



UNIVERSITÀ  
DEGLI STUDI DI MILANO-BICOCCA

## COURSE SYLLABUS

### Bioinformatics

2425-1-F0601Q114

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#### Aims

The course is focused on genomics technologies, on how they are used to generate omics data, and on the fundamental concepts and pitfalls in the analysis of these data. The course focuses on technologies relying on high-throughput sequencing approaches. Particular emphasis will be devoted to the study of genome-wide gene expression programs.

Knowledge and understanding.

Students will familiarize with the key genomic technologies and data types. They will learn good practise and key workflows in the field of genomics. Eventually, they will acquire key concepts in the field of bioinformatics and genomics, and they will familiarize with selected resources to which they shall reference in case of need during their future research activities.

Applying knowledge and understanding.

Students will be able to apply the acquired knowledge in other courses and in laboratory experiences and to use the comprehension skill in subsequent studies and/or research activities.

Making judgments.

Students will be able to process what they have learned and be able to recognize situations and problems in which the acquired knowledge can be used.

Communication skills.

At the end of the course, students will be able to express themselves appropriately in the description of issues related to genomics and bioinformatics by using language properties, as well as self-confidence.

Learning skills

At the end of the course, students will be able to survey the scientific literature related to the topics covered and will be able to analyse, apply and integrate the acquired knowledge with what learned in related courses.

## Contents

1. Genomics through high-throughput sequencing
2. Profiling of gene expression programs through RNA-seq
3. Determinants of gene expression programs (ChIP-seq and RIP-seq for regulatory factors, epigenetic marks, and RNA modifications)
4. Dynamics of RNA metabolism
5. The DNA 3D organization
6. The mutational landscape
7. Genomics at the single cell level
8. Integrative genomics
9. First steps as a bioinformatician
10. Key online resources

## Detailed program

1. Genomics through high-throughput sequencing: (i) Short reads sequencing (Ion Torrent, Illumina), (ii) Long reads sequencing (Pacific Biosciences, Oxford Nanopore Technologies)
2. Profiling of gene expression programs through RNA-seq: (i) Experimental design, (ii) Quality checks, (iii) Key analysis steps, (iv) Absolute vs differential expression, (v) Alternative splicing
3. Studying the determinants of gene expression programs: (i) Binding of regulatory factors to chromatin, (ii) Epigenetic marks, (iii) RNA modifications, (iv) Chromatin and RNA immunoprecipitation sequencing (ChIP-seq and RIP-seq)
4. Dynamics of RNA metabolism: (i) Nascent RNA, (ii) Post-transcriptional regulation, (iii) RNA polymerase life cycle
5. The DNA 3D organization
6. The mutational landscape
7. Genomics at the single cell level
8. Integrative genomics: (i) How to identify publicly available omics data, (ii) Pitfalls in the integration of heterogeneous omics data
9. First steps as a bioinformatician: (i) R-studio / Bioconductor, (ii) Python, (iii) The Unix shell, (iv) Galaxy
10. Key online resources: (i) Training / education, (ii) Genome-browsers, (iii) Online analysis tools

## Prerequisites

Background: basic notions of Molecular Biology.

Prerequisites: none

## Teaching form

21 x 2 hours-lectures composed by:

- a section of delivered didactics (Didattica erogativa, DE) focused on the presentation-illustration of contents by the lecturer
- a section of interactive teaching (Didattica Interattiva, DI) including teaching interventions supplementary to delivered didactic activities and short interventions by trainees.

Didactic activities are conveyed by means of face-to-face lectures.  
Teaching language: Italian.

## **Textbook and teaching resource**

Selected scientific papers, slides, and recording of the lessons will be available at the e-learning platform of the course.

Recommended textbooks:

- M.H. Citterich et al. "Fondamenti di Bioinformatica" Zanichelli

## **Semester**

Second semester

## **Assessment method**

Oral examination. Students will be asked to discuss a scientific paper on one of the topics covered during the course, followed by a conventional query on the course content. The ability to appropriately describe the scientific results, as well as their critical analysis will be positively evaluated.

## **Office hours**

By appointment through e-mail request to the lecturer.

## **Sustainable Development Goals**

GOOD HEALTH AND WELL-BEING

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