

Subject card

Subject name and code	Molecular phylogenetics versus taxonomy, PG_00150917						
Field of study	Medical Biology						
Date of commencement of studies	October 2025		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		
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		1.0		
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		dr hab. Marcin Górniak				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	15.0	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		3.0		7.0	25
Subject objectives	Introducing students to the molecular aspects of evolution and bioinformatics methods used in evolutionary studies. It will be demonstrated that the theory of evolution allows for the integration of seemingly disparate areas of biological research into a coherent system.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[BIOLMEDMU2_U01] can proficiently, but critically, use the scientific literature and databases necessary in the activities of medical biology and related disciplines	Is able to edit and align homologous DNA sequences obtained from a database. Can select the appropriate molecular marker to solve a given phylogenetic and taxonomic problem.	[SU4] test/exam - oral or written
	[BIOLMEDMU2_W03] knows the structure and functions of the human body, biological causes of disorders, lesions and social dysfunctions, and methods of their evaluation using biochemical, molecular, parasitological or neurobiological methods	The student knows: 1. The structures of nucleic acids and proteins, as well as the flow of genetic information in the cell. 2. The sources of genetic variability, types of molecular markers, their inheritance patterns, and the processes shaping genetic variability in populations. 3. Useful molecular techniques. 4. Selected methods for constructing and interpreting phylogenetic trees, primarily based on DNA sequences. 5. The principle of the molecular clock.	[SW4] test/exam - oral or written
	[BIOLMEDMU2_U03] is able to formulate and solve problems on the basis of the known laws and methods, including - using computer tools and statistical methods	Is able to construct, describe, and interpret simple phylogenetic trees. an provide examples of the applications of bioinformatics analyses in contemporary research.	[SU4] test/exam - oral or written
Subject contents	Genetic diversity at the molecular level: genes, genetic code, mutations. Genetic variability at the population level. Natural selection, neutral evolution, molecular evolution. Dynamics of DNA sequence changes and the molecular clock. Phylogeny and molecular taxonomy: application of bioinformatics methods.		
Prerequisites and co-requisites	The student should have previously completed the following courses:1. Biochemistry,2. Molecular Biology,3. Cell Biology,4. Biodiversity and Evolution,5. Statistics.		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Assessment in the form of a test with open-ended questions	51.0%	100.0%
Recommended reading	Basic literature	Markery molekularne, historia naturalna i ewolucja. Avise John C (2008) Warszawa. Wyd. UWŁatwe drzewa filogenetyczne. Hall Barry (2008) Warszawa, Wyd. UW	
	Supplementary literature	Selected scientific articles.	
	eResources addresses		
Example issues/ example questions/ tasks being completed	None		
Work placement	Not applicable		

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