organized around reading and discussing from posted lecture materials and computational method design for actual research problems (second part of the course). The students will be organized into working groups for the readings and will present the readings to the class. Final projects will involve designing and implementing a computational solution to an actual biological problem. The final project will be worked in teams.

Grades:

Grades for this course will be based on participation and on a final group project.

Following topics will be covered (pages from handout readings)

String search 1-16 to 1-26 (before Algorithm Complexity)
Algorithmic Complexity 1-26 to 1-32
Pattern detection and MCMC 1-33 to 1-39
Large-scale searching and BWT 1-40 to 1-49 (before BLAST)
Sequence alignment part 1: 1-50 to 1-63 (before optimal alignment)
Sequence alignment part 2: 1-63 to 1-68 (before multiple alignment)
Multiple alignment: 1-68 to 1-75
HMM part 1: 2-2 to 2-11 (before HMM computations)
HMM part 2: 2-11 (HMM computations) to 2-21 (before Box: Models…)
Box Models, parameters, and parameter estimation: 2-21 to 2-24
Phylogeny part 1: 2-25 2-30
Phylogeny part 2 (additive distance): 2-31 to 2-43 (exclude Box on Models)
Phylogeny part 3 (MP): 2-43 to 2-50
Phylogeny part 4 (tree optimization): 2-51 to 2-61 (before Unit 13)
Stochastic model of evolution: 2-61 to 2-70 (before MCMC)
MCMC computations: 2-71 to 2-74 (before Unit 14)
Property of estimators: 2-74 to 2-80
Data visualization and dimension reduction
Learning methods: Part 3 page 1 to page 10 (leave out yellowed text)
Kernel distances: Part 3 page 14 to page 22 (before convolution kernels)
Statistical properties of Learning Methods: Part 3 page 25 to 27 (before yellow part) and then page 30 Cross validation to 31 (before yellowed text)