



PRINCIPLES OF BIOINFORMATICS

Enrollment year	2019/2020
Academic year	2021/2022
Regulations	DM270
Academic discipline	BIO/11 (MOLECULAR BIOLOGY)
Department	DEPARTMENT OF BIOLOGY AND BIOTECHNOLOGY "LAZZARO SPALLANZANI"
Course	BIOLOGICAL SCIENCES
Curriculum	PERCORSO COMUNE
Year of study	3°
Period	2nd semester (01/03/2022 - 14/06/2022)
ECTS	6
Lesson hours	48 lesson hours
Language	Italian
Activity type	ORAL TEST
Teacher	LESCAI FRANCESCO (titolare) - 6 ECTS
Prerequisites	The student will be assumed to have basic knowledge of molecular biology and genetics (structure and function of a gene, transcripts, DNA, RNA, transcription and translation processes). Knowledge of biochemistry and cellular biology are not essential but recommended.
Learning outcomes	<p>At the end of the course, the student will be able to:</p> <ul style="list-style-type: none">- identify the most appropriate source, to retrieve biological information about whole organisms, genes or proteins and their functions- apply web-based bioinformatic tools and databases to execute searches and analyses- evaluate and compare the collected information in order to reach a conclusion about biological functions or inform experimental decisions- solve a biological question and communicate bioinformatics results in an integrated and coherent way

<p>Course contents</p>	<p>The course will provide commanding knowledge of widely known tools, which students will be able to use in any career path they would like to pursue in the future.</p> <p>In particular, we will deal with the following topics:</p> <ul style="list-style-type: none"> - genome browsers and biological databases - genome annotation - prediction of biological effect of mutations - retrieval of genome sequences from public databases - data generation and analysis of next generation sequencing information - retrieval of NGS data from public databases - sequence alignment and phylogenetic analysis - BLAST and sequence similarity searches - proteins and structure analysis - expression atlases - clinical relevance of mutations and rare variants - basics of biopython to speed-up bioinformatics analyses
<p>Teaching methods</p>	<p>The course will significantly use “blended learning” tools, which assume that one-way information transfer is limited during classes activity. Students will be instead expected to use the Kiro platform for readings and self-evaluation activities.</p> <p>Class activity will be focused to demonstrations, discussions and problem solving through interaction: demo, group work, quiz and real-time feedback.</p>
<p>Reccomended or required readings</p>	<p>The course will mostly use freely available material, video and tutorials. The use of a textbook will be discussed with the students during classes.</p>
<p>Assessment methods</p>	<p>The exam will take place in a single session, where the students:</p> <ul style="list-style-type: none"> - will be assigned a biological question (nature, function or characteristics of a gene, protein or genome) - will be asked to retrieve the information necessary to solve/answer the question, using the tools learnt during classes - will be asked to explain choices made to retrieve the information and illustrate their interpretation of the findings in order to answer the initial question.
<p>Further information</p>	<p>The Teacher will be available via email and for meetings to be agreed on, as well as through collaborative tools: a dedicated channel will be setup on Slack, for interacting with students and discussing different topics.</p>
<p>Sustainable development goals - Agenda 2030</p>	<p>The goals</p>