CSE 308 / 408
Bioinformatics: Issues and Algorithms

Spring Semester 2007
Meeting Dates & Times: TuTh 2:35 – 3:50
Room: PL 258

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1. Course Description

The past decade has witnessed explosive growth in the field of bioinformatics, with entire genomes for many organisms (including humans) now available online. Computer science plays a central role in the creation, analysis, and management of this data: from the sequencing and assembly of DNA, to searching vast databases of known nucleic acid or protein sequences, to the calculation of evolutionary trees, to attempts to predict the structure, and ultimately the function, of these macromolecules that form the basis for life. CSE 308 / 408 covers algorithms and computational models applied to problems from bioinformatics.

2. Target Audience / Prerequisites

This course is targeted at two audiences:

* computer science and bioengineering students who wish to learn about the field of bioinformatics and the ways in which computational methods are applied there,

* life sciences students who would like to understand the algorithmic techniques that lie behind the software tools they use.

Recognizing these distinct backgrounds, early lectures will be designed to bridge the disciplines and provide a common basis for later discussions.

This course is intended primarily for juniors, seniors, and graduate students. All students should have had some previous programming experience (including data structures) at the level of CSE 17, as well as a college-level understanding of discrete math, probability, and statistics. A previous course in algorithms is helpful but not required. Computer science students should note that no prior background in biology is assumed. For questions concerning prerequisites, contact the instructor.

In terms of the CSE Graduate Core Requirements, CSE 408 falls in the "Computer Applications" and the "Theory" categories.

3. Textbooks

Title: *An Introduction to Bioinformatics Algorithms*
Authors: Neil C. Jones and Pavel A. Pevzner
Publisher: MIT Press
ISBN: 0-262-10106-8

Title: *Bioinformatics Biocomputing and Perl*
Authors: Michael Moorhouse and Paul Barry
Publisher: John Wiley & Sons
ISBN-10: 047085331X

Additional readings will also be made available on the course Blackboard website.

4. Tentative Syllabus (subject to change)

* Introduction to molecular biology for non-biologists
  DNA, RNA, proteins, splicing, sequencing, gene structure

* Introduction to algorithms for non-computer scientists
  Correctness, iteration and recursion, time and space complexity, general methods

* Pairwise sequence alignment
  Homology, global and local alignment, dynamic programming
  Advanced alignment techniques: gap penalties, saving time and space

* Multiple sequence alignment
  Multidimensional dynamic programming
  Approximation techniques

* Physical mapping
  Restriction maps
  Double and partial digests

* Sequencing
  Shotgun sequencing
  Sequencing by hybridization, DNA microarray analysis, clustering
  Genome assembly

* Advanced topics
  Genome rearrangements
  Evolutionary relationships, phylogenetic trees

5. Accommodations for Students with Disabilities

If you have a disability for which you are or may be requesting accommodations, please contact both your instructor and the Office of Academic Support Services, University Center 212 (610-758-4152) as early as possible in the semester. You must have documentation from the Academic Support Services office before accommodations can be granted.