

Faculty of Chemistry					
SUBJECT CARD					
Name of subject in Polish	Genomika obliczeniowa				
Name of subject in English	Computational genomics				
Main field of study (if applicable):	Biotechnology				
Specialization (if applicable):	Bioinformatics				
Profile:	academic				
Level and form of studies:	2nd level, full-time				
Kind of subject:	obligatory				
Subject code					
Group of courses	NO				
	Lecture	Classes	Laboratory	Project	Seminar
Number of hours of organized classes in University (ZZU)	15		15		
Number of hours of total student workload (CNPS)	30		30		
Form of crediting	Examination		Crediting with grade		
For group of courses mark (X) final course					
Number of ECTS points	1		1		
including number of ECTS points for practical (P) classes			1		
including number of ECTS points for direct teacher-student contact (BU) classes	0,65		0,7		
PREREQUISITES RELATING TO KNOWLEDGE, SKILLS AND OTHER COMPETENCES					
1. Basic bioinformatics, genetics and molecular biology knowledge 2. Basic knowledge of computer science 3. Specialized English					
SUBJECT OBJECTIVES					
C1 Teaching elementary topics in genomics. C2 Introducing main genomics databases. C3 Teaching about methods of genomes sequencing and description. C4 Teaching about methods of comparative genomics. C5 Teaching about methods of gene expression and analysis. C6 Teaching about practical use of genomics research. C7. Acquainting students with the ethical aspects of genomics research and the use of genomic information.					

SUBJECT LEARNING OUTCOMES		
<p>relating to knowledge: PEK_W01 - knowledge of the basic concepts in genomics PEK_W02 - knowledge of the content and organization of genomic databases PEK_W03 - knowledge of the genome mapping, sequencing and description methods PEK_W04 - knowledge of the tools used to analyze and compare genomic sequences PEK_W05 - knowledge of the methods used in transcriptomic and their applications</p> <p>relating to skills: PEK_U01 - ability to search the genomic databases PEK_U02 - ability to select appropriate methods and tools for the studied problem PEK_U03 – ability to conduct basic genes or their elements predictions as well as genomic sequences alignment and comparison PEK_U04 - ability to analyze the obtained results</p> <p>relating to social competences: PEK_K01 - awareness of the ethical aspects of genomics research and challenges associated with data protection.</p>		
PROGRAMME CONTENT		
Lectures		Number of hours
Lec 1	Introductory lecture: the plan and content of the course and crediting rules. Introduction of the basic concepts in genomics, historical background of genomic research, applications and perspectives.	2h
Lec 2	Genomic information organization: sources of genomic information and principles of data collection and access. Introduction of genomic databases and data structure.	2h
Lec 3	Assembly of genome sequences: presentation of the gene assembly process based on homology approach and <i>de novo</i> . Introduction to the procedures and methods used for assembly of genome sequences.	2h
Lec 4	Structural genomics and description of genomes: overview of principles and methods of genome mapping including types of genomic maps. Presentation of main rules and methods of genes prediction and genome annotation.	2h
Lec 5	Functional and comparative genomics: the types of data gained from transcriptomic experiments, methods of its analysis and applications. Presentation of comparative genomics methods together with applications examples.	2h
Lec 6	Experimental techniques: presentation of basic experimental techniques used for the exploration of genomes including new generation techniques. Discussion of the application possibilities and the future of these field.	2h
Lec 7	Ethical aspects of genomic research: the ethical aspects of genomic research, the use of genomic information in science and industry and challenges of data safety.	2h
Lec 8	Written exam	1h
	Total hours	15h

Laboratory		Number of hours
Lab 1	Introductory classes: the program of laboratory classes, organization and rules of the computer lab. Introduction of basic tools and software used during the course.	2h
Lab 2	Genomic databases: introduction to the main genomic databases, data organization and presentation. Overview of related 'omics' databases.	2h
Lab 3	Description of the genome: Practical examples reflecting the genome annotation process. The use of genomic databases as a source of information including basic comparative analysis.	2h
Lab 4	Gene prediction: Practical examples of the principles of genes prediction including identification of coding sequences, ORFs, introns, exons, but also other genomic elements (e.g. promoters, motifs, non-translated sequences). Individual Project I	2h
Lab 5	Comparative genomics – part 1: introduction to the methods of sequence comparison and the specialized tools. Practical examples.	2h
Lab 6, Lab 7	Comparative genomics - part 2: Genomes evolution and phylogenetic analysis with elements of statistical analysis. Practical examples.	4h
Lab 8	Individual Project II	1h
	Total hours	15h

TEACHING TOOLS USED

N1. Lecture
 N2. Multimedia presentation
 N3. Practical usage of databases
 N4. Practical usage of software
 N5. Solving the exercises
 N6. Preparation of reports

EVALUATION OF SUBJECT LEARNING OUTCOMES ACHIEVEMENT

Evaluation (F – forming (during semester), C – concluding (at semester end))	Educational effect number	Way of evaluating educational effect achievement
C (Lecture)	PEK_W01- PEK_W05, PEK_U02, PEK_K01	Final exam
F1 (Laboratory)	PEK_W01-PEK_W02, PEK_U01-PEK_U03	Report from the Individual Project I
F2 (Laboratory)	PEK_W01- PEK_W04, PEK_U01-PEK_U04	Report from the Individual Project II

C (Laboratory) =F1+F2
PRIMARY AND SECONDARY LITERATURE
<u>PRIMARY LITERATURE:</u> <ol style="list-style-type: none"> 1. <i>Fundamentals of Bioinformatics and Computational Biology</i>, G.B. Singh, Springer-Verlag London, 2015 2. <i>MATLAB Programming for Biomedical Engineers and Scientists</i>, A.P. King, P. Aljabar, Academic Press, 2017 3. <i>Big Data Analytics in Genomics</i>, Wong, Ka-Chun, Springer-Verlag London, 2016. <u>SECONDARY LITERATURE:</u> <ol style="list-style-type: none"> 1. <i>Comparative Gene Finding, Models, Algorithms and Implementation</i>, M. Axelson-Fisk, Springer-Verlag London, 2015 2. <i>Genomes</i>, T. A. Brown, 4th Edition, Garland Science: New York, 2017
SUBJECT SUPERVISOR (NAME AND SURNAME, E-MAIL ADDRESS)
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