UNIVERSITÀ
DEGLI STUDI DI MILANO-BICOCCA

COURSE SYLLABUS

Computational Biology

2324-1-F0601Q095

Aims

The course of Computational Biology aims to give the theoretical knowledge and the practical skills for the usage of open source computational tools for search and analysis of biological data, as for protein structure and function prediction.

Knowledge and understanding. To acquire theoretical and methodological knowledge of computational resources, as open source web portal, database and tools for search and analysis of biological data.

Ability to apply knowledge and understanding. To be able to correctly use computational tools to collect and analyze biological data, and to recognize their salient aspects.

Autonomy of judgment. To be able to recognize the context for appropriate application of the computational tools learned during the course. To develop a critical vision for interpreting the results achieved.

Communication skills. To be able to elaborate computational data and describe them in an appropriate language with the correct technical terms.

Learning skills. To be able to correctly apply a computational analysis in contexts different from those used during the practical laboratory experience.

Contents

The course will explain the founding principles of the main algorithms devoted to protein structure and function prediction on the basis of the amino acid sequence and the procedures to extract information from dedicated databases.

Detailed program

Sequence databases
Global and heurystic sequence alignments
Multiple sequence alignments
Structure databases
Structural alignments
Molecular evolution
General issues in structural and functional prediction
Structural order/disorder prediction
Secondary structure prediction
Homology modeling
Fold recognition
De novo prediction
Structural genomics
Functional genomics

Prerequisites

Bases of molecular biology, protein biochemistry and molecular evolution

Teaching form

Frontal lesson and informatics laboratory exercises. Attendance to the laboratory is compelling for at least 75% of the scheduled hours.

Textbook and teaching resource

Slides shown at lessons will be made available on the e-learning platform.
Scientific papers for each topic will be given. They have to be used for exam preparation.
Suggested textbooks:
- Orengo et al. "Bioinformatics: Genes, Proteins and Computers" Bios Scientific Publishers Limited, 2002
- Durbin et al. "Biological sequence analysis" Cambridge University Press, 1998
- Tramontano "Bioinformatica" Zanichelli, 2002

Semester

Second semester

Assessment method

Composition of a project developed according to the laboratory exercises. Given a nucleotide sequence, the student is asked to individuate and characterize the encoded protein in terms of structure and function. The presentation is followed by a discussion dealing also with the theoretical aspects. The evaluation will focus on the basic notions acquired, the quality of the oral presentation, understanding of the specific matter, knowledge of methods and techniques, critical interpretation of the results, the capability to connect the different topics treated in the course, and the skills in facing a research project on protein structure and function prediction.

Office hours

Upon request by e-mail to lecturer

Sustainable Development Goals

GOOD HEALTH AND WELL-BEING