

**Subject card**

<b>Subject name and code</b>	Bioinformatics in diagnostics, PG_00147787						
<b>Field of study</b>	Genetics and Experimental Biology						
<b>Date of commencement of studies</b>	October 2024	<b>Academic year of realisation of subject</b>				2026/2027	
<b>Education level</b>	undergraduate studies	<b>Subject group</b>				Obligatory subject group in the field of study	
<b>Mode of study</b>	full-time studies	<b>Mode of delivery</b>				at the university	
<b>Year of study</b>	3	<b>Language of instruction</b>				Polish Polish	
<b>Semester of study</b>	6	<b>ECTS credits</b>				2.0	
<b>Learning profile</b>	academic	<b>Assessment form</b>					
<b>Conducting unit</b>	Pracownia Ewolucji Molekularnej i Bioinformatyki -> Katedra Genetyki Ewolucyjnej i Biosystematyki -> Faculty of Biology						
<b>Name and surname of lecturer (lecturers)</b>	Subject supervisor		prof. dr hab. Marek Ziętara				
	Teachers						
<b>Lesson types</b>	<b>Lesson type</b>	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	<b>Number of study hours</b>	30.0	0.0	0.0	0.0	0.0	30
	E-learning hours included: 0.0						
<b>Learning activity and number of study hours</b>	<b>Learning activity</b>	Participation in didactic classes included in study plan		Participation in consultation hours		Self-study	SUM
	<b>Number of study hours</b>	30		3.0		17.0	50
<b>Subject objectives</b>	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						
<b>Learning outcomes</b>	<b>Course outcome</b>		<b>Subject outcome</b>			<b>Method of verification</b>	
	[GBEL3_W08] information technology applied in genetics and experimental biology.		Knows the principles of operation of bioinformatic analysis programs and selected methods of construction and interpretation of phylogenetic trees based on DNA and protein sequences.			[SW4] test/exam - oral or written	
	[GBEL3_W01] Understanding the structure and properties of basic types of biological macromolecules, molecular mechanisms of metabolic pathways and genetic information flow, as well as sources of genetic variability in organisms and mechanisms of evolution; explaining the rules of inheritance, elucidating differences in the structure and functioning of prokaryotic and eukaryotic cells, and understanding the structure and functional relationships at the cellular and tissue levels.		It describes the structure and properties of macromolecules, as well as explains the rules of their inheritance.  He knows the principles of evolution sequences, structure and function of DNA.			[SW4] test/exam - oral or written	
<b>Subject contents</b>	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: passing the Bioinformatics exercises in diagnostics before admission to the exam.</p> <p>prerequisites: Knowledge and skills in Fundamentals of Bioinformatics.</p> <p>additional requirements:</p> <p>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.</p>								
Assessment methods and criteria	<table border="1"> <thead> <tr> <th data-bbox="459 651 786 680">Subject passing criteria</th> <th data-bbox="802 651 1137 680">Passing threshold</th> <th data-bbox="1153 651 1481 680">Percentage of the final grade</th> </tr> </thead> <tbody> <tr> <td data-bbox="459 685 786 714">Written exam</td> <td data-bbox="802 685 1137 714">51.0%</td> <td data-bbox="1153 685 1481 714">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>							
	<p>eResources addresses</p>	<p>Adresy na platformie eNauczanie:</p>							
Example issues/ example questions/ tasks being completed	Not applicable								
Work placement	Not applicable								

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