

General Information	MASTER DEGREE IN BIOTECHNOLOGIES
Title of the subject	Bioinformatics and Genome Analysis
Degree Course (class)	Industrial and Environmental Biotechnology (LM-8)
ECTS credits	9
Compulsory attendance	Yes
Language	Italian
Academic year	2020/2021

Subject Teacher		
Name and Surname	Ernesto Picardi	
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Place and time of reception	Room 49, Biology Building Reception time by email appointment	
ECTS credits details	Discipline sector (SSD)	Area
	BIO/11	Molecular Biology

Study plan schedule	Year of study plan		Semester	
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Time management	Lessons	Laboratory	Exercises	Total
CFU	7	2		9
Total hours	175	50		225
In-class study hours	56	24		80
Out-of-class study hours	119	26		145

Syllabus	
Prerequisites / Requirements	Basic knowledge of Molecular Biology and Genetics
Expected learning outcomes (according to Dublin descriptors)	
Knowledge and understanding	Acquisition of advanced knowledge in the field of bioinformatics and comparative genomics.
Applying knowledge	Use of specific bioinformatics methodologies and genomic platforms.
Making informed judgments and choices	Students will be able to independently and critically analyze genomic data with the most modern bioinformatics tools.
Communicating knowledge	Students will have adequate skills for the use of the main genomic and bioinformatics resources.
Capacities to continue learning	Students will have the ability to consult and use bioinformatics databases and the data contained therein through the use of ad hoc computational resources.
Study Program	
Content	Genomics: 1. Characteristics of prokaryotic, eukaryotic and organellar genomes. 2. Genomic Browsers (Ensembl and UCSC).

	<p>3. Sequencing strategies for whole genomes. 4. Sequencing technologies of nucleic acids. 5. Next Generation Sequencing.</p> <p>Transcriptomics:</p> <p>1. Methods for transcriptome analysis and their applications. 2. Untranslated regions of eukaryotic mRNAs. 3. The non-coding RNA fraction (ncRNA).</p> <p>Bioinformatics:</p> <p>1. Databases and sequence analysis tools. 2. Global and local alignment of biological sequences. 3. Database searches by similarity (BLAST, BLAT). 4. Bioinformatics methods for gene prediction. 5. The Python programming language (data structures, functions, script execution). 6. Use of the Python language to solve biological problems.</p>
Bibliography and textbooks	<p>Brown TA - Genomi 3 – Edises Pascarella, Paiardini – Bioinformatica – Zanichelli Amaldi, Benedetti, Pesole, Plevani – Biologia molecolare – Casa Editrice Ambrosiana (Zanichelli)</p>
Notes to textbooks	Can be integrated with other Molecular Biology and Bioinformatics texts
Teaching methods	Lectures and computer experiences.
Assessment methods (oral, written, ongoing assessment)	Oral
Evaluation criteria (describe criteria for each of the above expected outcomes)	The student will have to know the structural characteristics of the genomes and the main bioinformatics algorithms. It will have to be able to use the main genomic platforms and autonomously apply bioinformatics tools. He will be able to develop small bioinformatics programs for the analysis of biological sequences
Further information	