Subject card

Subject name and code	Elements of Bioinformatics, PG_00054280
Field of study	Informatics

Date of commencement of studies	February 2023	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	1	Language of instruction	Polish
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

Name and surname of lecturer (lecturers)	Subject supervisor	dr hab. inż. Michał Małafiejski
	Teachers	dr hab. inż. Michał Małafiejski dr inż. Joanna Raczek mgr inż. Krzysztof Pastuszak

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_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 chooses from the available models, algorithms or software libraries elements useful for carrying out bioinformatic analyzes.	[SU1] Assessment of task fulfilment
	[K7_W05] Knows and understands, to an increased extent, methods of process and function support, specific to the field of study.	The student knows the biological significance of DNA, RNA and protein sequences, understands formal models of their evolution and methods of obtaining information from such data.	[SW3] Assessment of knowledge contained in written work and projects
	[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 analyzes bioinformatic data using the software he creates, analyzes the obtained results, evaluates the usefulness of selected methods.	[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	The student implements bioinformatics software for aligning two or many biological sequences, modeling their evolution or analyzing phylogenetic history.	[SU4] Assessment of ability to use methods and tools
	[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	The student knows the mathematical methods supporting the acquisition of information from biological sequences and uses them in practice.	[SW3] Assessment of knowledge contained in written work and projects

Subject contents	
	1. Biological introduction.
	2. Linear matching of two sequences.
	3. Linear matching of multiple sequences.
	4. Modeling the evolution of biological sequences.
	5. Introduction to phylogenetics, distance methods.
	6. Reading evolution history: the parsimony method.
	7. Theme search, hidden Markov models.

Prerequisites and co-requisites	
	Basics of:
	- programming
	- algorithms and data structures or algorithm analysis
	- probability calculus and statistics

Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Midterm colloquium	44.0%	50.0%
	Project	52.0%	52.0% → 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: Elementy Bioinformatyki 2023 - Moodle ID: 30696 https://enauczanie.pg.edu.pl/moodle/course/view.php?id=30696
Example issues/ example questions/ tasks being completed		
Work placement	Not applicable	