

Subject card

Subject name and code	Population genetics, PG_00179661						
Field of study	Environmental Protection						
Date of commencement of studies	October 2026		Academic year of realisation of subject		2027/2028		
Education level	Master's studies		Subject group		Optional subject group		
Mode of study	full-time studies		Mode of delivery		at the university		
Year of study	2		Language of instruction		English		
Semester of study	4		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. Andre Viola De Moura				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	0.0	0.0	10.0	0.0	0.0	10
	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	10		5.0		10.0	25
Subject objectives	- Gain familiarity with bioinformatic methods to calculate core population genetics statistics - Understand basic workflows for quality control of genetic data - Become familiar with software packages commonly used for population genetic analyses - Correctly interpret population genetic statistics in terms of the underlying biological process						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[OŚMU2_U07] Has advanced skills in presenting the results of own research, discussions based on literature data and public speaking, including leading a debate.	- Provides correct biological interpretations of different population genetic patterns	[SU5] implementation of a problem task
	[OŚMU2_U02] Uses advanced measurement and analytical techniques used in environmental protection.	- Carries out population genetic analyses of provided datasets correctly in a manner appropriate for the problem presented	[SU5] implementation of a problem task
	[OŚMU2_W02] Has the thorough knowledge of statistical methods and modeling in environmental protection.	- Correctly uses a variety of commonly used population genetic analyses software	[SW5] implementation of a problem task
	[OŚMU2_K10] Has a need for continuous professional development.	- Provides correct biological interpretations of different population genetic patterns	[SK5] implementation of a problem task
	[OŚMU2_U04] Critically analyses experimental data on environmental protection by statistical methods and modelling using IT techniques and tools.	- Correctly uses a variety of commonly used population genetic analyses software - Provides correct biological interpretations of different population genetic patterns	[SU5] implementation of a problem task
	[OŚMU2_W04] Chooses methods, techniques and research tools used in environmental protection.	- Carries out population genetic analyses of provided datasets correctly in a manner appropriate for the problem presented	[SW5] implementation of a problem task
	[OŚMU2_U10] Uses Polish/ English in the field of environmental protection in accordance with the requirements specified for level B2+ of the Common European Framework of Reference for Languages.	- Carries out population genetic analyses of provided datasets correctly in a manner appropriate for the problem presented - Provides correct biological interpretations of different population genetic patterns	[SU5] implementation of a problem task
	[OŚMU2_K06] Recognises the importance of knowledge in solving encountered cognitive and practical problems and consults experts in the event of difficulties in solving a problem on her/his own.	- Provides correct biological interpretations of different population genetic patterns	[SK5] implementation of a problem task
Subject contents	- Calculation of fundamental genetic diversity measures, such as heterozygosity, F-statistics and Hardy-Weinberg equilibrium - Bioinformatic processing of genetic sequence data and microsatellite data - Basic genetic data quality control - Analytical methods to infer population structure - Core analytical methods for conservation genetics		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Classroom exercises	50.0%	100.0%

Recommended reading	Basic literature	Goudet, J., FSTAT (Version 1.2) (1995). A Computer Program to Calculate F-Statistics, <i>Journal of Heredity</i> 86: 485-486, Rozas, J., Ferrer-Mata, A., Sánchez-DelBarrio, J.C., Guirao-Rico, S., Librado, P., Ramos-Onsins, S.E., Sánchez-Gracia, A. (2017). DnaSP 6: DNA Sequence Polymorphism Analysis of Large Datasets. <i>Molecular Biology and Evolution</i> 34: 3299-3302 Peakall, R. and Smouse P.E. (2012) GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. <i>Bioinformatics</i> 28, 2537-2539. Pritchard, J.K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. <i>Genetics</i>, 155: 945-959 Waples, R.S. & Do, C. (2008), Ldne: a program for estimating effective population size from data on linkage disequilibrium. <i>Molecular Ecology Resources</i>, 8: 753-756 Piry, S., Luikart, G., Cornuet, J-M. (1999), Computer note. BOTTLENECK: a computer program for detecting recent reductions in the effective size using allele frequency data, <i>Journal of Heredity</i>, 90: 502-503
	Supplementary literature	Chybicki, I.J., Oleksa, A. & Kowalkowska, K. (2012) Variable rates of random genetic drift in protected populations of English yew: implications for gene pool conservation. <i>Conservation Genetics</i>, 13: 899-911 Moura AE, Tsingarska E, Dąbrowski MJ, Czarnomska SD, Jędrzejewska B, Pilot M (2014) Unregulated hunting and genetic recovery from a severe population decline: the cautionary case of Bulgarian wolves. <i>Conservation Genetics</i>, 15:405-417. Moura AE, Nielsen SCA, Vilstrup JT, Moreno-Mayar J V., Gilbert MTP, Gray H, Natoli A, Moller L, Hoelzel AR (2013) Recent Diversification of a Marine Genus (<i>Tursiops</i> spp.) Tracks Habitat Preference and Environmental Change. <i>Systematic Biology</i> 62:865-877.
	eResources addresses	
Example issues/ example questions/ tasks being completed	Calculate F-statistics for the provided dataset. Indicate the populations with the highest and lowest values of the relevant parameters. What does the F_{is} inbreeding coefficient tell us? Characterize the two populations, i.e., the pair of populations showing the highest levels of F_{st}, indicating potential divergence factors. Using data provided, perform the Wilcoxon test to infer a sudden reduction in population size. Which populations have experienced the 'bottleneck' effect in the recent history of the species?	
Work placement	Not applicable	

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