Subject card

Subject name and code	Introduction to Bioinformatics, PG_00053345		
Field of study	Biomedical Engineering, Biomedical Engineering, Biomedical Engineering		
Date of commencement of studies	February 2024	Academic year of realisation of subject	2024/2025
Education level	second-cycle studies	Subject group	Optional subject group 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	Polish
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	prof. dr hab. inż. Krzysztof Giaro
	Teachers	prof. dr hab. inż. Krzysztof Giaro

Lesson types and methods of instruction	Lesson type	Lecture	Tutorial	Laboratory	Project	Seminar	SUM
	Number of study hours	15.0	0.0	15.0	0.0	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	2.0	18.0	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_W09] Knows and understands, to an increased extent, the economic, legal and other conditions of various types of activities related to the given qualification, including the principles of protection of industrial property and copyright.	Not applicable	[SW3] Assessment of knowledge contained in written work and projects
	[K7_U01] can apply mathematical knowledge to formulate and solve complex and non-typical problems related to the field of study by: - appropriate selection of source information and its critical analysis, synthesis, creative interpretation and presentation, - application of appropriate methods and tools	The student knows the mathematical methods supporting the acquisition of information from biological sequences and uses them in practice by implementing bioinformatic tools.	[SU4] Assessment of ability to use methods and tools
	[K7_U03] can design, according to required specifications, and make a complex device, facility, system or carry out a process, specific to the field of study, using suitable methods, techniques, tools and materials, following engineering standards and norms, applying technologies specific to the field of study and experience gained in the professional engineering environment	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_W01] knows and understands, to an increased extent, mathematics to the extent necessary to formulate and solve complex issues related 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_K03] is ready to meet social obligations, inspire and organise activities for the social environment, initiate actions for the public interest, think and act in an entrepreneurial way	Not applicable	[SK3] Assessment of ability to organize work
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. Information Technologies (INT) 2. Linear Algebra 3. Probability Methods and Statistics		
Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
	Laboratory	52.0%	50.0%
	Midterm colloquium	44.0%	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	