The Hebrew University of Jerusalem

Syllabus

BIOINFORMATICS AND STRUCTURAL BIOCHEMISTRY - 71437

Last update 27-02-2022

HU Credits: 3

Degree/Cycle: 1st degree (Bachelor)

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 cocepts in bioinformatics, sequence and strucute of biological molecules. Sequence comparison, prediction of protein srtucture and function. Protein/protein interaction analysis.
Providing familiarity with bioinformatic tools.the use of bioinformatic in research. databases and webservers. Experience in different analysis during class exercise

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 alignments 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: