NAME OF THE COURSE	**Bioinformatics**						
Code	PMP140	Year of study	GU-2				
Course teacher	Ana Jeronči ć, PhD, Professor	Credits (ECTS)	6,0				
Associate teachers	Martina Perić Tomislav Ronč ević	Type of instruction (number of hours)	L	S	E	F	
			30		30		
Status of the course	Compulsory	Percentage of application of e-learning	20%				

COURSE DESCRIPTION		
Course objectives	The aim of the course is to introduce students with available tools used in bioinformatics for the analysis of sequences and protein structures and nucleic acids.	
Course enrolment requirements and entry competences required for the course	The learning outcomes of Bachelor programmes in physics, basic knowledge in molecular biology and biochemistry. For successful following of the bioinformatics course, it is necessary to have fundamental knowledge of biochemistry and biophysics. Specifically, it is necessary to know the structure and physico-chemical properties of the nucleotides and amino acids as covered by the previous college courses.	
Learning outcomes expected at the level of the course (4 to 10 learning outcomes)	On completion of this course a student should be able to: 1. use tools for comparing nucleic acid sequences 2. use tools for comparing protein sequences 3. use tools for predicting the protein structure 4. select tools according to the needs of the analysis 5. interpret results obtained using bioinformatic tools	
Course content broken down in detail by weekly class schedule (syllabus)	1. Introduction to bioinformatics, familiarity with the history and development of bioinformatics 2. Database knowledge (NCBI), database of gene and protein sequences (NCBI, SWISSPROT, UNIPROT, CATH, SCOP), protein structures (PDBs), functional domains of proteins (PFAMs) and complete genomes (ENSEMBL) 3. Aligning Nucleic Acid and Protein Sequence Tools: TCOFFEE, MCOFFEE, Clustal 4. Prediction of secondary and tertiary structure of proteins: modeling by homology and tools used for said prediction (PSI-PRED, Modeller, Phyre, Threader) 5. Protein structure visualization programs 6. Introduction to Molecular Dynamics of Proteins 7. Prediction of the secondary and tertiary structure of nucleic acids	
Format of instruction	☒ lectures ☒ seminars and workshops ☒ exercises ☐ on line in entirety ☐ partial e-learning ☐ field work	☒ independent assignments ☐ multimedia ☐ laboratory ☐ work with mentor ☐ homework assignments
Student responsibilities	Active participation in classes and assignments. Solving given problems, writing and presenting seminars.	

Screening student work *(name the proportion of ECTS credits for each activity so that the total number of ECTS credits is equal to the ECTS value of the course)*	Name	Ects	Name	Ects	Name	Ects
	Class attendance	1	Research		Experimental work	
	Oral exam	2	Report		Homework assignments	
	Seminar essay	1	Essay			
	Tests		Practical training	2		
	Written exam		Project			

Grading and evaluating student work in class and at the final exam	Evaluation of attendance of seminars and oral exam.

	Title	Number of copies in the library	Availability via other media
Required literature (available in the library and via other media)	[1] Arthur Lesk: Introduction to Bioinformatics	0	
	[2] Charles Cantor: Biophysical Chemistry Part I, The Conformation of biological Macromolecules	0	

Optional literature (at the time of submission of study programme proposal)	[1] Des Higgins and Willie Taylor's "Bioinformatics: Sequence Structure and Databanks [2] Scientific articles
Quality assurance methods that ensure the acquisition of exit competences	1. Analysis of the acquired learning outcomes at the end of the class, compared with the introductory work of students. 2. Monitoring the development of students in the subjects who followed the links with the success of the case 3. Exam results statistics and student evaluation through an anonymous survey at the end of the course. The survey is conducted according to the regulations of the University of Split.
Other (as the proposer wishes to add)	