

Subject card

Subject name and code	Bioinformatics for biologists, PG_00132656						
Field of study	Biology						
Date of commencement of studies	October 2024	Academic year of realisation of subject			2026/2027		
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	3	Language of instruction			Polish Polish		
Semester of study	5	ECTS credits			1.0		
Learning profile	academic	Assessment form			credit		
Conducting unit	Laboratory of Molecular Evolution and Bioinformatics -> Department of Evolutionary Genetics and Biosystematics -> Faculty of Biology -> Rector						
Name and surname of lecturer (lecturers)	Subject supervisor		prof. dr hab. Marek Ziętara				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	0.0	0.0	0.0	15
	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	15		2.0		8.0	25
Subject objectives	To introduce students to advanced bioinformatics tools for the basics: molecular phylogenetics, structural bioinformatics, genomics and proteomics, and genetic variation analysis.						
Learning outcomes	Course outcome		Subject outcome		Method of verification		
	[BIOLL3_W12] The graduate knows and understands the principles of using IT tools for data analysis and interpretation of natural phenomena and processes		The student knows the principles of analysis of the structure and function of DNA and proteins.		[SW4] test/exam - oral or written		
	[BIOLL3_W11] The graduate knows the basic methods of statistical analysis and their importance in the interpretation of phenomena and processes		The student has knowledge of the operation of programs for bioinformatic analyses and methods of construction and interpretation of phylogenetic trees based on DNA and protein sequences.		[SW4] test/exam - oral or written		
Subject contents	Introduction to biological databases. Sequence comparison. Models of DNA substitution. Introduction to molecular phylogenetics. Construction of phylogenetic trees on a selected research model - methods and programs. The principle of the molecular clock. Predicting genes and promoters. Structural bioinformatics. Mapping, assembling and comparing genomes. Introduction to functional genomics and proteomics. Analysis of genetic variation.						

Prerequisites and co-requisites	<p>formal requirements: passing Bioinformatics exercises for biologists before admission to the exam.</p> <p>additional requirements:</p> <ol style="list-style-type: none"> 1. The student is obliged to participate in classes, and in the event of absence, it must be excused in accordance with paragraph 12 of the UG Study Regulations. 2. The condition for passing the lecture is attendance at least 80% of classes. 3. The student is obliged to fill in the gaps in knowledge and skills caused by the absence from lectures on his/her own, while the gaps in knowledge and skills caused by the absence from the classes in the manner and on the date indicated by the Lecturer. 								
Assessment methods and criteria	<table border="1"> <thead> <tr> <th data-bbox="448 620 798 651">Subject passing criteria</th> <th data-bbox="802 620 1142 651">Passing threshold</th> <th data-bbox="1147 620 1477 651">Percentage of the final grade</th> </tr> </thead> <tbody> <tr> <td data-bbox="448 658 798 689">Written test</td> <td data-bbox="802 658 1142 689">51.0%</td> <td data-bbox="1147 658 1477 689">100.0%</td> </tr> </tbody> </table>			Subject passing criteria	Passing threshold	Percentage of the final grade	Written test	51.0%	100.0%
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Written test	51.0%	100.0%							
Recommended reading	Basic literature	<p>A. Literature required for the final credit of the course:A1. used during classes: Jin Xiong, Podstawy bioinformatyki. Wydawnictwo Uniwersytetu WarszawskiegoA2. Self-studied by the student: Barry G. Hall Łatwe drzewa filogenetyczne. Wydawnictwo Uniwersytetu Warszawskiego</p>							
	Supplementary literature	<p>B. Supplementary literature:</p> <ul style="list-style-type: none"> • Baxevanis A.D., Oullette B.F. (red.) (2005) Bioinformatyka - podręcznik do analizy genów i białek. PWN, ISBN 83-01-142111 • Paul G. Higgs, Teresa K. Attwood (2008) Bioinformatyka i ewolucja molekularna. PWN, ISBN 978-83-01-15494-3 • scientific articles indicated by the lecturer 							
	eResources addresses								
Example issues/ example questions/ tasks being completed	No applicable								
Work placement	Not applicable								

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