

Subject card

Subject name and code	Genes and Populations in Time and Space, PG_00156401						
Field of study	Bioinformatics						
Date of commencement of studies	October 2025		Academic year of realisation of subject		2027/2028		
Education level	Bachelor's studies		Subject group		Optional subject group		
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		3.0		
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 Aleksandra Naczka				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	30.0	0.0	0.0	30
	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	30		0.0		45.0	75
Subject objectives	Understand the basics of heritable and non-heritable variation, methods of describing it and the effects of various evolutionary factors shaping genetic equilibrium in populations, over time and space.						
Learning outcomes	Course outcome		Subject outcome		Method of verification		
	[BIOINL3_W04] Has knowledge of basic research techniques and tools used in bioinformatics		Identifies evolutionary processes affecting patterns of genetic variation in natural populations. Understands the causes of variation in trait frequency in natural populations. Understands the distributions of genetic variation of local populations over space.		[SW1] oral statement/ conversation/discussion [SW2] presentation/project/paper/ report [SW3] text preparation/written work		
	[BIOINL3_U02] Graduate is able to apply knowledge of natural sciences and science to formulate, analyze and solve problems related to bioinformatics		Be able to calculate and analyse parameters of genetic variation in plant and animal populations using formulas and computer programs. Can apply knowledge of genetic variation in plant and animal populations to formulate and solve bioinformatics problems.		[SU1] oral statement/conversation/ discussion [SU2] presentation/project/paper/ report [SU3] text preparation/written work		

Subject contents	1. Heritable and non-heritable variation. 2. Genetic polymorphism. 3. Gene flow in populations over time and space. 4. The problem of inbred depression in endangered species conservation. 5. Factors disturbing genetic equilibrium in populations. 6. Geographical variation in selected plant and animal species. 7. Conservation genetics. 8. Population genetic structure. 9. Haplotype networks. 10. Effective population size.		
Prerequisites and co-requisites	- entry requirements: The student, after completing the compulsory subjects in the first three semesters, has the knowledge and skills that qualify him/her to participate and pass the subject - formal requirements: Completed subjects: Biodiversity and fundamentals of taxonomy; Cell biology and metabolism; Molecular biology and genetics		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Student's own work as part of the work cards for each exercise	51.0%	100.0%
Recommended reading	Basic literature	A. Literature required for final course credit (passing the exam): A.1. used during the class - Hartl D.L. Clark A.G. Podstawy genetyki populacji Uniwersytet Warszawski, Warszawa 2009 - Freeland J.R. Ekologia molekularna. PWN, Warszawa 2008 - Frankham R. Introduction to conservation genetics. Cambridge University Press, 2010 H. Fletcher, I. Hickey, P. Winter. Genetyka. Krótkie wykład. PWN, 2010 A.2. Studied independently by the student Scientific publications made available by the teacher	
	Supplementary literature	none	
	eResources addresses		

Example issues/ example questions/ tasks being completed	Using the ARLEQUIN programme, the frequency of haplotypes will be estimated, neutrality tests will be performed, and the degree of genetic variation based on F statistics and AMOVA molecular variance analysis will be determined. Search for regions influenced by natural selection. Assessment of effective population size.
Work placement	Not applicable

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