UNIVERSITÀ
DEGLI STUDI DI MILANO-BICOCCA

COURSE SYLLABUS

Computational Tools For Bioinformatics

2021-1-F0802Q045

Aims

The goal of the course is to enable master students to get deep knowledge of the most popular computational methodologies employed in the context of structural bioinformatics. More specifically, both static properties and dynamic behavior of biological macromolecules will be addressed and characterized in detail. The course also aims to give a comprehensive survey of the implementation of such methodologies in the most popular software and computational platforms.

Knowledge and understanding. At the end of the course, the student will:
1) know the computational strategies generally used to discern structure-function relationships in biological systems.
2) comprehend the algorithms on which such computational strategies rely.
3) understand the difference between molecular mechanics and quantum mechanics, both from theoretical and practical standpoints, and their role in the study of biological macromolecules.
4) know in detail what conformational search, molecular docking (protein-ligand and protein-protein) and molecular dynamics are.

Applying knowledge and understanding.
At the end of this training activity, the student will be able to apply the gained knowledge, using it to recognize (theoretically and practically) potentialities and (eventual) limits of the bioinformatic strategies seen during the course.

Making judgments.
At the end of the course, the student will be able to choose the most suitable computational method to address a specific biological-chemical issue. He will be also able to critically analyze results obtained from computational calculations and to interpret them properly.

Abilità comunicative.
This training activity will allow the student to express himself adequately, and with scientific language, in the explanation of the various addressed topics.

Learning skills.
At the end of the course the student will dispose of all the tools that are necessary to apply his knowledge to address issues others than those presented during the course. He will be able to plan bioinformatic calculations on the basis of his gained knowledge, together with skills of literature reading and understanding.

Contents

1.Determination and computational modelling of protein structure.
2.Relatioship between molecular structure and energy.
3.Molecular Mechanics (MM).
4.Global and local search algorithms
5.Molecular Docking
6.Molecular Dynamics.

Detailed program

1.Determination and computational modelling of protein structure: survey on the experimental techniques used in the characterization of protein 3D structure and how to handle pdb files; introduction to bioinformatics.
2.Relatioship between molecular structure and energy: structure-energy relationship in molecules; the harmonic approximation; molecular conformation, Z-matrix and degrees of freedom; the PES and the mathematical definition of stationary points; hints on linear algebra.
3.Molecular Mechanics (MM): differences between molecular mechanics and quantum mechanics, both in theory and practice; hybrid methods QM-MM; the functional forms of the Force Field and its parametrization; mathematic description of the forces involved in molecular interactions; solvation models;
4.Global and local search algorithms: local search algorithms (of zero, first and second order); global search algorithm in the conformational sampling of the PES (both stochastic and systematic).
5.Molecular Docking: the recognition process between macromolecules and exogeneous molecules (drugs or enzymatic substrates); the role of molecular docking in the drug design process; the “architecture” of molecular docking; search algorithms and scoring functions; potential energy grid; covalent docking and its utility; macromolecule-macromolecule docking and its utility; survey on the most popular software and web server for molecular docking; successes and limits of the technique; results rationalization (also thanks to practical exercises seen/done during classes).
6.Molecular Dynamics: classification of MD techniques; application areas and limits; statistical thermodynamics, thermodynamic ensambles; Verlet integration; thermostats vs barostats; trajectories analysis and simulation interpretation.

Prerequisites

Background.
Specific knowledge of other topics is not required. It is preferable being motivated toward in silico investigations of molecular basis of biochemical processes.

Prerequisites. None

Teaching form

Classroom lectures including training in a series of softwares and web servers.
Teaching language: italian.

Textbook and teaching resource

Slides. Available at the e-learning platform of the course.
Handouts. Available at the e-learning platform of the course.
Bibliography. Selected scientific papers and reviews
Textbooks
 “Bioinformatica” , Stefano Pascarella, Alessandro Paiardini
"Introduction to Computational Chemistry", Frank Jensen (chapter 2).

Semester

Second semester

Assessment method

Written examination: preparation of a detailed report regarding the practical exercises seen and/or done during classes, followed by oral examination.

Office hours

Contact: on demand by email to the lecturer.