



# Course program and reading list

Semester 1 Year 2024

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

## Algorithms in Computational Biology

### Lecturer:

Prof. Ilan Gronau [ilan.gronau@runi.ac.il](mailto:ilan.gronau@runi.ac.il)

### Teaching Assistant:

Ms. Tal Bamberger [tal.bamberger@post.runi.ac.il](mailto:tal.bamberger@post.runi.ac.il)

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

Course Requirements :	Group Code :	Language:
Final Paper	241357100	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
  - 3141 - Machine Learning from Data
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## 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

### Hidden Markov Models (HMMs):

- Markovian processes and definition of 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
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## 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.

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## Grading

- 70% homework assignments (4 assignments)
  - 30% concluding home assignment
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## Learning Outcomes

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

Tuesday, 17:00 in my office (C127), and via Zoom.

See details and link on Piazza: <https://piazza.com/runi.ac.il/fall2023/cs3571/staff>

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## Additional Notes

Course material slightly modified due to condensed 10-week semester.

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## Reading List

1. **Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids.**  
Richard Durbin (Editor), S. Eddy, A. Krogh, G. Mitchison (Contributor), Cambridge University Press, Cambridge, UK.  
[http://books.google.co.il/books/about/Biological\\_sequence\\_analysis.html?id=R5P2GJvjqC&redir\\_esc=y](http://books.google.co.il/books/about/Biological_sequence_analysis.html?id=R5P2GJvjqC&redir_esc=y)
2. **Inferring Phylogenies.** Joseph Felsenstein, Sinauer Associates, Sunderland, Massachusetts  
<http://www.sinauer.com/inferring-phylogenies.html>