UNIVERSITÀ
DEGLI STUDI DI MILANO-BICOCCA

COURSE SYLLABUS

Data and Computational Biology

2627-2-F1802Q118

Aims

The "Data and Computational Biology" course for the master (laurea) degree will give students the opportunity to acquire knowledge about some of the most important techniques used in the field. The course will primarily focus on biological systems modeling and on the integration of experimental data (gene-expression, proteomics, sequencing). The course will also present some of the current research activities of the DCB lab, with special regard to intestinal crypts modeling and the analysis of tumors based on "Single-cells" analysis techniques.

Contents

The course is composed of three main parts/topics.

- Introduction to Biology and Biochemical Network Modeling
- Modeling and Simulation of Biological systems.
- Data Analysis of biomedical phenomena, with special attention to oncological progression phenomena.

Detailed program

The syllabus listed hereafter may be subject to changes. The topics list is long and may or may not be covered in its completeness; new topics may be added during in the syllabus as needed.

- Representations of biological systems: models and computational issues.
- Model databases and and metabolic, regulatory, and intra- and intercellular signaling networks (e.g., BioModels and KEGG); SBML, KGML and CellML formats.
- Simulation systems for metabolic, regulatory and intra- and intercellular signaling networks.

- Gillespie algorithm and variants: limits and relationship with Montecarlo methods.
- Spatio-temporal models: in-lattice and off-lattice simulations.
- Boolean models, their generation, and their interpretation as "interaction networks".
- Multicellular and multiscale simulation.
- Gene-expression, sequencing and proteomic data integration in simulation frameworks, by means of statistical analysis and modeling of biological phenomena variation and progression at the biomolecular level.
- Temporal ordering reconstruction of samples on the basis of genomic measures.
- Epidemiological models (SIR and derivatives).

Prerequisites

Introductory courses (undegraduate or master level) on Mathematics, Probability and Statistics, and/or Biology and Biochemistry. Some knowledge of R, Python (et al.) programming.

Teaching form

The course will be offered as a set of standard lectures during the term. “e-Learning” support will also be provided for the distribution of course material, exercises and project descriptions. Moreover there will be laboratory sessions where the students will learn to program with the programming languages introduced during the course.

As a possible guideline, subject to contingency, the course will be organized as

- 12 2 hours lectures: traditional lecture in presence.
- 4 2 hours lectures: traditional and interactive lecture in presence.
- 10 2 hours recitations: traditional and interactive recitations activities in presence.

Textbook and teaching resource

Lecture slides will be made available on the Moodle platform.

Many bibliographic references can be found within the course slides, especially the most recent ones.

Some useful text are suggested below. The first one is especially recommended for students who do not have a biology and biochemistry background.

- Lawrence E. Hunter, The Processes of Life, An Introduction to Molecular Biology, MIT Press, 2009 (very much recommended for Computer Scientists)
- Keener and Sneyd, Mathematical Physiology (Vol I), Spinger, 2009
- J Marketa Zvelebil and Jeremy O. Baum, Understanding Bioinformatics, Garland Science, 2008
- Weinberg, Biology of Cancer, Garland Science, 2006
- Original papers by Gillespie (1976, 1977, 1994)
- U. Alon, “An Introduction to Systems Biology; Design Principles of Biological Circuits”, Chapman & Hall/CRC, 2007
- J. M. Bower, H. Bolouri (eds.), “Computational Modeling of Genetic and Biochemical Networks”, MIT Press, 2001

- R. Schwartz, “Biological Modeling and Simulation”, MIT Press, 2008

Semester

Fall semester.

Assessment method

The evaluation of a student's work enrolled in the "Data and Computational Biology" course will be based on class participation, the completion of periodic homework assignments and on a final pubic presentation.

The final presentation is an oral test where the student will describe a deeper analysis of one of the topics covered during the course. The presentation will provide the student's colleagues with a concise and useful summary of papers and software artifacts that can be used to analyze data, simulate models, or make inferences about interesting characteristics of a biomedical phenomenon under study.

Office hours

By appointment, either in-person or via teleconference.

Sustainable Development Goals

GOOD HEALTH AND WELL-BEING