



## Syllabus

# 3D DATA PROCESSING IN STRUCTURAL BIOLOGY - 76562

*Last update 03-03-2019*

HU Credits: 3

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](mailto:dina.schneidman@mail.huji.ac.il)

Coordinator Office Hours:

Teaching Staff:

Dr. Dina Schneidman

Course/Module description:

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*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:*

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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%).*