

Subject card

Subject name and code	Introduction to phylogenetic analysis, PG_00207258						
Field of study	Biology						
Date of commencement of studies	October 2026		Academic year of realisation of subject		2026/2027		
Education level	Master's studies		Subject group		Obligatory subject group in the field of study Optional subject group Subject group related to scientific research in the field of study		
Mode of study	full-time studies		Mode of delivery		at the university		
Year of study	1		Language of instruction		Polish		
Semester of study	2		ECTS credits		1.0		
Learning profile	academic		Assessment form		exam		
Conducting unit	Laboratory of Mammalian Evolutionary Genomics -> Department of Evolutionary Genetics and Biosystematics -> Faculty of Biology -> Rector						
Name and surname of lecturer (lecturers)	Subject supervisor		prof. dr hab. Małgorzata Pilot				
	Teachers						
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						
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		1.0		9.0	25
Subject objectives	To familiarize students with phylogenetic methods based on nucleic acid sequence analysis. To provide knowledge about molecular and statistical methods enabling the identification of individuals/genotypes and the assessment of genetic diversity. To inform students about the basic steps of sequential data analysis. Shaping the ability to construct trees of phylogenetic relationships based on molecular data. To provide information to understand the mechanisms, advantages and disadvantages and applications of basic methods of phylogenetic analyses.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[BIOLMU2_W05] has an in-depth knowledge and understanding of the dynamic development of the biological sciences and is well versed in new research trends and disciplines	The graduate understands the advantages, disadvantages and limitations of the use of individual methods of phylogenetic analyses	[SW4] test/exam - oral or written
	[BIOLMU2_W04] has in-depth knowledge of the chosen specialization in the biological sciences	The graduate knows the basic methods of phylogenetic analysis and understands their practical importance, can explain the principles of operation of basic methods of phylogenetic analyses	[SW4] test/exam - oral or written
	[BIOLMU2_W01] has a deep knowledge and understanding of natural phenomena and processes at various levels of complexity	The graduate knows the basic methods of phylogenetic analysis and understands their practical importance, can explain the principles of operation of basic methods of phylogenetic analyses	[SW4] test/exam - oral or written
	[BIOLMU2_U05] is able to use statistical methods and IT techniques and tools to describe biological phenomena and analyze specialized data	The graduate chooses an appropriate computer program and method of phylogenetic analyses depending on the output data	[SU1] oral statement/conversation/discussion [SU4] test/exam - oral or written
	[BIOLMU2_U03] is able to critically analyze and select biological information, especially from electronic sources	The graduate is able to interpret the results of phylogenetic analyses	[SU1] oral statement/conversation/discussion [SU4] test/exam - oral or written
	[BIOLMU2_K01] shows initiative and is ready to act independently and feels the need for lifelong learning	The graduate understands the need for lifelong learning and updating knowledge in the field of phylogenetic analyses and their practical application	[SK1] oral statement/conversation/discussion
Subject contents	Application of phylogenetic analyses. Basic concepts used in phylogeny reconstruction, comparison of phenetic and cladistic analysis techniques, cladogram construction, types of data matrices, algorithmic methods and methods based on the optimization criterion, network analyses, models of nucleotide and amino acid sequence evolution, the problem of finding the best tree, difficulties in phylogeny reconstruction and its reliability, stages of computer phylogenetic analysis of sequence data, overview of computer programs used for phylogenetic analyses.		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	test assessment with open questions	50.0%	100.0%
Recommended reading	Basic literature Futuyma E. J. 2009. Evolution, Second Edition. Sinauer Associates. Sunderland, MA Hall B.G. 2004. Phylogenetic trees made easy: A how to manual. Sinauer Associates, Sunderland, MA.		

	Supplementary literature	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. Hall B.G. 2004. Phylogenetic trees made easy: A how to manual. Sinauer Associates, Sunderland, MA.
	eResources addresses	
Example issues/ example questions/ tasks being completed	Basic concepts used in phylogeny reconstruction, cladogram construction, types of data matrices, algorithmic methods and methods based on the optimization criterion, network analyses, models of nucleotide and amino acid sequence evolution, the problem of finding the best tree, difficulties in phylogeny reconstruction and its reliability, stages of computer phylogenetic analysis of sequence data, computer programs used for phylogenetic analyses	
Work placement	Not applicable	

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