University of Gdańsk

Subject card

Subject name and code	Bioinformatics for biologists, PG_00079748		
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	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 Beata Guzow-Krzemińska dr Natalia Olędrzyńska dr hab. Marcin Górniak dr hab. Andre Viola De Moura	

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 his/her own and others' safety at work and to recognise risk 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
[BIOLL3_W12] the graduate knows and understands the principles of using IT tools for data analysis and interpretation of natural phenomena and processes	The effect demonstrated in the lecture.	[SW4] test/exam - oral or written
[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 effect demonstrated in the lecture.	[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

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.

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.

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
Average of partial grades	51.0%	40.0%
Colloquium	51.0%	60.0%

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	Not applicable	
Work placement	Not applicable	

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