Subject card

Subject name and code	Bioinformatics in diagnostics, PG_00090770		
Field of study	Genetics and Experimental 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	6	ECTS credits	2.0
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 dr Beata Guzow-Krzemińska dr Natalia Olędrzyńska mgr Michalina Kijowska	

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:						

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	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
[GBEL3_U02] The graduate is able to: use computer programmes for analysis and calculation, and use databases and bioinformatics tools to solve biological problems	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
[GBEL3_U04] The graduate is able to: read scientific texts in English and Polish with comprehension, synthesise the knowledge they contain, prepare well-documented papers on biological problems and on the commercialisation of research	Can read and understand scientific texts in bioinformatics in English and prepare their translation into Polish.	[SU1] oral statement/conversation/discussion [SU8] observation of student's independent or team work
[GBEL3_K08] The graduate is prepared to: takes responsibility for equipment/materials entrusted to it and respects the work of others	Is responsible for the computer equipment/materials entrusted to him/her, his/her own work and respects the work of others.	[SK1] oral statement/conversation/discussion [SK8] observation of student's independent or team work

<table>
<tr><td>Subject contents</td><td colspan="2">Exercises: Reconstruction of phylogenetic relationships of diagnosed taxa in a selected research model. Use of bioinformatics tools for detailed description of phylogenetic trees for their presentation and interpretation. Estimation of phylogenetic compounds using the molecular clock method. Application of bioinformatics methods to predict selected RNA/protein structures. Application of bioinformatics methods to map, assemble and compare genomes. Use of specialized software (e.g. MEGA, Seaview, BEAST, MrBayes, tRNAscan-SE).</td></tr>
<tr><td>Prerequisites
and co-requisites</td><td colspan="2">prerequisites: knowledge and skills in Fundamentals of Bioinformatics.

formal requirements: the student is obliged to participate in the lecture Bioinformatics in diagnostics

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.

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.</td></tr>
<tr><td>Assessment methods
and criteria</td><td colspan="2"><table>
<tr><th>Subject passing criteria</th><th>Passing threshold</th><th>Percentage of the final grade</th></tr>
<tr><td>Colloquium</td><td>51.0%</td><td>60.0%</td></tr>
<tr><td>Average of partial grades</td><td>51.0%</td><td>40.0%</td></tr>
</table></td></tr>
<tr><td rowspan="3">Recommended reading</td><td>Basic literature</td><td>A. Literature required for the final passing of the course (passing the exam):

A.1. used during classesJ

in Xiong. Podstawy bioinformatyki. Wydawnictwa Uniwersytetu Warszawskiego

A.2. studied by the student on his or her own

Barry G. Hall Łatwe drzewa filogenetyczne. Wydawnictwa Uniwersytetu Warszawskiego

scientific articles indicated by the lecturer</td></tr>
<tr><td>Supplementary literature</td><td>B. Supplementary literature

Baxevanis A.D., Ouellette 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</td></tr>
<tr><td>eResources addresses</td><td></td></tr>
<tr><td>Example issues/
example questions/
tasks being completed</td><td colspan="2">Nie dotyczy</td></tr>
<tr><td>Work placement</td><td colspan="2">Not applicable</td></tr>
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