

BME280/CSE277/CSE377: BIOINFORMATICS
Fall 2007

Lectures: TTh 3:30-4:45pm, ITEB 125

Instructor: Ion Mandoiu
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Textbook: Neil C. Jones and Pavel A. Pevzner, *An Introduction to Bioinformatics Algorithms*, MIT Press, 2004. Textbook website: <http://www.bioalgorithms.info/>.

Prerequisites: BIOL 107, CSE 254, and either STAT 220 or STAT 224, or equivalent background in biology, discrete math, and statistics.

Course outline: This course is an introduction to the fundamental mathematical models and algorithmic techniques used in bioinformatics. Emphasis will be placed on modeling computational problems arising in biology as graph-theoretic, statistical, or mathematical optimization problems, and on designing, analyzing, and implementing efficient combinatorial algorithms for the latter. Covered algorithmic techniques will include exhaustive search, integer programming, greedy algorithms, dynamic programming, divide-and-conquer, graph algorithms, combinatorial pattern matching, clustering, hidden Markov models, and randomized algorithms. Biological applications covered will include restriction mapping, DNA sequencing, motif finding, pairwise and multiple sequence alignment, gene prediction, evolutionary trees, and genome rearrangements.

Tentative Schedule:

Week	Lecture dates	Topics	Notes
1	Aug 28 & 30	Molecular biology (Ch. 3), Exhaustive search (Ch. 4)	Hw1
2	Sept 4 & 6	Exhaustive search (contd.), Integer programming (handouts)	Prog1
3	Sept 11 & 13	Greedy algorithms (Ch. 4)	Hw2
4	Sept 20	Dynamic programming (Ch. 6)	No class Sept 18
5	Sept 25 & 27	Dynamic programming (contd.)	Hw3, Prog2
6	Oct 2 & 4	Divide and conquer (Ch. 7)	
7	Oct 9 & 11	Graph algorithms (Ch. 8)	Hw4
8	Oct 16	Graph algorithms (contd.)	No class Oct 18
9	Oct 23 & 25	Pattern matching (Ch. 9)	Hw5
10	Oct 30 & Nov 1	Clustering (Ch. 10)	
11	Nov 6 & 8	Phylogenetic trees (Ch. 10)	Hw6
12	Nov 13 & 15	Hidden Markov models (Ch. 11)	
13	Nov 27 & 29	Hidden Markov models (contd.)	Hw7
14	Dec 4 & 6	Randomized algorithms (Ch. 12)	

Grading and course policies: Grading will be based on homework assignments (30%), programming assignments (20%), and a final project (50%). Homeworks will be mostly theoretic in nature and will be assigned bi-weekly. There will be 2 individual programming assignments requiring you to implement complete solutions to specified bioinformatics problems in the programming language of your choice. The final project will give you the opportunity to study a bioinformatics problem in more depth. Suitable final project topics include surveys of bioinformatics topics not covered in the lectures, design and implementation of novel algorithms, and empirical evaluation of existing methods. A list of potential topics will be provided towards the middle of the semester, although you are encouraged to devise your own. You will be required to submit a written

final report of 15-20 pages and give a short presentation of your project at the end of the semester. When appropriate, projects can be done in teams.

HuskyCT: We have a HuskyCT (formerly Vista/WebCT) site for the class; you can access it by logging in with your NetID and password at <https://vista.uconn.edu/>. You must check HuskyCT regularly for class materials, grades, problem clarifications, changes in class schedule, and other class announcements.

Academic honesty: You are expected to adhere to the highest standards of academic honesty. Unless otherwise specified, collaboration on assignments is not allowed. Use of published materials is allowed, but the sources should be explicitly stated in your solutions. Violations will be reviewed and sanctioned according to the University Policy on Academic Integrity.

Students with disabilities: If you have a documented disability for which you are or may be requesting an accommodation, you are encouraged to contact the instructor and the Center for Students with Disabilities or the University Program for College Students with Learning Disabilities as soon as possible to better ensure that such accommodations are implemented in a timely fashion.