School: Efi Arazi School of Computer Science M.Sc.

Algorithms in Computational Biology

Lecturer:

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Teaching Assistant:

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Course No.: 3571  Course Type: Elective  Weekly Hours: 3  Credit: 3

Course Requirements: Final Exam

Group Code: 211357101  Language: English

Prerequisites:

Prerequisite:

52 - Calculus I
53 - Calculus II
54 - Linear Algebra I
55 - Linear Algebra II
56 - Discrete Mathematics
59 - Data Structures
69 - Logic And Set Theory
77 - Algorithms
109 - Introduction To Probability
417 - Introduction To Computer Science
Course Description

Sequence alignment:
- Dynamic programming algorithms for global and local pairwise sequence alignment
- Heuristics for saving time and space implemented in the BLAST algorithm
- Scoring functions for alignment

Probabilistic models:
- Markov models and hidden Markov models (HMMs)
- Inference algorithms in HMMs – forward / backward / Viterbi
- The Baum Welch algorithm for learning parameters of the HMM
- The Expectation-Maximization (EM) algorithm

Phylogenetic Inference:
- Maximum Parsimony
- Probabilistic substitution models
- Distance-based phylogenetic reconstruction

Course Goals
The course introduces classical problems and algorithms in computational biology. It connects concepts in theoretical computer science with practical problems in biological research.

Grading
- 40% homework assignments (5 assignments total)
- 60% final exam

Learning Outcomes
- Dynamic programming algorithms for sequence alignment
- Hidden Markov Models (HMMs)
- Algorithms for phylogenetic inference
Lecturer Office Hours

Thursday, 17:00 (or by e-mail appointment) via Zoom

Reading List

   http://books.google.co.il/books/about/Biological_sequence_analysis.html?id=R5P2GJvijQC&redir_esc=y

2. **Inferring Phylogenies.** Joseph Felsenstein, Sinauer Associates, Sunderland, Massachusetts
   http://www.sinauer.com/inferring-phylogenies.html