



UNIVERSITÀ  
DEGLI STUDI DI MILANO-BICOCCA

## COURSE SYLLABUS

### Computational Biology

2425-1-F0601Q124

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#### 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 heuristic 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 LESSONS

Seventeen 2-hour lectures + one 1-hour lecture composed by:

- a section of delivered didactics, focused on the presentation-illustration of contents by the lecturer.
- a section of interactive teaching, including teaching interventions supplementary to delivered didactic activities, short interventions by trainees, demonstrations of practical applications (case study, journal club, etc.).

Didactic activities are conveyed by means of face-to-face lectures

### LABORATORY

Four 2-hour laboratory activities + two 1-hour laboratory activities, delivered by interactive teaching

Attendance is compulsory.

## 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

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