

221. 4424 Algorithms in Comparative Genomics

Time: Monday 14:00-17:00], Madrega 1006

Instructor: Prof Sagi Snir, **Email:** , ssagi@research.haifa.ac.il

Office Hours: [Thursday] [14:00-16:00], Room [m14], [58774]

Course Level: (BA+MA)

Course Type & Format: [Elective], [Lecture]

Number of Hours/Credits: 3

Prerequisites: Courses in algorithms and discrete mathematics

Course Overview (Short Abstract):

In light of the genomic revolution and the availability of immense genomic data, fundamental questions that only recently seemed unsolvable, are now being studied intensively. This has given rise to basic computational issues associated with such questions. Specifically, the COVID-19 pandemic has brought back evolutionary questions to the top of research agenda.

The course deals with algorithmic issues and methods that arise from comparative genomics that analyze molecular biological sequences. The approach to the material will be algorithmic, meaning that the computational aspects of the various problems (complexity, approximations, heuristics and applications) will be studied

Learning Outcomes (What are the skills, abilities, or major concepts a student is expected to acquire in this course?) – At the end of the course students will be able to:

1. Introduction to general molecular Biology and the Central Dogma
2. Introduction to general Computational Biology
3. Introduction to general theoretical Computer Science (complexity, approximations, heuristics and applications)

Assessment (Assessment Method and Grade Composition):

Attendance – 0%

[Exam] – 80-100%

[Homework assignments] – [0-20]%

[Requirement] – [Number]%

Week-by-Week Content and Assignments:

Wee k #	Topic	Assignment
1	Dynamic programming	
2	Sequence alignment	

3	Genomic distances	
4	Models of sequence evolution	
5	Phylogenetic tree construction	
6	Gene tree / species tree reconciliation	
7	Genome rearrangement	
8	Prediction of RNA folding	
9	Viral evolution	
10		
11		
12		
13		
14		

Reading List:

- Dan Gusfield **Algorithms on Strings, Trees and Sequences**, Cambridge University Press; 1997
- Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison, **Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids**, Cambridge University Press; 1999
- Neil C. Jones, Pavel A. Pevzner, **An Introduction to Bioinformatics Algorithms**, The MIT Press, 2004