



## Subject card

Subject name and code	Bioinformatics, PG_00037406						
Field of study	Biotechnology						
Date of commencement of studies	October 2020	Academic year of realisation of subject				2022/2023	
Education level	first-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	3	Language of instruction				Polish	
Semester of study	5	ECTS credits				2.0	
Learning profile	general academic profile	Assessment form				assessment	
Conducting unit	Department of Pharmaceutical Technology and Biochemistry -> Faculty of Chemistry						
Name and surname of lecturer (lecturers)	Subject supervisor		dr hab. inż. Marek Wojciechowski				
	Teachers		dr hab. inż. Marek Wojciechowski				
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	The aim of this subject is to familiarise the students with the idea of algorithms and basic computational methods used in the analysis of various genomics and molecular biology problems. Students get acquainted with protein sequence and structure analysis methods, structural and sequence databases and the tools for effective data analysis. In the laboratory course students have the opportunity to use the knowledge and practice their skills in solving real bioinformatics problems.						
Learning outcomes	Course outcome		Subject outcome			Method of verification	
	K6_K02		Student is aware of the speed of changes taking place in biotechnology development and understands the need for continuous training in this field			[SK5] Assessment of ability to solve problems that arise in practice	
	K6_U11		Student is able to use remote and local tools to solve problems in the field of bioinformatics			[SU4] Assessment of ability to use methods and tools	
	K6_K03		Student is aware of the importance of modern technologies, including computer science and molecular biology, for the development of the economy of the country			[SK4] Assessment of communication skills, including language correctness	
	K6_W11		Student knows the basic IT tools useful for solving various tasks in the field of molecular biology and is able to use them efficiently..			[SW3] Assessment of knowledge contained in written work and projects	
Subject contents	Definition of an algorithm. Basic data structures and programming strategies. Abstract data structures: lists, trees, stacks, queues. Rule and divide strategy, dynamic programming, greedy algorithm, recursion. Computational complexity. Information processing in living cells. Genetic code. Replication, transcription and translation. Protein sequence, structure and function relationship. Local and remote databases. Aminoacids substitution matrices. Protein sequence comparison. Protein sequence databases. Heuristic algorithms for sequence database searching. Phylogenetic analysis. Multiple sequence alignment. Sequence motifs, profiles and regular expressions. Structural protein databases. Databases of protein families. Protein sequence and structure alignment. Analysis of protein structure and function. Protein tertiary structure prediction methods.						
Prerequisites and co-requisites							

Assessment methods and criteria	Subject passing criteria	Passing threshold	Percentage of the final grade
		60.0%	50.0%
		60.0%	50.0%
Recommended reading	Basic literature	1) Educational materials provided by the lecturer. 2) Bioinformatics and Molecular Evolution, PG. Higgs, TK. Attwood, Blackwell publishing 2005.	
	Supplementary literature	1) Introduction to algorithms T.H.Cormen, Ch.E.Leiserson, R.L.Rivest, MIT Press 2009. 2) BIOINFORMATICS, ed. Paul H. Dear, SCION Publishing ltd, 2007.	
	eResources addresses		
Example issues/ example questions/ tasks being completed	1) Classification and protein function analysis based on its primary structure. 2) Protein structure prediction from its amino acid sequence.		
Work placement	Not applicable		