Subject card

Subject name and code	Methods of phylogenetic analyses in diagnostics, PG_00203470		
Field of study	Medical Biology		
Date of commencement of studies	October 2026	Academic year of realisation of subject	2028/2029
Education level	Bachelor’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	3	Language of instruction	Polish
Semester of study	6	ECTS credits	1.0
Learning profile	academic	Assessment form	credit
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	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 introduce students to molecular and statistical methods enabling the identification of individuals/genotypes and the assessment of genetic diversity. Presentation of the basic steps of sequential data analysis. Shaping the ability to construct trees of phylogenetic relationships based on molecular data. To familiarize students with the mechanisms, advantages and disadvantages as well as the applications of basic methods of phylogenetic analyses in diagnostics.

Learning outcomes

Course outcome	Subject outcome	Method of verification
[BIOLMEDL3_W16] has an advanced knowledge of the experimental methods and the most important techniques of biological sciences that can be applied to medical biology and diagnostics	The graduate is able to explain the theoretical basis of research techniques used for the analysis of genetic variation and knows their application in medical biology and diagnostics	[SW4] test/exam - oral or written [SW1] oral statement/ conversation/discussion
[BIOLMEDL3_W14] describes the principles of using computer tools to analyze data and interpretation of biological phenomena and processes	The graduate knows the basic methods of phylogenetic analysis and understands their importance in molecular and biochemical diagnostics	[SW4] test/exam - oral or written [SW1] oral statement/ conversation/discussion
[BIOLMEDL3_U08] can interpret scientific data related to the profession of medical biologist	The graduate is able to interpret the results of phylogenetic analyses	[SU1] oral statement/conversation/ discussion [SU8] observation of student's independent or team work
[BIOLMEDL3_U04] applies basic statistical methods and computer algorithms and techniques to describe phenomena and data analysis	The graduate applies statistical methods as well as bioinformatics techniques and tools to the analysis of molecular data; selects the appropriate computer program and method, depending on the output data available, performs a simple phylogenetic analysis	[SU1] oral statement/conversation/ discussion [SU8] observation of student's independent or team work
[BIOLMEDL3_K01] understands the need for lifelong learning and to update his/her knowledge of medical biology and related disciplines	The graduate understands the need for lifelong learning and updating knowledge in the field of phylogenetic analyses and their application in medical biology	[SK1] oral statement/conversation/ discussion

Subject contents

Scope of applications of phylogenetic analyses: m.in. veterinary medicine, epidemiology, microorganism typing, forensic medicine, environmental protection, food industry. The use of DNA markers for genotyping and polymorphism assessment. Problems of selecting the appropriate molecular marker. The relationship of genetic polymorphism with morbidity and treatment effectiveness. Molecular methods for identifying microorganisms. Barcoding. Comparative phylogenetics. Basic concepts used in the reconstruction of phylogeny. Data matrix types. An overview of methods used in phylogenetic analyses. Models of the evolution of nucleotide and amino acid sequences, the problem of finding the best tree, difficulties in reconstructing phylogeny and its reliability.

Prerequisites and co-requisites

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
graded assessment: test with open questions	50.0%	100.0%

Recommended reading

Basic literature	Baxevanis A. D., Quellette B. F. F. (eds.). Bioinformatics: A Practical Guide to the Analysis of Genes & Proteins (third editon). New York: John Wiley & Sons. Brown T. A. 2023. Genomes. CRC Press. Boca Raton. Futuyma DJ, Kirkpatrick M. 2022. Evolution, 5th ed. Oxford University Press. 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, Sunder-land, MA. Hall B.G. 2004. Phylogenetic trees made easy: A how to manual. Sinauer Associates, Sunderland, MA. Hills D. M. i in. (red.). 1996. Molecular systematic. Sinauer Associates, Sunderland, MA. Salemi M. Vandamme A.M. 2003. The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny. Cambridge University Press
	eResources addresses	
Example issues/ example questions/ tasks being completed	- Advantages and disadvantages of various genetic markers used for genotyping and polymorphism assessment;- How to select the appropriate molecular marker;- Application of barcoding and metabarcoding in the identification of microorganisms;- Modeling the evolution of nucleotide and amino acid sequences;- Methods of phylogenetic tree construction;- Ways to search the treespace to find the best tree;- Methods of assessing the reliability of phylogenetic trees;- Interpretation of phylogenetic trees for diagnostic purposes	
Work placement	Not applicable	