

Subject card

Subject name and code	Bioinformatics sequence analysis, PG_00156236						
Field of study	Bioinformatics						
Date of commencement of studies	October 2024		Academic year of realisation of subject		2025/2026		
Education level	Bachelor'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		Polish		
Semester of study	3		ECTS credits		6.0		
Learning profile	academic		Assessment form				
Conducting unit	Intercollegiate Faculty of Biotechnology UG-MUG -> Rector						
Name and surname of lecturer (lecturers)	Subject supervisor		dr hab. Stanisław Oldziej				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	45.0	0.0	0.0	60
	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	60		0.0		90.0	150
Subject objectives	The aim of the course is to familiarize students with the basic tools used in bioinformatics for the analysis of nucleotide and amino acid sequences and the ability to use them. Students will also become familiar with the basic databases used in bioinformatics and methods of searching for information, and will learn about the problem of dynamic changes in methods and means of collecting and processing information.						
Learning outcomes	Course outcome		Subject outcome		Method of verification		
	[BIOINL3_K01] Graduate knows the limitations of his own knowledge and skills; he demonstrates a willingness to constantly improve, update his knowledge and enhance his qualifications in bioinformatics		Student is able to critically evaluate the results of analyses		[SK2] presentation/project/paper/report [SK3] text preparation/written work		
	[BIOINL3_U03] Graduate applies fundamental mathematical and statistical methods to describe phenomena and analyze data; has the ability to perform basic data analysis in professional databases used in bioinformatics		Uses basic bioinformatics methods to select and analyze data found in specialized databases.		[SU2] presentation/project/paper/report		
	[BIOINL3_U05] Graduate has the ability to use scientific literature, including English-language sources on bioinformatics; has ability to use appropriate databases		The student has the ability to search for and select information stored in specialized databases.		[SU2] presentation/project/paper/report		
	[BIOINL3_W04] Has knowledge of basic research techniques and tools used in bioinformatics		Knows basic bioinformatics methods for data analysis, knows basic experimental methods for acquiring biological data.		[SW2] presentation/project/paper/report [SW3] text preparation/written work		

Subject contents	Lecture content: • Experimental methods for obtaining amino acid and nucleotide sequences with particular emphasis on high-throughput methods • Databases collecting biological data (amino acid sequences, nucleotide sequences, biomolecule structures, metabolic pathways, medical data) • Substitution matrices • Algorithms for sequence comparison • Algorithms for multiple sequence alignment Laboratory exercise content: • Searching for information stored in biological databases • Comparing protein and/or nucleic acid sequences • Comparing multiple sequences, creating alignments, and analyzing them • Visualizing results		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	final tests	51.0%	100.0%
Recommended reading	Basic literature	• P.G. Higgs, T.K. Attwood. Bioinformatyka i ewolucja molekularna, PWN, 2008 • A.D. Baxevanis, B.F.F. Ouellette (red.) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. Wiley-Liss, Inc. 2005.	
	Supplementary literature	literature recommended by the lecturers during the classes	
	eResources addresses	Basic https://www.ncbi.nlm.nih.gov/genbank/ - GenBank - database of nucleotide sequences, genes, and genomes. Bioinformatics tools for nucleotide sequence analysis. https://www.rcsb.org/ - PDB (Protein Data Bank) database of biomolecule structures. https://www.uniprot.org - Amino acid sequence database, tools for bioinformatic analysis of amino acid sequences https://www.genome.jp/kegg/ - KEEG (Kyoto Encyclopedia of Genes and Genomes) database. A database integrating genes, gene products, and metabolism.	
Example issues/ example questions/ tasks being completed	n		
Work placement	Not applicable		

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