The Hebrew University of Jerusalem

Syllabus

3D DATA PROCESSING IN STRUCTURAL BIOLOGY - 76562

Last update 03-03-2019

HU Credits: *3*

Degree/Cycle: *1st degree (Bachelor)*

Responsible Department: *Computer Science & Computational Biology*

Academic year: *0*

Semester: *2nd Semester*

Teaching Languages: *Hebrew*

Campus: *E. Safra*

Course/Module Coordinator: *Dina Schneidman*

Coordinator Email: *dina.schneidman@mail.huji.ac.il*

Coordinator Office Hours:

Teaching Staff:
Dr. Dina Schneidman

Course/Module description:
Introductory course to computational structural biology. The course will focus on general methods for processing three-dimensional datasets, such as pattern recognition, surface and volume matching.
We will learn how these algorithms are used in Computational Structural Biology for structural modeling of macromolecules.

Course/Module aims:
Review of methods for processing 3D data with applications in structural modeling of macromolecules.

Learning outcomes - On successful completion of this module, students should be able to:
The course will give the students the tools to read and understand state-of-the-art papers in computational structural biology. In addition the goal is to learn to develop new algorithms for structural modeling of macromolecules, as well as 3D object recognition.

Attendance requirements(%):
100%

Teaching arrangement and method of instruction: Frontal teaching
Small groups guidance for final projects

Course/Module Content:
1.Introduction to macromolecular structure
2.Pattern recognition by point matching, structural alignment of proteins (pairwise and multiple)
3.Pattern recognition by surface matching, algorithms for assembly of macromolecular complexes (pairwise and multiple)
4.Volumetric matching algorithms, structural modeling with Electron Microscopy (EM) data
5.Structural modeling with distance distribution from Small Angle X-ray Scattering (SAXS)experiments
6.Structural modeling with distance restraints based on cross-linking mass

spectrometry datasets
7.Integration of multiple datasets
8.Handling uncertainty in the data

Required Reading:
N/A

Additional Reading Material:

Course/Module evaluation:
End of year written/oral examination 0 %
Presentation 0 %
Participation in Tutorials 10 %
Project work 0 %
Assignments 20 %
Reports 0 %
Research project 70 %
Quizzes 0 %
Other 0 %

Additional information:
No biological background is needed. The course is focused on general methods for 3D datasets with applications in Structural Biology.
The grade consists mainly of the research project (70%), 3-4 exercises (20%) and class participation (10%).