



UNIVERSITÀ  
DEGLI STUDI DI MILANO-BICOCCA

## SYLLABUS DEL CORSO

### Bioinformatica

2122-1-F0901D043-F0901D087M

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#### Aims

The main objective of the module is to introduce students to the main problems related to the computational analysis of biological sequences (DNA, RNA, proteins). Students will acquire the basic knowledge and concepts related to computational methods and techniques for collecting, managing and analyzing data in molecular biology, such as sequence data generated by Next Generation Sequencing (NGS) technologies, and will master the main computational tools necessary to extract information of interest for biomedical research from the main sequencing databases.

#### Contents

Introduction to bioinformatics: motivations, problems and methodologies.

Data generation: NGS technologies

Organization and management of data: the main databases; access, query, data entry

Data analysis: genome reconstruction and annotation; sequence comparison: global, local and multiple alignment algorithms; reconstruction of phylogenies; transcriptome analysis.

#### Detailed program

1. Data management in life sciences
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Basic knowledge of computer science and molecular biology

## **Teaching form**

Standard classes (if possible)

## **Textbook and teaching resource**

M. Helmer Citterich, F. Ferrè, G. Pavesi, C. Romualdi, G. Pesole, Fondamenti di bioinformatica (Zanichelli editore)

Teachers notes

## **Semester**

First semester

## **Assessment method**

Oral exam at the end of the course, on all the topics covered in the course. The evaluation will take into account the specific knowledge of the topics, the clarity of exposition and the ability to connect the computational tools to the biological problems to be solved.

## **Office hours**

To be defined with the student by email contact

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