

Subject card

Subject name and code	Introduction to phylogenetic analysis, PG_00154710						
Field of study	Biology						
Date of commencement of studies	October 2024		Academic year of realisation of subject		2024/2025		
Education level	postgraduate 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 if there is a need, the lecture can be conducted in English		
Semester of study	2		ECTS credits		1.0		
Learning profile	academic		Assessment form				
Conducting unit	Pracownia Genomiki Ewolucyjnej Ssaków -> Katedra Genetyki Ewolucyjnej i Biosystematyki -> Faculty of Biology						
Name and surname of lecturer (lecturers)	Subject supervisor		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		2.0		8.0	25
Subject objectives	To familiarize students with diagnostic 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_U03] the graduate can critically analyse and select biological information, especially from electronic sources	The graduate is able to interpret the results of phylogenetic analyses	[SU8] observation of student's independent or team work
	[BIOLMU2_K01] the graduate is ready for initiative and independence of action 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
	[BIOLMU2_W05] the graduate knows and understands the dynamic development of the biological sciences and new research directions 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_W01] the graduate knows and understands natural phenomena and processes at different 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] the graduate is able to use statistical methods and computer techniques and tools to describe biological phenomena and analyse specialised data	The graduate chooses an appropriate computer program and method of phylogenetic analyses depending on the output data	[SU8] observation of student's independent or team work
	[BIOLMU2_W04] the graduate has an in-depth knowledge of the chosen specialisation 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
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	Podstawowe https://ksiegarnia.pwn.pl/Ewolucja,68958708,p.html - Evolution by Douglas J. Futuyma is a foundational textbook of evolutionary biology for students of all fields of biology, environmental protection, medicine, veterinary medicine and other agricultural sciences. In Evolution, Futuyma refers to the latest examples from laboratory and field research, and his book has an extremely reader-friendly form. Numerous colour photographs, illustrations, diagrams and charts, as well as frames and tables present the discussed problems in an accessible way, and each chapter ends with an excellent summary and a set of problems to solve on your own. This textbook is very popular at universities around the world. https://ksiegarnia.pwn.pl/Latwe-drzewa-filogenetyczne,68600742,p.html - Easy phylogenetic trees. The User Guide is a kind of "cookbook" in the field of molecular phylogeny, providing very accessible instructions for performing a meaningful phylogenetic analysis based on nucleic acid and protein sequences with relatively little effort. It discusses all the basic methods of modern molecular phylogenetics, which is currently an indispensable tool of modern biology (not only evolutionary) - from the simplest to the most advanced. The reader is led "by hand" through the entire process of building phylogenetic trees using various methods and checking their reliability. For those more interested in the theory of tree structure, there is information deepening knowledge about various phylogenetic methods and concepts. Uzupełniające Adresy na platformie eNauczanie:
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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