GDAŃSK UNIVERSITY OF TECHNOLOGY

Subject card

Subject name and code	BASIC OF BIOINFORMATICS, PG_00063453			
Field of study	Biotechnology			
Date of commencement of studies	October 2024	Academic year of realisation of subject		2024/2025
Education level	second-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	1	Language of instruction		Polish
Semester of study	1	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
	[K7_K02] is aware of the potential risks and opportunities associated with the development of science and technology for the natural environment and society	Student is aware of both the threats and opportunities for the environment and society associated with the development of science and technology.	[SK5] Assessment of ability to solve problems that arise in practice
	[K7_W04] selects methods of data analysis, including bioinformatics, statistical and molecular modeling, useful for solving technological and scientific problems in biotechnology and related fields	Student selects appropriate bioinformatics and statistical methods for analyzing data related to a specific problem and applies molecular modeling techniques useful for solving various biotechnology and molecular biology related problems.	[SW3] Assessment of knowledge contained in written work and projects
	[K7_U05] proposes solutions to technological and scientific problems in biotechnology and related fields using experimental methods and bioinformatics, statistics and specialized databases	Student proposes solutions to problems in biotechnology and molecular biology by utilizing results from experimental methods and bioinformatics resources, including databases.	[SU4] Assessment of ability to use methods and tools

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
	Test of lecture material knowledge	60.0%	50.0%
	Practical project	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

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