

Subject card

Subject name and code	Bioinformatics for biologists, PG_00079747						
Field of study	Biology						
Date of commencement of studies	October 2023	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	3	Language of instruction			Polish		
Semester of study	5	ECTS credits			1.0		
Learning profile	academic	Assessment form			credit		
Conducting unit							
Name and surname of lecturer (lecturers)	Subject supervisor		prof. dr hab. Marek Ziętara				
	Teachers		prof. dr hab. Marek Ziętara				
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						
	Additional information: The number of hours a student works consists of 15 hours of classes, 2 hours of consultations, and 8 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	15	0.0	0.0	15		
Subject objectives	The aim of the course is to familiarize students with advanced bioinformatics tools, with the techniques of molecular phylogenetics, with elements of structural bioinformatics and with the basics of genomics.						
Learning outcomes	Course outcome	Subject outcome			Method of verification		
	[BIOLL3_W11] the graduate has an advanced knowledge of 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		
	[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_U04] the graduate can apply statistical methods and computer algorithms and techniques to describe phenomena and analyse biological data	Effect achieved in exercises.			[SU2] presentation/project/paper/report		
	[BIOLL3_K05] the graduate is ready to be responsible for his/her own and others' safety at work and to recognise risk situations and take appropriate action	Effect achieved in exercises.			[SK8] observation of student's independent or team work		

Subject contents	Lecture: Molecular evolution in bioinformatics terms. Discussion of phylogenetic relationships of diagnosed taxa in the selected research model. Characteristics and interpretation of phylogenetic trees (discussion of the reliability of tree topology, the phenomenon of gene duplication - orthologs and paralogues, the phenomenon of incomplete sorting of phylogenetic lines, the phenomenon of attraction of long branches, hybridization, the problem of the outer group). The issue of the molecular clock. Selected RNA/protein structures. Discussion and comparison of genomes in the selected research model.								
Prerequisites and co-requisites	<p>formal requirements:</p> <p>passing the Bioinformatics exercises in diagnostics before admission to the exam.</p> <p>prerequisites: Knowledge and skills in Fundamentals of Bioinformatics. 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" data-bbox="448 775 1487 846"> <thead> <tr> <th data-bbox="448 775 794 808">Subject passing criteria</th> <th data-bbox="794 775 1141 808">Passing threshold</th> <th data-bbox="1141 775 1487 808">Percentage of the final grade</th> </tr> </thead> <tbody> <tr> <td data-bbox="448 808 794 846">Written exam</td> <td data-bbox="794 808 1141 846">51.0%</td> <td data-bbox="1141 808 1487 846">100.0%</td> </tr> </tbody> </table>			Subject passing criteria	Passing threshold	Percentage of the final grade	Written exam	51.0%	100.0%
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Written exam	51.0%	100.0%							
Recommended reading	<p>Basic literature</p>	<p>A. Literature required for the final passing of the course (passing the exam):</p> <p>A.1. used during classes</p> <p>Jin Xiong. Podstawy bioinformatyki. Wydawnictwa Uniwersytetu Warszawskiego</p> <p>A.2. studied by the student on his or her own</p> <p>Barry G. Hall Łatwe drzewa filogenetyczne. Wydawnictwa Uniwersytetu Warszawskiego</p> <p>scientific articles indicated by the lecturer</p>							
	<p>Supplementary literature</p>	<p>B. Supplementary literature</p> <p>Baxevanis A.D., Ouellette B.F. (red.) (2005) Bioinformatyka - podręcznik do analizy genów i białek. PWN, ISBN 83-01-142111</p> <p>Paul G. Higgs, Teresa K. Attwood (2008) Bioinformatyka i ewolucja molekularna. PWN, ISBN: 978-83-01-15494-3</p>							
	eResources addresses								
Example issues/ example questions/ tasks being completed	Nie dotyczy								
Work placement	Not applicable								

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