University of Gdańsk

Subject card

Subject name and code	Methods of phylogenetic analyses in diagnostics, PG_00203469		
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	2.0
Learning profile	academic	Assessment form	credit

Conducting unit	Department of Evolutionary Genetics and Biosystematics -> Faculty of Biology -> Rector	
Name and surname of lecturer (lecturers)	Subject supervisor	mgr Michalina Kijowska
	Teachers	

Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	15.0	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	4.0	31.0	50

Subject objectives	To learn molecular and statistical methods for identifying individuals/genotypes and assessing genetic variation. To learn the basic steps of sequence data analysis. To form 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 analysis in diagnostics. To learn the basic computer programs necessary for phylogenetic analyses.

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	explains the theoretical basis of research techniques used to analyze genetic variation and knows their application in medical biology and diagnostics	[SW2] presentation/project/paper/ report
[BIOLMEDL3_W14] describes the principles of using computer tools to analyze data and interpretation of biological phenomena and processes	knows the basic methods of phylogenetic analysis and understands their importance in molluscan-biochemical diagnostics	[SW2] presentation/project/paper/ report
[BIOLMEDL3_U04] applies basic statistical methods and computer algorithms and techniques to describe phenomena and data analysis	applies statistical methods and bioinformatics techniques and tools to analyze molecular data; selects the appropriate computer program and method, depending on the output data available, performs simple phylogenetic analysis	[SU5] implementation of a problem task [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	understands the need for lifelong learning and updating knowledge of phylogenetic analysis and its application in medical biology	[SK8] observation of student's independent or team work
[BIOLMEDL3_U08] can interpret scientific data related to the profession of medical biologist	can interpret the results of phylogenetic analyses	[SU5] implementation of a problem task [SU8] observation of student's independent or team work

Subject contents

Analysis of molecular data. Construction of cladograms: algorithmic methods and methods based on the optimization criterion. Network analyses. Gene Bank as a source of information: analyses of genetic polymorphism (e.g., HBV, HPV, HIV) and species identification; determination of relatedness, subtypes, tracing sources and routes of infection and viral spread using viruses (including HIV) as examples. Steps in computer phylogenetic analysis of sequence data. Review of computer programs used for phylogenetic analysis. Use of scientific literature on population and evolutionary genetics. Planning and performing simple research tasks in the field of diagnostics, population and evolutionary genetics under the guidance of a mentor.

Prerequisites and co-requisites

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
final report	51.0%	60.0%
worksheets	51.0%	40.0%

Recommended reading

Basic literature	Baxevanis A. D., Quellette B. F. F. (ed.). Bioinformatics, Polish Scientific Publishers PWN, Warsaw, 2005 Brown T. A. Genomes. Polish Scientific Publishers PWN, Warsaw, 2001 Futuyma E. J. Evolution. Warsaw University Publishing House, Warsaw, 2008 Hall B.G. Phylogenetic trees made easy. Warsaw University Publishing House, Warsaw, 2008

	Supplementary literature	Felsenstein J. Inferring Phylogenies. Sinauer Associates, Sunderland, MA, 2004 Graur D., Wen-Hsiung L. Fundamentals of Molecular Evolution. Second Edition. Sinauer Associates, Sunder-land, MA, 2000 Hall B.G. Phylogenetic trees made easy: A how to manual. Sinauer Associates, Sunderland, MA, 2004 Hills D. M. i in. (ed.). Molecular systematic. Sinauer Associates, Sunderland, MA, 1996 Salemi M. Vandamme A.M. The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phyloge-ny. Cambridge University Press, 2003
	eResources addresses	
Example issues/ example questions/ tasks being completed	Case study: A 61-year-old HIV-negative patient underwent surgery during which no blood transfusion was given. She then began to show symptoms of HIV infection and was shown to be seropositive. Using phylogenetic analysis tools, answer the question: was the patient infected by the hospital's medical staff?	
Work placement	Not applicable	