



## *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](mailto:Masha.Niv@mail.huji.ac.il)

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

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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

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*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*