



The Hebrew University of Jerusalem

Syllabus

BIOINFORMATICS AND STRUCTURAL BIOCHEMISTRY - 71437

Last update 24-02-2015

HU Credits: 3

Degree/Cycle: 1st degree (Bachelor)

Responsible Department: Biochemistry and nutrition science

Academic year: 3

Semester: 2nd Semester

Teaching Languages: Hebrew

Campus: Rehovot

Course/Module Coordinator: Dr. Masha Niv

Coordinator Email: Masha.Niv@mail.huji.ac.il

Coordinator Office Hours: sunday 11:30-12:30

Teaching Staff:

Prof Masha Niv
Ayana Wiener

Course/Module description:

Basic concepts in bioinformatics, sequence and structure of biological molecules. Sequence comparison, prediction of protein structure and function. Protein/protein and DNA/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(%):

100 in tutorials

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:

Essential bioinformatics / Jin Xiong:
Introduction to bioinformatics / Arthur M. Lesk
Bioinformatics for dummies By Jean-Michel Claverie Ph. D.,
Cedric Notredame Ph.D.
Introduction to Protein Structure, John Tooze
Understanding bioinformatics / Zvelebil & Baum
Bioinformatics, sequence and genome analysis/ D.Mount

Course/Module evaluation:

End of year written/oral examination 40 %
Presentation 0 %
Participation in Tutorials 10 %
Project work 0 %
Assignments 40 %
Reports 0 %
Research project 10 %
Quizzes 0 %
Other 0 %

Additional information:

None