

Subject card

Subject name and code	Bioinformatics and Molecular Modeling_laboratory, PG_00117384						
Field of study	Marine Biotechnology						
Date of commencement of studies	October 2024	Academic year of realisation of subject			2025/2026		
Education level	postgraduate studies	Subject group					
Mode of study	full-time studies	Mode of delivery			at the university		
Year of study	2	Language of instruction			English english		
Semester of study	3	ECTS credits			1.0		
Learning profile	academic	Assessment form					
Conducting unit	Laboratorium Badawczo-Wdrozeniowe -> Instytut Biotechnologii UG -> Intercollegiate Faculty of Biotechnology UG-MUG						
Name and surname of lecturer (lecturers)	Subject supervisor	dr Agata Motyka-Pomagruk					
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	10.0	0.0	0.0	10
	E-learning hours included: 0.0						
Learning activity and number of study hours	Learning activity	Participation in didactic classes included in study plan		Participation in consultation hours		Self-study	SUM
	Number of study hours	10		3.0		15.0	28
Subject objectives	Acquainting students with practical skills from the field of bioinformatics, allowing for usage of bioinformatic methods and tools for marine biotechnology-related research Students will search, download and interpret scientific information, in particular from databases containing information indispensable in carrying out operations in bioinformatic analyses Students will collect and analyze the sequencing and other biological data with the use of the publicly available and commercial software in addition to following pipelines designated for newly gathered data for their deposition in public databases. Students will design experiments in silico.						
Learning outcomes	Course outcome		Subject outcome		Method of verification		
	[MBMU2-KU02] Can collect and interpret empirical data; applies statistical methods and computer tools in data analysis; formulates conclusions based on empirical data		The student is able to use publicly available databases and bioinformatics software, obtain the necessary information (including sequencing data) and perform bioinformatics analyses using these tools.		[SU5] implementation of a problem task [SU6] demonstration of practical skills		
	[MBMU2-KU03] Can use and critically analyze available scientific information; can prepare and present - orally or in writing - a paper covering detailed problems in the field of marine biotechnology on the basis of the scientific information or their own work, with the use of scientific language, including specialized terminology and conceptual apparatus; has the ability to conduct discussions		The student is able to describe and interpret the results of bioinformatic analyses and draw conclusions of biological significance from them. The student is able to prepare a report of the performed bioinformatic analyses and conclude on the significance of the results in the context of marine biotechnology.		[SU4] test/exam - oral or written		

Subject contents	<p>Self-performing bioinformatic analyses: Browsing through sequential databases and popular bioinformatics servers. Review of the most popular sequence formats generated or required by bioinformatic software. Searching for similar sequences in databases. Search parameters and statistical analysis of results (BLAST). Sequence analysis with various software (Chromas, Bioedit, Geneious, Ugene, Bionumerics). Sequence Alignments (Pairwise comparison) with various software (e.g. Clustal, Bioedit, MEGA, Geneious, Bionumerics). Comparing similarities between nucleotide and amino acid sequences. Phylogenetic analysis: selection of the model of nucleotide and amino acids substitution, construction of phylogenetic trees by means of various methods: maximum parsimony genetic distance, maximum Bayesian probability and reasoning, verification of the correctness of phylogenetic trees (Geneious, MEGA, and other software) Assembling reads from Sanger sequencing into consensus and searching for open reading frames (ORF-Finder) Designing starters with various software: PRIMER3, PrimerQuest, OligoAnalyzer. Searching for chimeric sequences (e.g. Bellerophon, Decipher software). Metagenomics: Determination of the operational taxonomic units (OTU) and ASVs (K-base, mothur) Good practices in using AI in scientific work. Genome assembling and annotation (RAST, Geneious, KEGG, BioCyc) Searching for the gene clusters encoding secondary metabolites (antiSMASH platform) Searching for plasmids (plasmidfinder software), prophages (Phastest), mobile genetic elements (ICEfinder) in NGS data Basic comparative genomics (constructing phylogenetic profiles, searching for genome plasticity regions using various platforms: Integrated Microbial Genomes - IMG, Microbial Genome Annotation & Analysis Platform, Edgar 3, K-base, KEGG). Computation of the overall genome relatedness indices (OGRI) methods: DNA-DNA hybridization in silico (TYGS), ANI (platform Jspecies) Pangenomic analysis - pangenome, core genome, dispensable and unique genes, pangenomic studies using various platforms: Integrated Microbial Genomes - IMG, Microbial Genome Annotation & Analysis Platform, Edgar 3, K-base)</p>		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	The acquired skills will be verified by independent performance of bioinformatic tasks during practical exam. The correctness of the analysis and interpretation of the results will be assessed.	0.0%	100.0%
Recommended reading	Basic literature	Applied Bioinformatics - An Introduction, Paul M. Selzer Richard J. Marhöfer, Oliver Koch. Second Edition.2018 Bioinformatics. A Practical Guide to the Analysis of Genes and Proteins. Redakcja naukowa: A.D. Baxevanis, B.F.F. Ouellette. Bioinformatics and Molecular Evolution. Paul G. Higgs, Teresa K. Attwood.	
	Supplementary literature	The acquired skills will be assessed by self-performed bioinformatics analysis, interpretation of the results and their presentation in a form of a report. Reports will be required to pass the course.	
	eResources addresses	Adresy na platformie eNauczanie:	
Example issues/ example questions/ tasks being completed	The covered tasks include practical experience in: obtaining information from publicly available bioinformatic databases, performing sequence alignments, obtaining consensus sequences, performing phylogenetic analyses, good practices with the use of AI in scientific work, searching for genes and determining their function, performing analyses in the field of metagenomics and comparative genomics.		
Work placement	Not applicable		

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