



Syllabus

BIOINFORMATICS AND STRUCTURAL BIOCHEMISTRY - 71437

Last update 27-02-2022

HU Credits: 3

Responsible Department: Biochemistry & Food Sciences

Academic year: 0

Semester: 2nd Semester

Teaching Languages: Hebrew

Campus: Rehovot

Course/Module Coordinator: Prof. Masha Niv

Coordinator Email: masha.niv@mail.huji.ac.il

*Coordinator Office Hours: Please send email for appointment or contact via
0546575622*

Teaching Staff:

*Prof Masha Niv,
Mr. Yaron Benshoshan*

Course/Module description:

Basic concepts in bioinformatics, sequence and structure of biological molecules. Sequence comparison, prediction of protein structure and function. Protein/protein interaction analysis.

Providing familiarity with bioinformatic tools, the use of bioinformatics in research, databases and web servers. Experience in different analysis during class exercises

Course/Module aims:

The goal of the course is to introduce basic concepts in bioinformatics and to use bioinformatics tools that are available on the web. The course will focus on sequence analysis, structure prediction and protein interactions.

Learning outcomes - On successful completion of this module, students should be able to:

On successful completion of this module, the students should be able to run BLAST for sequence searches, use sequence alignment tools and explain the meaning of phylogenetic trees. The students will know how to visualize and carry out basic analysis of 3D structures of protein. The students should be able to suggest suitable bioinformatics tools to representative biological questions.

Attendance requirements(%):

full attendance is expected

Teaching arrangement and method of instruction: lectures and tutorials

Course/Module Content:

*Introduction
Database Searches
Sequence search, pairwise alignment
Pairwise sequence alignment
Multiple sequence alignments
Motif searches
Regular expressions
PSSM
Phylogenetic trees
Primary, secondary, 3D structure
Levinthal paradox, protein folding
Protein structure determination (NMR, Xray)
PDB databank of structures, folds*

*Protein Structure prediction competition(CASP(
Homology modeling
Protein-protein interactions (physical and co-expression maps, network)
Protein/protein docking methods
Docking, protein-protein, protein-small molecules*

Required Reading:

Papers that appear in the Moodle site of the course

Additional Reading Material:

Appears in Moodle

Course/Module evaluation:

End of year written/oral examination 0 %

Presentation 0 %

Participation in Tutorials 0 %

Project work 0 %

Assignments 30 %

Reports 0 %

Research project 40 %

Quizzes 30 %

Other 0 %

Additional information: