



## 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"><li>- identify the most appropriate source, to retrieve biological information about whole organisms, genes or proteins and their functions</li><li>- apply web-based bioinformatic tools and databases to execute searches and analyses</li><li>- evaluate and compare the collected information in order to reach a conclusion about biological functions or inform experimental decisions</li><li>- solve a biological question and communicate bioinformatics results in an integrated and coherent way</li></ul>

Course contents	<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"> <li>- genome browsers and biological databases</li> <li>- genome annotation</li> <li>- prediction of biological effect of mutations</li> <li>- retrieval of genome sequences from public databases</li> <li>- data generation and analysis of next generation sequencing information</li> <li>- retrieval of NGS data from public databases</li> <li>- sequence alignment and phylogenetic analysis</li> <li>- BLAST and sequence similarity searches</li> <li>- proteins and structure analysis</li> <li>- expression atlases</li> <li>- clinical relevance of mutations and rare variants</li> <li>- basics of biopython to speed-up bioinformatics analyses</li> </ul>
Teaching methods	<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>
Reccomended or required readings	<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>
Assessment methods	<p>The exam will take place in a single session, where the students:</p> <ul style="list-style-type: none"> <li>- will be assigned a biological question (nature, function or characteristics of a gene, protein or genome)</li> <li>- will be asked to retrieve the information necessary to solve/answer the question, using the tools learnt during classes</li> <li>- 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.</li> </ul>
Further information	<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>
Sustainable development goals - Agenda 2030	<p><a href="#">\$Ibl legenda sviluppo sostenibile</a></p>