

year	code	course name	ECTS	type	semester	educational activity type	ECTS	hours	faculty
2	F1801Q109	Computational Biology	6	elective	First semester	lecture	5	40	Antoniotti Marco
						practice exercise	1	10	Antoniotti Marco

Professors' CV: <http://www.unimib.it/go/176181440>

### Contents

The “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 BIMIB lab, with special regard to intestinal crypts modeling.

### Course objectives

The student will acquire the necessary “hands-on” experience to access and manipulate bioinformatics models and databases.

**Prerequisites** Mathematics and Programming experience. Basic knowledge of Biology.

### Teaching methods

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

### Learning assessments

Exam type: Written and oral

Evaluation type: Final grade

**Extended syllabus**

1 Representations of biological systems: models and computational issues.

2 Network inference.

3 Model databases and and metabolic, regulatory, and intra- and intercellular signaling networks (e.g., BioModels and KEGG); SBML, KGML and CellML formats.

4 "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."

5 "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."