



## Subject card

Subject name and code	Basic Bioinformatics, PG_00054940						
Field of study	Biotechnology						
Date of commencement of studies	October 2022		Academic year of realisation of subject		2024/2025		
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						
Name and surname of lecturer (lecturers)	Subject supervisor		dr hab. inż. Marek Wojciechowski				
	Teachers						
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_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		
	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_W06		Student has basic knowledge of cell biology, molecular biology, immunology and enzymology		[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		
	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	Adresy na platformie eNauczanie:
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	