University of Gdańsk

Subject card

Subject name and code	Bioinformatics and molecular modeling - laboratory classes, PG_00193132		
Field of study	Marine Biotechnology		
Date of commencement of studies	October 2026	Academic year of realisation of subject	2027/2028
Education level	Master's studies	Subject group	Obligatory subject group in the field of study
Mode of study	full-time studies	Mode of delivery	at the university
Year of study	2	Language of instruction	English
Semester of study	3	ECTS credits	2.0
Learning profile	academic	Assessment form	credit
Conducting unit	Research and Development Laboratory -> UG Institute of Biotechnology -> Intercollegiate Faculty of Biotechnology UG-MUG -> Rector		
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	20.0	0.0	0.0	20
	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	20	1.0	29.0	50

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

<table>
<tr><td>Subject contents</td><td colspan="2">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, MEGA, Geneious). Sequence alignments with various software (*e.g.* MEGA, Geneious). 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 (*e.g.* MEGA, Geneious). Assembling reads from Sanger sequencing into consensus and searching for open reading frames (ORF-Finder) Designing primers with various software: PRIMER3, PrimerQuest, OligoAnalyzer. Searching for chimeric sequences (e.g. Bellerophon).</td></tr>
<tr><td>Prerequisites and co-requisites</td><td colspan="2"></td></tr>
<tr><td>Assessment methods and criteria</td><td colspan="2"><table>
<tr><th>Subject passing criteria</th><th>Passing threshold</th><th>Percentage of the final grade</th></tr>
<tr><td>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.</td><td>51.0%</td><td>100.0%</td></tr>
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<tr><td rowspan="3">Recommended reading</td><td>Basic literature</td><td>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.

Students will search for publicly-available materials independently, using, among others, electronic sources of information.</td></tr>
<tr><td>Supplementary literature</td><td>Bioinformatics. Sequence and genome analysis". D.W. Mount. 2001.</td></tr>
<tr><td>eResources addresses</td><td></td></tr>
<tr><td>Example issues/ example questions/ tasks being completed</td><td colspan="2">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.</td></tr>
<tr><td>Work placement</td><td colspan="2">Not applicable</td></tr>
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