University of Gdańsk

Subject card

Subject name and code	Molecular Phylogenetics, PG_00193530		
Field of study	Bioinformatics		
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 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	5	ECTS credits	5.0
Learning profile	academic	Assessment form	exam

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	prof. dr hab. Marek Ziętara
	Teachers	

Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	30.0	0.0	45.0	0.0	0.0	75
	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	75	0.0	50.0	125

Subject objectives	The aim of the course is to familiarize students with the methods of phylogenetic analyses using DNA and protein sequences. Students will learn both the theoretical foundations of these analyses (KW_02) as well as acquire knowledge and skills to carry them out independently (KW_04, KU_01). Students will acquire the ability to independently interpret their own and published results of phylogenetic analyses, including the ability to propose evolutionary scenarios based on these results (KU_05).

Learning outcomes

Course outcome	Subject outcome	Method of verification
[BIOINL3_U05] Graduate has the ability to use scientific literature, including English-language sources on bioinformatics; has the ability to use appropriate databases	Can obtain sequences for phylogenetic analyses. Can use literature sources and computer resources in English.	[SU1] oral statement/conversation/ discussion [SU2] presentation/project/paper/ report [SU4] test/exam - oral or written
[BIOINL3_W02] Has advanced scientific knowledge necessary to understand the basic processes in living organisms.	Knows the molecular markers used in phylogenetic taxonomy. He knows the concepts of genealogy and coalescence. He knows the theoretical foundations of phylogeography, molecular clock, speciation, hybridization of species. He knows the differences between gene and species trees. He knows the mechanisms of gene duplication and differentiation.	[SW4] test/exam - oral or written [SW3] text preparation/written work
[BIOINL3_W04] Has advanced knowledge of research techniques and tools used in bioinformatics	He knows models of the evolution of DNA sequences. He knows the principles of phylogenetic tree reconstruction. Knows methods of verification of phylogenetic trees. Knows the principles of predicting ancestral sequences.	[SW4] test/exam - oral or written [SW3] text preparation/written work
[BIOINL3_U01] Graduate is able to program using modern programming tools, including tools dedicated to bioinformatics	He can align sequences and calculate the model of evolution. Can reconstruct phylogenetic trees using specialized software. Can independently interpret phylogenetic trees. Can evaluate the topology of phylogenetic trees using specialized software. Can reconstruct ancestral sequences using phylogenetic methods.	[SU1] oral statement/conversation/ discussion [SU2] presentation/project/paper/ report [SU3] text preparation/written work

Subject contents	*Taxonomy and molecular phylogenetics* Lecture 16 hours Molecular markers used in taxonomy. Analysis of sequencing results. Relationship and intraspecific genealogy (coalescence). Phylogeography, molecular clock, speciation and hybridization. Models of molecular evolution of DNA sequences. Phylogenetic trees of species. Phylogeny of species and phylogeny of genes. A review of software for the construction and verification of phylogenetic trees, including: MEGA, Beast, jModelTest, PhyML, MrBayes. Laboratory/computer exercises 24 hours Acquisition and preparation of DNA sequences for phylogenetic analyses. Sequence compilation and adjustment of the evolution model. Reconstruction of phylogenetic trees using distance methods (NJ and ME), trait-based methods (MP), maximal likelihood (ML) and Bayesian methods. Assessment of the reliability of phylogenetic trees. Application of the molecular clock. *Phylogenetics and molecular evolution of proteins* Lecture 14 hours Models of molecular evolution of protein sequences. Reconstruction of phylogenetic trees based on protein sequences. Methods of verification of phylogenetic trees. Phylogeny of protein-coding genes and phylogeny of species. The rate of molecular evolution and the molecular clock. Neutral theory of evolution and types of selection acting on protein-coding genes. Duplication, horizontal transfer and evolution of protein-coding gene families. Predicting the sequence of ancestors of protein-coding genes. Laboratory/computer exercises 21 hours Acquisition and preparation of protein sequences for phylogenetic analyses. Sequence alignment and adjustment of the evolution model. Reconstruction of phylogenetic trees using maximum likelihood and Bayesian methods. Assessment of the reliability of phylogenetic trees. Application of the molecular clock. Reconstruction of phylogenetic trees of protein-coding gene families and their interpretation. Phylogenetic reconstruction of ancestral sequences.

Prerequisites and co-requisites

prerequisites: After completing compulsory subjects in the first four semesters, the student has the knowledge and skills qualifying him or her to participate in and pass the course.

formal requirements: Passed: Biodiversity and Basics of Taxonomy, Bioinformatics Sequence Analysis, Molecular Biology and Genetics, Genomics, Basics of Stochastic Processes for Bioinformatics Specialists

additional requirements:

1. Attendance at classes is obligatory, and in the event of absence, it must be justified in accordance with paragraph 12 of the UG Study Regulations.

2. The condition for passing the lecture is attendance at least 80% of classes, while the condition for passing the classes is participation in at least 85% of classes.

3. The condition for admission to the exam is passing the exercises. In the case of test questions, the student will choose one of the possible answers and briefly justify their choice or synthetically answer open questions. The questions can be illustrated with an appropriate chart, diagram, etc. The exam will test both the student's knowledge and skills.

4. A negative grade in the written exam must be corrected during the resit exam held on the basis of the same rules as the exam on the first date.

5. The skills acquired during the exercises will be verified on an ongoing basis by the lecturers. During the exercises, the facilitator will also check the students' knowledge directly related to the acquired skills (questions, discussion). The teacher will assess the skills and knowledge of each student so that at the end of the exercises each student will have a minimum of 4 grades.

Assessment methods and criteria

Subject passing criteria	Passing threshold	Percentage of the final grade
Written exam	51.0%	60.0%
Laboratory - average of partial marks	51.0%	40.0%

Recommended reading

Basic literature	A. Literature required for the final passing of the course (passing the exam): • Original scientific publications and studies prepared by the teacher and made available to students during classes. • Bioinformatyka i ewolucja molekularna. PG Higgs i TK Atwood, Wydawnictwo Naukowe PWN, Warszawa 2008. • Bioinformatyka- podręcznik do analizy genów i białek. AD Baxevanis BFF Ouellette Wydawnictwo Naukowe PWN, Warszawa 2004. • Markery molekularne, historia naturalna i ewolucja. JC Avise Uniwersytet Warszawski, Warszawa, 2008 • Łatwe drzewa filogenetyczne. Hall Barry (2008) Warszawa, Wyd. UW.
Supplementary literature	B. Supplementary literature: • Genomes 3 T.A. Brown , 2007, Garland Science. • Ekologia molekularna. Joanna R. Freeland (2008) Warszawa PWN. • Brown T.A. Genomy, wyd. II, przekład pod red. P. Węgleńskiego, Wydawnic
eResources addresses	

Example issues/ example questions/ tasks being completed

Not applicable

Work placement

Not applicable