School of Computer Science
Tel Aviv University
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Algorithms for Molecular Biology

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http://www.math.tau.ac.il/~rshamir/algmb/algmb00.html

Instructor: Prof. Ron Shamir

TA: Itsik Pe'er

Time: Fall Semester, Mondays 4-7pm, Shenkar 222

Office hours:
Ron Shamir: Thursdays 5-6pm Schreiber 014.
Itsik Pe'er: Mondays 3-4 Schreiber 011.

Course Outline

This course will discuss algorithms for some important computational problems in Molecular Biology. In particular, we shall study problems that are pertinent to the Human Genome Project and to the so-called "post-Genome era".

We shall study exact algorithms for those problems which can be solved efficiently, as well as complexity, approximation algorithms and heuristics for the more difficult problems. We shall concentrate on discrete realistic models for the biological problems. Many biological examples will be presented. The subjects that will be covered include:

- sequence comparison
- sequence alignment
- hidden Markov models
- gene finding
- physical mapping
- bioinformatics tools and resources (guest lecture - Dr. Racheli Zakarin)
- phylogeny
- genome rearrangement
- DNA chips
- structural computational biology (guest lecture - Prof. Haim Wolfson)
- gene expression
- gene networks

- proteomics

Prerequisites

This is a graduate course which is open also to third year undergraduates.
No prior knowledge in biology is needed. The required background will be given during the course.

Course assignments and grading

Each student (or a pair of students, depending on course enrollment) will scribe (i.e., to prepare lecture notes) one lecture. The notes should be prepared in LaTeX and returned to the TA *within a week* after the lecture. They will be corrected by the TA or the lecturer, and then revised by the student and returned in final form *within five days* after the students were informed of the corrections. Notes should contain all the material presented in class, written in clear and accurate fashion, as well as the relevant references. Using figures and diagrams when necessary in order to clarify things is recommended. In most lectures, the scribes of lectures given in previous years can be used as a basis. Some of those require little update, but others may need substantial revisions!

There will be no final exam. The exercise sets will serve as a take home exam. Solutions should be done **independently** by each student and without help from others. Use of books and articles for the solutions is allowed and will not affect the grading, but the sources should be noted in the solutions. Assignments are a mixture of theoretical, web-based and programming work. Most assignments contain built-in bonus, so by completing some 85-90% worth of all exercises you will be given full score.

Final grade: 75% from exercise sets + 25% from scribe.

Scribe grade will be reduced by one point (out of the maximum of 25) for each late day past each of the two deadlines. This is done in order to ensure that scribes are completed and made available to the whole group promptly.

Course information, handouts and lecture notes from previous years can be accessed through the course homepage.