Subject card

Subject name and code	Marine OMICS - lecture, PG_00192697		
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 Subject group related to scientific research 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	exam
Conducting unit	Intercollegiate Faculty of Biotechnology UG-MUG -> Rector		
Name and surname of lecturer (lecturers)	Subject supervisor	dr hab. Paulina Czaplewska	
	Teachers		

Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	28.0	0.0	0.0	0.0	0.0	28
	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	28	2.0	20.0	50

Subject objectives	The aim of the course is to familiarize the student with the basics of metabolomics, genomics, transcriptomics and proteomics as techniques used in broadly understood research related to the sea and its ecosystem. Additionally, as part of the course, students will learn next-generation sequencing (NGS) techniques and the analysis of microbiomes in marine environments.

Learning outcomes

Course outcome	Subject outcome	Method of verification
[MBMU2-KW03] Has an in-depth knowledge and understanding of complex biological phenomena at the molecular level, understands their significance for an organism, marine environment and marine biotechnology	KW_01: Understands complex biological phenomena at the molecular level, knows their importance for biotechnology and their connections with other fields and disciplines of science K_W04: Knows the basic principles of occupational safety, understands the risks associated with laboratory work, knows the risks associated with conducting laboratory research, knows the risks associated with working with pathogenic organisms and GMOs	[SW4] test/exam - oral or written
[MBMU2-KW01] Has an in-depth knowledge and understanding of the significance, limitations and potential applications of natural marine resources in the context of the complex biological, environmental and technological factors influencing the development of biotechnology.	KU_01: Has the skills necessary for laboratory work; is able to plan and carry out an experiment, is able to document his own operations and results; in laboratory work, under the supervision of the instructor, uses complex techniques and research tools, is able to use laboratory equipment. Collects and interprets empirical data, uses statistical methods and IT tools in data analysis, draws conclusions based on empirical data (K_U05)	[SW4] test/exam - oral or written

Subject contents

Organization and genetic content of prokaryotic (bacteria, archaea) and eukaryotic (yeast, humans, plants) genomes. The Human Genome Project. The importance of mobile genetic elements for the organization and size of genomes. Genome and mitochondrial genomeplastids. Viral genomes. Comparative genomics. The impact of genomics on medicine and society.

Next generation sequencing (NGS) techniques: Collecting environmental samples from the seas, securing samples, isolating genetic material, preparing a library for high-throughput sequencing, conducting the sequencing process.Metagenomic data analysis: Manipulation and analysis of collected metagenomic data, interpretation of results regarding microbiomes of marine environments.The use of ancient DNA ingenomics. Evolution of genomes.Introduction to mass spectrometry, physical basis for measuring MS spectra, equipment and basics of recording MS spectra. Qualitative and quantitative analysis in proteomic analysis using mass spectrometry Methods of sample preparation for MS analysis, registration and analysis of peptide and protein spectra (ESI, MALDI) Analysis of post-translational modifications in MS Protein loss before MS analysis, digestion in solution and digestion in gel Analysis of MS data using MS spectra and protein databases. Protein digestion, recording of MS/MS spectra, data analysis. The influence of various factors on changes in the metabolite profile.

Chimeric sequences. OTU (operational taxonomic units) determination, Metagenomics

Genomics and projects of genome sequencing

Genome assembly and annotation

Comparative genomics. Phylogenetic profiles and regions of genome plasticity.

Pangenomics. Pangenome, core genome and dispensable genes discrimination.

Overall Genome Related Index (OGRI) methods: ANI/AAI, DNA-DNA hybridisation in silico.

Phylogenomics.

Searching for the gene clusters encoding secondary metabolites

Searching for plasmids, prophages, and mobile genetic elements in NGS data.

<table>
<tr><td>Prerequisites and co-requisites</td><td colspan="2">Formal requirements - no formal requirementsIt is required to obtain knowledge, skills and competences for specific subjects: Biochemistry (lecture), Organic chemistry (lecture), Biodiversity and basics of taxonomy, Bioinformatic sequence analysis, Molecular biology and geneticsAfter passing the compulsory subjects in the first three semesters, the student has the knowledge and skills that qualify him to participate and pass the course</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>Exam</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>Scientific publications and studies prepared by the teacher and made available to students during classes. Genomes 3 T.A. Brown, 2007, Garland Science Brown T.A. "Genomes", ed. II, translation edited by P. Węgleński, Wydawnictwo Naukowe PWN, Warszawa 2009. Molecular Biology of the Gene, 7th edition, 2014, Pearson Johnstone Robert A.W. I Malcolm E.Rose, Mass spectrometry, PWN 2001 De Hoffmann, Edmond, Charette, Jean Joseph, Stroobant, Vincent, Mass Spectrometry, Wydawnictwa Naukowo-Techniczne 1998 Materials provided by the teacher</td></tr>
<tr><td>Supplementary literature</td><td>Primers for Proteomics https://doi.org/10.1142/13595 | May 2024 Pages: 250 Edited by: Paulina Czaplewska (<i>University of Gdańsk, Poland & Medical University of Gdańsk, Poland</i>), Katarzyna Macur (<i>University of Gdańsk, Poland & Medical University of Gdańsk, Poland</i>), and Paweł Ciborowski (<i>University of Nebraska Medical Center, USA</i>)

Metagenomics: Techniques, Applications, Challenges and Opportunities; Reena Singh Chopra, Chirag Chopra, Neeta Raj Sharma; 2020, Springer
https://doi.org/10.1007/978-981-15-6529-8</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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