University of Gdańsk

Subject card

Subject name and code	Bioinformatics and Molecular Modeling - tutorials, PG_00117383						
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-Wdrożeniowe -> 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	10.0	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		2.0		13.0	25
Subject objectives	Acquainting students with knowledge in the field of bioinformatics, allowing to consciously use bioinformatics methods and tools applied in marine biotechnology Students will acquire an ability to use scientific information, in particular databases containing information indispensable in carrying out operations in bioinformatic analyses Students will be familiarized with approaches on how to collect and analyze the data with the use of the publicly available and commercial software in addition to cognition of pipelines for newly gathered data for deposition in public databases. Students will acquire an ability to design experiments in silico.						

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	[BIOTECHMU2_W05] The graduate knows and understands the methods used in exact and natural sciences, necessary to comprehend biological phenomena and processes at the molecular level. The student possesses knowledge on methods used in bioinformatics. [BIOTECHMU2_U02] The graduate is able to collect and interpret empirical data; apply statistical methods and bioinformatic tools for data analysis; draw conclusions based on empirical data. The student is able to collect sequencing data, perform analyses using bioinformatic tools and draw conclusions based on the obtained results. [BIOTECHMU2_U04] The graduate is able to proficiently use scientific information, including English-language information on marine biotechnology; analyze and critically select information; use web-based resources; use appropriate databases. The student is able to use publicly available bioinformatic databases in order to retrieve the desired information and critically analyze it.	[SW4] test/exam - oral or written [SW2] presentation/project/paper/ report [SW5] implementation of a problem task

Subject contents

Theoretical introduction, instructions and FAQs on: 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). Good practices in using AI in scientific work. Metagenomics: Determination of the operational taxonomic units (OTU) and ASVs (K-base, mothur) 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)

Prerequisites and co-requisites

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
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.	0.0%	50.0%
Theoretical knowledge acquired during this course will be verified in quizzes (one quiz per meeting).	0.0%	50.0%

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	Bioinformatics. Sequence and genome analysis". D.W. Mount. 2001. The students will independently search for materials using, among other things, electronic information sources.
	eResources addresses	Adresy na platformie eNauczanie:
Example issues/ example questions/ tasks being completed	The covered tasks include theoretical preparation for: obtaining information from publicly available bioinformatic databases, performing sequence alignments, obtaining consensus sequences, performing phylogenetic analyses, good practices in 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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