Subject card

Subject name and code	Elements of Bioinformatics, PG_00055358
Field of study	Informatics

Date of commencement of studies	October 2022	Academic year of realisation of subject	2023/2024
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	mgr inż. Krzysztof Pastuszak 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_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.	[SW3] Assessment of knowledge contained in written work and projects [SW1] Assessment of factual knowledge
	[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 understands the physical and biochemical context of the bioinformatics problems he analyzes.	[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_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.	[SU2] Assessment of ability to analyse information [SU1] Assessment of task fulfilment

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
	Project	26.0%	50.0%
	Midterm colloquium	25.0%	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	Adresy na platformie eNauczanie:
Example issues/ example questions/ tasks being completed		
Work placement	Not applicable	