



Subject card

Subject name and code	Basic Bioinformatics, PG_00054940						
Field of study	Biotechnology						
Date of commencement of studies	October 2024	Academic year of realisation of subject			2026/2027		
Education level	first-cycle studies	Subject group			Obligatory subject group 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 -> Faculties of Gdańsk University of Technology						
Name and surname of lecturer (lecturers)	Subject supervisor	dr hab. inż. Marek Wojciechowski					
	Teachers						
Lesson types	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_W06	Student has basic knowledge of cell biology, molecular biology, immunology and enzymology			[SW3] Assessment of knowledge contained in written work and projects		
	K6_U11	Student is able to use remote and local IT tools to solve problems in the field of bioinformatics			[SU4] Assessment of ability to use methods and tools		
	K6_W11	Student knows basic IT tools useful in carrying out tasks in the field of molecular biology and is able to use them effectively			[SW3] Assessment of knowledge contained in written work and projects		
	K6_U01	Student is able to use mathematical tools to analyze the results of experiments in the field of genetics and molecular biology			[SU1] Assessment of task fulfilment		
Subject contents	Course content – lecture 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		
	Practical project	60.0%			50.0%		
	Final test of the lecture material	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	
Practical activities within the subject	Not applicable	

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