



Subject card

Subject name and code	Elements of Bioinformatics, PG_00055358						
Field of study	Informatics						
Date of commencement of studies	October 2023		Academic year of realisation of subject		2024/2025		
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	2		Language of instruction		English		
Semester of study	3		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						
Name and surname of lecturer (lecturers)	Subject supervisor		dr inż. Piotr Mironowicz				
	Teachers		dr inż. Piotr Mironowicz				
Lesson types and methods of instruction	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		5.0		15.0	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_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	Student describes the biological function of DNA, RNA and polypeptides. Student can model the evolution of sequences in terms of Markov chain. Student describes and uses computer algorithms for two sequence alignments and multi-alignments, performs phylogenetic analysis and searches genes in DNA.	[SU1] Assessment of task fulfilment [SU2] Assessment of ability to analyse information
	[K7_U41] can select methods of modelling and analysis of information systems and applications using selected elements of theoretical computer science and modern programming tools	The student is able to choose the appropriate bioinformatic algorithm for the indicated biological problem and use the programming environment for its implementation.	[SU4] Assessment of ability to use methods and tools
	[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 understands the physical and biochemical context of the bioinformatics problems he analyzes.	[SU2] Assessment of ability to analyse information
	[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_W05] Knows and understands, to an increased extent, methods of process and function support, specific to the field of study.	Student describes the biological function of DNA, RNA and polypeptides. Student can model the evolution of sequences in terms of Markov chain. Student describes and uses computer algorithms for two sequence alignments and multi-alignments, performs phylogenetic analysis and searches genes in DNA.	[SW1] Assessment of factual knowledge [SW3] Assessment of knowledge contained in written work and projects
Subject contents	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		
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	<p>1. P. Winter, G. Hickey, H. Fletcher, "BIOS Instant Notes in Genetics", Taylor & Francis, 2006.</p> <p>2. D. Gusfield, "Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology", Cambridge University Press, 1997.</p> <p>3. M. Waterman, "Introduction to Computational Biology: Maps, Sequences and Genomes", Chapman & Hall, 1995.</p> <p>4. M. Nei, S. Kumar, "Molecular Evolution and Phylogenetics", Oxford University Press, 2000.</p>
	eResources addresses	<p>Adresy na platformie eNauczenie:</p> <p>Elements of Bioinformatics 24-25 - Moodle ID: 41692</p> <p>https://enauczenie.pg.edu.pl/moodle/course/view.php?id=41692</p>
Example issues/ example questions/ tasks being completed		
Work placement	Not applicable	

Document generated electronically. Does not require a seal or signature.