



Subject card

Subject name and code	Elements of Bioinformatics, PG_00064513						
Field of study	Informatics						
Date of commencement of studies	February 2027	Academic year of realisation of subject			2027/2028		
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			English		
Semester of study	2	ECTS credits			2.0		
Learning profile	general academic profile	Assessment form			assessment		
Conducting unit	Department of Algorithms and Systems Modelling -> Faculty of Electronics Telecommunications and Informatics -> Faculties of Gdańsk University of Technology						
Name and surname of lecturer (lecturers)	Subject supervisor	dr hab. inż. Piotr Mironowicz					
	Teachers	dr hab. inż. Piotr Mironowicz dr hab. inż. Michał Małafiejski					
Lesson types	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	0.0	15.0	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		4.0		16.0	50
Subject objectives	Bioinformatics is a relatively new branch of computer science whose aim is to support biological research by computers. The scope of methods used by bioinformatics is very wide: we have fast text processing, discrete optimization algorithms, statistical analysis, artificial intelligence and machine learning, computational geometry and even computational models of physical systems. This subject is devoted to presentation of selected computational problems connected with the analysis of information obtained from biological data e.g. DNA and protein sequences.						

Learning outcomes	Course outcome	Subject outcome	Method of verification
	[K7_W02] knows and understands, to an increased extent, selected laws of physics and physical phenomena, as well as methods and theories explaining the complex relationships between them, constituting advanced general knowledge in the field of technical sciences related to the field of study	Student learned physical processes and models of higher-level phenomena, such as models of DNA mutation or the formation of species traits.	[SW1] Assessment of factual knowledge
	[K7_U02] can perform tasks related to the field of study as well as formulate and solve problems applying recent knowledge of physics and other areas of science	The student is able to formulate and solve selected computational problems arising in the analysis of biological data, in particular DNA and protein sequences, using algorithmic methods, statistical tools and mathematical models commonly applied in bioinformatics.	[SU2] Assessment of ability to analyse information
	[K7_U08] while identifying and formulating engineering tasks specifications and solving these tasks, can: - apply analytical, simulation and experimental methods, - notice their systemic and non-technical aspects, - make a preliminary economic assessment of suggested solutions and engineering work	The student is able to identify problems in the analysis of biological data and select appropriate computational methods, including sequence alignment algorithms, phylogenetic tree reconstruction methods, and mutation models, using analytical and simulation-based approaches.	[SU3] Assessment of ability to use knowledge gained from the subject
[K7_U43] can apply information technologies in market economy and information society conditions as well as algorithmize and computerize cognitive and decision-making processes in other areas of knowledge	The student is able to algorithmically formulate selected problems in biological data analysis and apply computational tools for processing and interpreting sequence data in the context of biological research.	[SU4] Assessment of ability to use methods and tools	
Subject contents	Course content – lecture 1. Biology introduction. 2. Pairwise alignment. 3. Multiple alignment methods. 4. Modeling of biological sequences evolution. 5. Introduction to phylogenetics, distance methods. 6. Building phylogenetic trees - parsimony. 7. Patterns searching, hidden Markov models. Course content – project Independent or team implementation of selected computational problems in the field of bioinformatics algorithms.		
Prerequisites and co-requisites	Subjects: 1. Practice of Programming (PPR) 2. Algorithms and Data Structures (ADST) lub Fundamentals of Algorithm Analysis (FAA) 3. Probability and Mathematical Statistics (PMS)		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Midterm colloquium	25.0%	50.0%
	Project	26.0%	50.0%
Recommended reading	Basic literature	1. P. Higgs, T. Attwood, "Bioinformatics and Molecular Evolution", Wiley-Blackwell, 2005. 2. A. Baxevanis, B. Ouellette i inni, "Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins", Wiley-Interscience, 2004. 3. R. Durbin, S. Eddy, A. Krogh, G. Mitchison, "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids", Cambridge University Press, 1999.	
	Supplementary literature	1. P. Winter, G. Hickey, H. Fletcher, "BIOS Instant Notes in Genetics", Taylor & Francis, 2006. 2. D. Gusfield, "Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology", Cambridge University Press, 1997. 3. M. Waterman, "Introduction to Computational Biology: Maps, Sequences and Genomes", Chapman & Hall, 1995. 4. M. Nei, S. Kumar, "Molecular Evolution and Phylogenetics", Oxford University Press, 2000.	
	eResources addresses		
Example issues/ example questions/ tasks being completed	Discuss methods for aligning DNA sequences. Discuss the basic concepts of phylogenetics. Identify the main models of DNA evolution.		

Practical activities within the subject	Not applicable
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