

Subject card

Subject name and code	Phylogenesis in practice, PG_00154742						
Field of study	Biology						
Date of commencement of studies	October 2024		Academic year of realisation of subject		2025/2026		
Education level	postgraduate studies		Subject group		Obligatory subject group in the field of study Optional subject group		
Mode of study	full-time studies		Mode of delivery		at the university		
Year of study	2		Language of instruction		Polish		
Semester of study	3		ECTS credits		2.0		
Learning profile	academic		Assessment form				
Conducting unit	Faculty of Biology						
Name and surname of lecturer (lecturers)	Subject supervisor		dr hab. Marcin Górniak				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	30.0	0.0	0.0	0.0	30
	E-learning hours included: 0.0						
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		5.0		15.0	50
Subject objectives	Students are learning diagnostic techniques based on nucleic acid sequences. They are taught molecular and statistical methods for identifying individuals/genotypes and assessing genetic diversity. They gain basic knowledge about sequence data analysis and the skill of constructing phylogenetic trees from molecular data. Information about the mechanisms, advantages, disadvantages, and applications of phylogenetic analysis methods in diagnostics is provided. They also become familiar with basic computer programs for phylogenetic analysis.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[BIOLMU2_U03] the graduate can critically analyse and select biological information, especially from electronic sources	Is able to interpret the results of phylogenetic analysis.	[SU2] presentation/project/paper/report
	[BIOLMU2_W05] the graduate knows and understands the dynamic development of the biological sciences and new research directions and disciplines	Understands the advantages, disadvantages, and limitations of applying individual methods of phylogenetic analysis.	[SW4] test/exam - oral or written [SW1] oral statement/conversation/discussion
	[BIOLMU2_W01] the graduate knows and understands natural phenomena and processes at different levels of complexity	Is familiar with basic methods of phylogenetic analysis and understands their significance in practice, explaining the principles of operation of fundamental methods of phylogenetic analysis.	[SW4] test/exam - oral or written [SW1] oral statement/conversation/discussion
	[BIOLMU2_W04] the graduate has an in-depth knowledge of the chosen specialisation in the biological sciences	Is familiar with basic methods of phylogenetic analysis and understands their significance in practice, explaining the principles of operation of fundamental methods of phylogenetic analysis.	[SW4] test/exam - oral or written [SW1] oral statement/conversation/discussion
	[BIOLMU2_U05] the graduate is able to use statistical methods and computer techniques and tools to describe biological phenomena and analyse specialised data	Selects the appropriate computer program and method for phylogenetic analysis depending on the available output data.	[SU2] presentation/project/paper/report
	[BIOLMU2_U01] the graduate is able to select and apply research techniques and tools appropriate to the problems of the biological sciences specialisation studied	Is able to conduct a basic analysis of sequence data.	[SU2] presentation/project/paper/report
	[BIOLMU2_K01] the graduate is ready for initiative and independence of action and feels the need for lifelong learning	Understands the need for lifelong learning and updating knowledge in the field of phylogenetic analysis and its practical application.	[SK1] oral statement/conversation/discussion
Subject contents	Applications of phylogenetic analysis. Fundamental concepts used in phylogeny reconstruction, comparison of phenetic and cladistic analysis techniques, construction of cladograms, types of data matrices, algorithmic methods, and optimization-based methods, network analysis, models of evolution of nucleotide and amino acid sequences, the problem of finding the best tree, difficulties in phylogeny reconstruction and its reliability, stages of computerized analysis of sequence data, overview of computer programs used for phylogenetic analysis. Analysis of molecular data. Gene Bank as a source of information: analysis of genetic polymorphism (including Sars-CoV2, HIV viruses) and species identification; determination of relatedness, subtypes, tracking sources and routes of infections, and virus spread using the example of viruses (including HIV). Stages of computerized analysis of sequence data. Overview of computer programs used for phylogenetic analysis.		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Passing a test with open-ended questions and/or multiple-choice questions	51.0%	70.0%
	Overall assessment based on partial grades received.	51.0%	30.0%
Recommended reading	Basic literature	Futuyma E. J. 2008. Evolution. Wydawnictwo Uniwersytetu Warszawskiego, Wa-wa. Hall B.G. Phylogenetic Trees Made Easy A How-To Manual Fifth Edition.	
	Supplementary literature	articles published in current scientific journals with global reach. Felsenstein J. 2004. Inferring Phylogenies. Sinauer Associates, Sunderland, MA. Graur D., Wen-Hsiung L. 2000. Fundamentals of Molecular Evolution. Second Edition. Sinauer Associates, Sunderland, MA.	
	eResources addresses	Adresy na platformie eNauczanie:	
Example issues/ example questions/ tasks being completed	None		

Work placement	Not applicable
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