The Hebrew University of Jerusalem

Syllabus

BIOINFORMATICS AND STRUCTURAL BIOCHEMISTRY - 71437

Last update 05-03-2019

<u>*HU Credits:*</u> *3*

<u>*Degree/Cycle:*</u> *1st degree (Bachelor)*

<u>*Responsible Department:*</u> *Biochemistry & Food Sciences*

<u>*Academic year:*</u> *0*

<u>*Semester:*</u> *2nd Semester*

<u>*Teaching Languages:*</u> *Hebrew*

<u>*Campus:*</u> *Rehovot*

<u>*Course/Module Coordinator:*</u> *Prof. Masha Niv*

<u>Coordinator Email:</u> masha.niv@mail.huji.ac.il

<u>*Coordinator Office Hours:*</u> *I will meet you gladly, please send email for appointment*

<u>Teaching Staff:</u>
  Prof Masha Niv
Mr.

<u>Course/Module description:</u>
  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

<u>Course/Module aims:</u>
  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.

<u>Learning outcomes - On successful completion of this module, students should be
able to:</u>
  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.

<u>Attendance requirements(%):</u>
  100% attendance of tutorials

Teaching arrangement and method of instruction: lectures and tutorials

<u>Course/Module Content:</u>
  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 10 %
Project work 10 %
Assignments 10 %
Reports 0 %
Research project 50 %
Quizzes 20 %
Other 0 %

Additional information: