MOLECULAR MODELING AND SIMULATION

Basic Information

This is a course, which contributes to MSc award in Biology

Title of the Academic Program	Master's Degree Programs in English "Medical and Biological Physics"
Type of the course	elective
Course period	Fall semester, 1 semester (16 weeks)
Study credits	4 ECTS credits
Duration	144 hours
Language of instruction	English
Academic requirements	- BSc degree in Biology, Physics, Biophysics, Chemistry , Biochemistry, Environmental Sciences or equivalent (transcript of records), - good command of English (certificate or other official document)

Course Description

The practical course "Molecular Modeling and Simulation" is designed for students who wish to master specific practical skills allowing to perform basic types of molecular modeling simulations and use bioinformatics tools for various types of analysis of biological data. The course acquaints students with the principles of sequence and structural alignment, homology modeling, visualization software (VMD, Chimera, Pymol), protein-ligand docking, calculation of electrostatic potential of biomolecules using APBS, molecular mechanics, and basics of molecular dynamics.

Course Aim

The aim of the course is to enable students to acquire knowledge and skills with which they can independently do basic computer analyzes of the structure and function of biomolecules.

Course Objectives

The course objectives are:

- to familiarize students with the basic principles of molecular modeling and simulation,

- to enable students to apply various computational approaches for studying the structure and function of small molecules and large biomolecules,

- to enable students to visualize and analyze structures of biomolecules and the results of molecular simulations.

Learning Outcomes of the Course (module)[1]

By the end of the course, students will be able to:

1. Independently search databases containing molecular structures, and identify different types of computational records of molecular structures;

2. apply specialized software appropriate to various molecular modeling tasks, including structure optimisation, calculation of the electrostatic potential of a biomolecule, molecular docking, simulation of molecular dynamics trajectory;

3. combine different methods to solve structural bioinformatics and molecular modeling problems;

4. plan a computer simulation of a biomolecular system to study its behavior and properties.

Teaching and Learning Methods

The course implies interactive practical works, where students carry out a set of computational experiments and discuss each step with the lecturer. At the beginning of each practical session a brief summary of the theory and computational details will be provided.

Course Structure

Learning Activities	Hours
Lectures	-
Practice sessions	36
Self-study Assignments	72
Final Exam (including preparation)	36
Total study hours	**144**

Course Outline

Week	Learning activities	Assignments	Hours
1-2	Mini-lecture “Introduction to Molecular Modeling and	Home work “Analysis of	4/9

	Visualization of Biomolecules” Practice “Organization of PDB documents and algorithms for displaying molecules on computers.”	protein structural domains and active site using VMD”	
3-4	Mini-lecture “Sequence alignment” Practice “Identification of functional regions using sequence alignment”	Home work “Local sequence alignment”	4/9
5-6	Mini-lecture “Homology modelling and the reconstruction of proteins” Practice “SWISS-MODEL, MODELLER and Alphafold”	Home work “Homology modeling of your favorite enzyme”	4/9
7-8	Mini-lecture “Continuum electrostatics” Practice “Electrostatic potential of an enzyme”	Home work “Electrostatic potential of an enzyme and its active site”	4/9
9-10	Mini-lecture “Protein-ligand docking” Practice “Docking of a small molecule into the active site of an enzyme using AutoDock Vina”	Home work “Protein-ligand interaction”	6/9
11-12	Mini-lecture “Molecular modeling I” Practice “Building molecules and optimizing their structure”	Home work “Analysis of conformations using Pymol”	4/9
13-14	Mini-lecture “Molecular modeling II” Practice “Molecular dynamics of small molecules”	Home work “Analysis of MD trajectory”	6/9
15-16	Mini-lecture “Protein stability” Practice “Analysis of protein structure stability”	Home work “Analysis of PONDR results”	4/9
	Final Exam		**36**

Course Instructors, Contact information

Anna A. Deeva
PhD in Biophysics, research fellow and assistant professor at the Biophysics Department, School of Fundamental Biology and Biotechnology, Siberian Federal University, Krasnoyarsk, Russia
Email: adeeva@sfu-kras.ru

Lev A. Sukovaty
Junior research associate at the Biophysics Department, School of Fundamental Biology and Biotechnology, Siberian Federal University, Krasnoyarsk, Russia
Email: lsukovaty@sfu-kras.ru

Assessment

The overall course percentage grade consists of the grades for eight lab reports and home work assignments. Students are expected to prepare at least six lab reports and upload them to E-learning SibFU website. Lab reports should be prepared in accordance with the template and comprehensive answers are given to concept testing questions.

Attendance Policy

Since almost each class includes material, which is not presented in literature in compact form, and conducting computational experiments with specific software, attendance of all of them is obligatory.

Web page of the course

The webpage of the course is available through E-learning SibFU web site: https://e.sfu-kras.ru/course/view.php?id=34943. You must be logged in to access

this course. Course Guide and all accompanying materials are also available at the course web-page.

Core reading

1. Van Gunsteren W. F. et al. Biomolecular modeling: goals, problems, perspectives //Angewandte Chemie International Edition. – 2006. – Т. 45. – №. 25. – С. 4064-4092.

2. Biomolecular Modeling and Simulation: A Field Coming of Age, T. Schlick, R. Collepardo-Guevara, L. A. Halvorsen, S. Jung and X. Xiao, Quarterly Reviews of Biophysics, 44, 191-228 (2011)

3. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (Methods of Biochemical Analysis, 43) Andreas D. Baxevanis and B. F. Francis Ouellette (Editors) 2nd Edn: John Wiley & Sons, New York; 2001; ISBN 0-471-38390-2; 470 pp.

4. Kollman PA, Massova I, Reyes C, et al. (December 2000). "Calculating structures and free energies of complex molecules: combining molecular mechanics and continuum models". Acc Chem Res. 33 (12): 889–97.

5. Matthias G. Ullmann and Elisa Bombarda, Chapter 6, Continuum Electrostatic Analysis of Proteins: http://www.bisb.uni-bayreuth.de/PDF/Ullmann2014-book.pdf

6. Biomolecular Electrostatics and Solvation: A Computational Perspective,P. Ren, J. Chun, D. G. Thomas, M. J. Schnieders, M. Marcho, J. Zhang and N. A. Baker, Quarterly Reviews of Biophysics, 45, 427-491 (2012)

7. “Vina Tutorial” on the official Web page: http://vina.scripps.edu/tutorial.html

8. Introduction to Molecular Dynamics Simulation, M. P. Allen, Computational Soft Matter, NIC Series, 23, 1-28 (2004)

9. Babu M. M. The contribution of intrinsically disordered regions to protein function, cellular complexity, and human disease //Biochemical Society Transactions. – 2016. – Vol. 44. – №. 5. – P. 1185-1200.

Facilities, Equipment and Software

Linux machines with the required preinstalled software are available at the Biophysics Department.