University of Gdańsk

Subject card

Subject name and code	Bioinformatics and Molecular Modeling_Lecture, PG_00099386						
Field of study	Marine Biotechnology						
Date of commencement of studies	October 2025		Academic year of realisation of subject		2026/2027		
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		1.0		
Learning profile	academic		Assessment form		exam		
Conducting unit	Intercollegiate Faculty of Biotechnology UG-MUG -> Rector						
Name and surname of lecturer (lecturers)	Subject supervisor	dr hab. Małgorzata Waleron, prof. UG					
	Teachers						

Lesson types

Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
Number of study hours	10.0	0.0	0.0	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	0.0	0.0	10

Subject objectives

Getting students acquainted with the basic knowledge in the area of bioinformatics that allows students to consciously use bioinformatics methods and tools applied in marine biotechnology and other fields of science.

Students will widen their knowledge in the related areas and disciplines of science that will allow them to see relationships and dependencies in nature, in particular those essential for marine biotechnology.

Learning outcomes

Course outcome	Subject outcome	Method of verification
[MBMU2-KW04] Knows and deeply understands advanced research methods used in marine biotechnology and related sciences	The student has knowledge in the field of bioinformatic methods applied in marine biotechnology. The student has an extended knowledge of the interpretation of bioinformatics analyses and their use in marine biotechnology	[SW4] test/exam - oral or written

Subject contents

1. Overview of sequence databases.
2. Collection, storage and processing of sequences for deposit in public databases.
3. Sequence formats and conversion.
4. Sequence comparison (pair-wise sequence comparison, multiple sequence comparison).
5. Searching for similar sequences in databases.
6. Operon assembly and annotation.
7. Open reading frame search.
8. Protein function prediction.
9. Evolutionary models.
10. Phylogenetic prediction.
11. Predicting the 3D structure of a protein based on its amino acid sequence using the AlphaFold database.
12. Protein Structure Database.

Prerequisites and co-requisites

<table>
<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 theoretical knowledge acquired during the course will be verified by means of a written examination.</td><td>51.0%</td><td>100.0%</td></tr></table></td></tr>
<tr><td rowspan="3">Recommended reading</td><td>Basic literature</td><td>Applied Bioinformatics : An Introduction, Paperback by Selzer,Paul M. (EDT) Springer 2018
Bioinformatics. A Practical Guide to the Analysis of Genes and Proteins. A.D. Baxevanis, B.F.F. Ouellette. 1998
Bioinformatics and Molecular Evolution. Paul G. Higgs, Teresa K.Attwood. 2004</td></tr>
<tr><td>Supplementary literature</td><td>• Bioinformatics. Sequence and genome analysis". D.W. Mount. 2001.
• Students individually search for materials concerning classes using electronic resources.</td></tr>
<tr><td>eResources addresses</td><td></td></tr>
<tr><td>Example issues/ example questions/ tasks being completed</td><td colspan="2"></td></tr>
<tr><td>Work placement</td><td colspan="2">Not applicable</td></tr>
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