University of Gdańsk

Subject card

Subject name and code	Bioinformatics and molecular modeling - lecture, PG_00192720		
Field of study	Marine Biotechnology		
Date of commencement of studies	October 2027	Academic year of realisation of subject	2028/2029
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	1.0	14.0	25

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

<table>
<tr><td>Subject contents</td><td>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.</td></tr>
<tr><td>Prerequisites and co-requisites</td><td></td></tr>
<tr><td>Assessment methods and criteria</td><td><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>Recommended reading</td><td><table>
<tr><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>
</table></td></tr>
<tr><td>Example issues/ example questions/ tasks being completed</td><td></td></tr>
<tr><td>Work placement</td><td>Not applicable</td></tr>
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