

# CSE 308-408

## Bioinformatics: Issues and Algorithms

Spring 2007 • TuTh 2:35 pm – 3:50 pm • Packard Lab 258

- Instructor**      **Professor Daniel Lopresti**  
 Office PL 404B • Ext 85782 • Email [dal9@lehigh.edu](mailto:dal9@lehigh.edu)  
 Office Hours 4:00 – 6:00 Th (or by appointment)
- Biology Advisor**    **Professor Jutta Marzillier**  
 Ext 84902 • Email [jym2@lehigh.edu](mailto:jym2@lehigh.edu)
- Textbooks**        *An Introduction to Bioinformatics Algorithms*, Neil C. Jones and Pavel A. Pevzner  
 MIT Press, ISBN 0-262-10106-8. (IBA)
- Bioinformatics Biocomputing and Perl*, Michael Moorhouse and Paul Barry  
 John Wiley & Sons, ISBN 047085331X. (BB&P)

**Blackboard**        Lecture slides, assignments, etc. will be available @ <http://ci.lehigh.edu>

- Grading**
- Homework assignments = 250 points
  - Programming assignments = 250 points
  - Final project or paper = 500 points
  - Scribe duty (CSE 408 only) = 100 points

- Notes**
- Homework / programming assignments will generally be posted to Blackboard by 9:00 am and due by 5:00 pm on the specified day. Carefully follow all instructions when naming your programs and submitting your work.
  - Assignments turned in up to one week late will received ½ credit. After that point, no credit will be given. Extensions must be approved by Professor Lopresti.
  - If you already consider yourself proficient in Unix and Perl programming, you may choose to skip the lectures marked with an asterisk (\*). Please skim the indicated reading, however, and review the lecture notes online in Blackboard.

| Date    | Topics   | Readings      | Activities |
|---------|--|---------------|------------|
| Tu 1/16 | Course introduction  |               |            |
| Th 1/18 | Intro to molecular biology<br><i>genetics and genomes, analyzing DNA</i>                               | IBA 3, BB&P 1 |            |
| Tu 1/23 | Intro to algorithms<br><i>correctness, recursion, iteration, time complexity</i>                       | IBA 2, BB&P 2 |            |
| Th 1/25 | Intro to Unix; Perl programming 1 *<br><i>getting started, control flow, variables, arrays, hashes</i> | BB&P 3-4      |            |
| Tu 1/30 | Perl programming 2 *<br><i>subroutines, scoping rules, file I/O</i>                                    | BB&P 5-6      | HW #1 out  |
| Th 2/1  | Sequencing (Prof. Marzillier)  | Reading TBA   |            |
| Tu 2/6  | Perl programming 3<br><i>pattern matching, regular expressions, sorting</i>                            | BB&P 7-8      |            |
| Th 2/8  | Restriction mapping<br><i>biology, full and partial digests, brute-force and practical algorithms</i>  | IBA 4.1-4.3   | HW #1 due  |
| Tu 2/13 | Motifs, search trees<br><i>regulatory motifs, profiles, search trees, motif-finding</i>                | IBA 4.4-4.9   | HW #2 out  |
| Th 2/15 | Genome rearrangements<br><i>biology, sorting by reversals, greedy and approximation algorithms</i>     | IBA 5         |            |

| <b>Date</b> | <b>Topics</b>  | <b>Readings</b> | <b>Activities</b>     |
|-------------|--|-----------------|-----------------------|
| Tu 2/20     | Sequence comparison & alignment 1  | IBA 6.1-6.7     |                       |
|             | <i>biology, comparison models, dynamic programming, global alignment</i>         |                 |                       |
| Th 2/22     | Sequence comparison & alignment 2  | IBA 6.8-6.10    | HW #2 due             |
|             | <i>local alignment, gap penalties, multiple alignment</i>                        |                 |                       |
| Tu 2/27     | Sequence comparison & alignment 3  | IBA 7           | HW #3 out             |
|             | <i>saving time and space, divide-and-conquer</i>                                 |                 |                       |
| Th 3/1      | Sequencing & assembly 1  | IBA 8.1-8.9     |                       |
|             | <i>biology, graph theory, shortest superstrings, sequencing by hybridization</i> |                 |                       |
| Tu 3/6      | Spring break   |                 |                       |
| Th 3/8      | Spring break   |                 |                       |
| Tu 3/13     | Sequencing & assembly 2  | IBA 8.10-8.15   |                       |
|             | <i>protein sequencing, spectral analysis</i>                                     |                 |                       |
| Th 3/15     | Genetic pattern matching 1   | IBA 9.1-9.5     | HW #3 due             |
|             | <i>repeat-finding, suffix trees</i>  |                 |                       |
| Tu 3/20     | Genetic pattern matching 2   | IBA 9.6-9.8     | HW #4 out             |
|             | <i>heuristics: FASTA and BLAST</i>   |                 |                       |
| Th 3/22     | Tools, datasets, and applications  | BB&P 17-18      |                       |
|             | <i>EMBL/GenBank, SWISS-PROT/PIR, ClustalW, BLAST</i>                             |                 |                       |
| Tu 3/27     | DNA microarrays (Prof. Marzillier)   | Reading TBA     |                       |
| Th 3/29     | Clustering for expression analysis   | IBA 10.1-10.4   | HW #4 due             |
|             | <i>biology, hierarchical clustering, k-means</i>                                 |                 |                       |
| F 3/30      |  |                 | Project proposals due |
| Tu 4/3      | Evolutionary trees 1   | IBA 10.5-10.7   | HW #5 out             |
|             | <i>biology, distance-based tree reconstruction, additive trees</i>               |                 |                       |
| Th 4/5      | Evolutionary trees 2   | IBA 10.8-10.11  |                       |
|             | <i>character-based tree reconstruction, parsimony (small and large)</i>          |                 |                       |
| Tu 4/10     | Proteomics (Prof. Marzillier)  | Reading TBA     |                       |
| Th 4/12     | No class: inauguration of President Gast   |                 | HW #5 due             |
| Tu 4/17     | RNA and protein structure prediction   | Reading TBA     |                       |
|             | <i>RNA secondary structure prediction, protein threading</i>                     |                 |                       |
| Th 4/19     | Bioethics  | Reading TBA     |                       |
| Tu 4/24     | History of the Genetic Code  | Reading TBA     |                       |
| Th 4/26     | Student final project presentations  |                 |                       |
| F 4/27      |  |                 | Final projects due    |

**University Policy on Disabilities** If you have a disability for which you are or may be requesting accommodations, please contact both your professor and the Office of Academic Services, Room 212, University Center or call (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.

**Academic Integrity** The work you submit in CSE 308-408 must be entirely your own. While we encourage you to discuss basic concepts and strategies with friends and classmates, the copying or sharing of solutions to homework or programming assignments, or of final papers or projects, is never acceptable. Such cases will be referred to the University Committee on Discipline and, if found guilty, you may be given the failing grade WF in the course.

You should keep in mind that computer programs exhibit an individual's "style" just as much as other forms of authorship. Changing variable names, editing comments, or making other trivial updates in an attempt to hide plagiarism is rarely effective.

If you have questions about this policy at any point throughout the semester, ask. It is far better to be safe than sorry when your academic career may be on the line.