

Subject card

Subject name and code	Bioinformatics for biologists, PG_00079748						
Field of study	Biology						
Date of commencement of studies	October 2022		Academic year of realisation of subject		2024/2025		
Education level	Bachelor's studies		Subject group				
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		2.0		
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		prof. dr hab. Marek Ziętara dr Aleksandra Naczek dr Beata Guzow-Krzemińska dr Natalia Olędrzyńska dr hab. Marcin Górniak				
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	30.0	0.0	0.0	30
	E-learning hours included: 0.0						
	Additional information: The number of hours a student works consists of 30 hours of classes, 2 hours of consultations, and 18 hours of independent work.						
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	30		0.0		0.0	30
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_K05] the graduate is ready to be responsible for the safety of his own work and that of others, and to recognize dangerous situations and take appropriate action		The student is responsible for the entrusted computer equipment, materials, his/her own work and respects the work of others.		[SK8] observation of student's independent or team work		
	[BIOLL3_U04] the graduate can apply statistical methods and computer algorithms and techniques to describe phenomena and analyse biological data		The student uses bioinformatics tools to classify biological data and obtain the structures of second- and third-order biological molecules.		[SU2] presentation/project/paper/report		
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	formal requirements: the student is required to participate in the lecture Bioinformatics for biologists.		
	additional requirements:		
	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 exercises is participation in at least 85% of classes.		
Assessment methods and criteria	3. The student is obliged to fill in the gaps in knowledge and skills caused by absence from classes in the manner and on the date indicated by the Lecturer.		
	Subject passing criteria	Passing threshold	Percentage of the final grade
	Colloquium	51.0%	60.0%
	Average of partial grades	51.0%	40.0%
Recommended reading	Basic literature	A. Literature required for the final passing of the course:	
		A1. used during classes: Jin Xiong, Podstawy bioinformatyki. Wydawnictwo Uniwersytetu Warszawskiego	
		A2. Self-studied by the student: Barry G. Hall Łatwe drzewa filogenetyczne. Wydawnictwo Uniwersytetu Warszawskiego	
	Supplementary literature	B. Supplementary literature:	
	- 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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