



Subject card

Subject name and code	Phylogenetics, PG_00070038						
Field of study	InfoBioChem						
Date of commencement of studies	February 2026		Academic year of realisation of subject		2026/2027		
Education level	second-cycle 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	1		Language of instruction		Polish		
Semester of study	2		ECTS credits		3.0		
Learning profile	general academic profile		Assessment form		exam		
Conducting unit	Department of Functional Materials Engineering -> Faculty of Electronics Telecommunications and Informatics -> Faculties of Gdańsk University of Technology						
Name and surname of lecturer (lecturers)	Subject supervisor		dr inż. Milena Marycz				
	Teachers						
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	30.0	0.0	30.0	0.0	0.0	60
	E-learning hours included: 0.0						
	eNauczanie source addresses: Moodle ID: 9130 Filogenetyka 2026/2027 https://enauzanie.pg.edu.pl/2025/course/view.php?id=9130						
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	60		5.0		10.0	75
Subject objectives	Introduction to the fundamentals of molecular and computational phylogenetics and their applications in biological data analysis. Familiarization with methods for data preparation and the reconstruction, evaluation, and interpretation of phylogenetic trees. Development of practical skills in applying bioinformatics tools to phylogenetic analyses.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[K7_U02] is able to use IT tools for operations on nucleotide and protein sequences.	Can use bioinformatics tools to search, compare, analyse and process nucleotide and protein sequences for phylogenetic analyses.	[SU1] Assessment of task fulfilment [SU4] Assessment of ability to use methods and tools
	[K7_U04] is able to accurately select and apply research methods and tools appropriate to the curriculum in the field of biological, medical, and chemical sciences, including molecular, systems, and medical biology, biotechnology, and bioinformatics.	Can select and apply appropriate bioinformatics methods and tools for sequence analysis and for the reconstruction and evaluation of phylogenetic trees.	[SU3] Assessment of ability to use knowledge gained from the subject [SU4] Assessment of ability to use methods and tools
	[K7_K04] is ready to effectively organize their work time, including reliably meeting deadlines for completing specific tasks.	Is ready to independently and effectively organise their work and complete assigned tasks in phylogenetic analysis within the specified deadlines.	[SK3] Assessment of ability to organize work
	[K7_W07] has a thorough knowledge and understanding of the structure and operating principles of components and systems related to the field of study, including theories, methods, and complex relationships between them, as well as selected specific issues relevant to the curriculum InfoBioChem	Knows and understands in depth the theoretical foundations, methods and tools of phylogenetic analysis, as well as the principles of reconstructing, evaluating and interpreting phylogenetic trees based on molecular data.	[SW1] Assessment of factual knowledge
Subject contents	<p>Course content – lecture</p> <p>Introduction to molecular and computational phylogenetics and the fundamental concepts of molecular evolution. Representation, structure, and interpretation of phylogenetic trees. Types of data used in phylogenetic analyses, homology, and methods for sequence comparison and alignment. Fundamentals of molecular evolution and substitution models, as well as selected methods for phylogenetic tree reconstruction. Tree space and basic concepts related to searching for and comparing tree topologies. Methods for assessing the reliability and uncertainty of phylogenetic analysis results. Analysis of multiple trees, including consensus trees and supertrees. Challenges and limitations of phylogenetic analyses. Selected contemporary applications of phylogenetics and future directions in the development of computational methods for biological data analysis.</p>		
	<p>Course content – laboratory</p> <p>Acquisition and preparation of sequence data for phylogenetic analyses. Sequence alignment and comparison. Reconstruction, visualization, evaluation, and interpretation of phylogenetic trees using selected bioinformatics methods and tools. Comparison of phylogenetic analysis results. Implementation of a basic phylogenetic analysis workflow – from data preparation to the interpretation of results.</p>		
Prerequisites and co-requisites			
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Lectures - written examination	60.0%	50.0%
	Laboratory classes - assessment based on the completion and evaluation of laboratory tasks specified in the instructions for individual laboratory exercises	60.0%	50.0%
Recommended reading	Basic literature	<ol style="list-style-type: none"> 1. Scientific publications and materials prepared by the course instructor and made available to students during classes. 2. Brown, T.A. „Genomes”, 2nd ed., Polish translation edited by P. Węgleński, Wydawnictwo Naukowe PWN, Warsaw, 2009. 3. Higgs, P.G., Attwood, T.K. „Bioinformatics and Molecular Evolution”, Wydawnictwo Naukowe PWN, Warsaw, 2008. 4. Baxevanis, A.D., Ouellette, B.F.F. „Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins”, Wydawnictwo Naukowe PWN, Warsaw, 2004. 	
	Supplementary literature	<ol style="list-style-type: none"> 1. Avise, J.C. „Molecular Markers, Natural History and Evolution”, University of Warsaw, Warsaw, 2008. 2. Hall, B.G. „Phylogenetic Trees Made Easy”, University of Warsaw Press, Warsaw, 2008. 3. Freeland, J.R. „Molecular Ecology”, Wydawnictwo Naukowe PWN, Warsaw, 2008. 4. Brown, T.A. „Genomes 3”, Garland Science, 2007. 	
	eResources addresses		

Example issues/ example questions/ tasks being completed	<ol style="list-style-type: none"> 1. Acquisition, preparation, alignment, and comparison of biological sequences using selected databases and bioinformatics tools. 2. Reconstruction and interpretation of phylogenetic trees using selected computational methods. 3. Assessment of the reliability of phylogenetic analysis results and comparison of the resulting trees. 4. Analysis and interpretation of relationships among sequences and taxa based on phylogenetic data. 5. Implementation of a basic phylogenetic analysis workflow—from sequence data preparation to the interpretation of the results.
Practical activities within the subject	Not applicable

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