UNIVERSITÀ DI PAVIA

Anno Accademico 2021/2022

BIOINFORMATICS	
Enrollment year	2020/2021
Academic year	2021/2022
Regulations	DM270
Academic discipline	ING-INF/06 (ELECTRONIC AND INFORMATION BIOENGINEERING)
Department	DEPARTMENT OF BIOLOGY AND BIOTECHNOLOGY "LAZZARO SPALLANZANI"
Course	EXPERIMENTAL AND APPLIED BIOLOGY
Curriculum	Scienze biomediche molecolari
Year of study	2°
Period	1st semester (01/10/2021 - 14/01/2022)
ECTS	6
Lesson hours	48 lesson hours
Language	Italian
Activity type	WRITTEN AND 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. Basic knowledge of biostatistics will be useful.
Learning outcomes	At the end of the course, the student will be able to: - identify the most appropriate sequencing method, to answer a biological or genetic question; - use the most appropriate programming environment (Python, R, or a combination of both) to process files and information, and design data analysis; - apply the suitable bioinformatics tools and online databases to analyse data generated with different methods; - evaluate and compare the results of the analysis, in order to answer

	the initial question or take further experimental decisions; - solve a biological question and communicate bioinformatics results in an integrated and coherent way, using reproducible research methods.
Course contents	The course will cover the most common analysis methods, to deal with key applications of next generation sequencing technology. In particular, students will cover the bases of the following programming environments: - shell / bas - python - R and RStudio GUI Then, the course will cover the following activities, using the most appropriate computing and programming environments: - data retrieval from biological databases - data manipulation and format conversion - tool-specific APIs and REST APIs - targeted sequencing analyses (germline and somatic) - analysis of RNAseq data - analysis of ChipSeq data - rendering of reproducible and parametric reports - bases of data visualization
Teaching methods	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. Class activity will be focused to demonstrations, discussions and problem solving through interaction: demo, group work, quiz and real-time feedback. Virtual machines and code editors will be used in classes, to improve learning python, R and the other command-line tools used in the course.
Reccomended or required readings	The course will mostly use freely available material, video and tutorials. The use of a textbook will be entirely optional, and we suggest the following: Bioinformatics with Python Cookbook Tiago Antao Packt Publishing 2018 R Bioinformatics Cookbook Dan MacLean Packt Publishing, 2019 These textbooks will be made available by the Sciences Library in an e-book version. The teacher will provide supporting materials and tutorials throughout the classes.
Assessment methods	The student will receive a simplified dataset, to be analised using one of the tools or methods learnt during the course. The student will then be asked to explain the results of the analysis, and demonstrate a critical approach to answering the biological question proposed; the knowledge of tools and methods will be verified at this stage as well.

Further information

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.

Sustainable development

| goals - Agenda 2030 | $lbl_legenda_sviluppo_sostenibile |