Nazwa zajęć/*Course title*:	**Podstawy bioinformatyki**				ECTS	4
Nazwa zajęć w j. angielskim/ *Course title in English*:	**Basics of bioinformatics**					
Zajęcia dla kierunku studiów/ *Degree program name*:	Biotechnology					

Język kursu/ *Course language*:	English			Poziom studiów/*Study level:*	I	
Typ studiów/ *Form of studies*:	**x** intramural .. extramural	Status zajęć/ *Course status*	X podstawowe/ *Basic* kierunkowe/ *major*	X obowiązkowe/ *mandatory* do wyboru/ *elective*	Semestr/*Semester:* 5	x semestr zimowy/ *winter semester* semestr letni/ *summer semester*
		Rok akademicki/*Academic year:*		**2022/2023**	Numer katalogowy/ *Catalogue number:*	**BBT_BTa-1S-5Z-36**

Koordynator zajęć/Course coordinator:	**Prof. dr hab. Marcin Filipecki**
Prowadzący zajęcia/ *Teachers responsible for the course:*	Prof. dr. hab. Marcin Filipecki, Prof. dr hab. Grzegorz Bartoszewski
Założenia, cele i opis zajęć/ *Aims, objectives and description of the course:*	The aim of teaching the subject "Fundamentals of bioinformatics" is to introduce the basic concepts related mainly to the analysis of the rapidly increasing sequential, structural and functional data. These data are widely available to masses of scientists and the basic skill of every biotechnologist today is to compare and analyze their own results in the context of other genome data (transcripts, proteomes, metabolomes). In the last dozen or so years, many databases and many computer programs have been created that allow the use of the above-mentioned information. Therefore, a biotechnologist should be able to choose an appropriate bioinformatics tool, use and properly interpret the obtained results. Course content: What is and what does bioinformatics, genome sequencing projects, model organisms, sequence - structure - function, bioinformatics institutes, bioinformatics and transcriptome, proteome, metabolome, basic sequence information. Biological databases, data formats, inquiry form. Comparing 2 sequences, amino acid similarity, similarity tables, similarity factor, similarity search in databases, FASTA and BLAST algorithms, expect value. Methods of reading and processing sequence data (Sequence editing using Chromas: chromatogram interpretation, motif search, "cutting" vector sequences, saving sequences in various formats, generating complementary and inverted sequences. Preparation of a restriction map using the REMAP program from the EMBOSS package. reading frames using an application from the EMBOSS package (PLOT ORF, SHOW ORF and GET ORF). Generating a protein sequence based on a nucleotide sequence using the TRANSEQ program from the EMBOSS package. Basic sequence databases (DDBJ, EMBL, GenBank). Effective use of databases, ENTREZ program. Protein sequence databases. Genomic browsers. Reaching various sources of biological information via ExPASy server, databases: Swiss Prot, PROSITE. Designing PCR primers. Principles of primer design, basic and advanced parameters, programs: OLIGO, eprimer3 (EMBOSS)), PRIME (GCG). Sequence comparison and searching databases with local BLAST and FASTA algorithms. Parameters: gap penalty, gap extension penalty, word size, expect. Selection of the similarity table. Amenities (blastx, tblastx etc.)
Formy dydaktyczne, liczba godzin/ *Teaching forms, number of hours*:	a) laboratory classes…………… ……………………… …… number of hours 45
Metody dydaktyczne/*Teaching methods:*	Classes take place in the computer lab, where each student has to perform the planned tasks independently. the possibility of using distance learning when necessary
Wymagania formalne i założenia wstępne/ *Formal requirements and prerequisites*	Introductory subjects and prerequisites: genetics, molecular biology, basic computer skills, use of a web browser The student has knowledge of the basics of gene functioning, methods of inheriting traits, and theoretical knowledge of basic experimental techniques in molecular biology.

Efekty uczenia się/*Learning outcomes:*		treść efektu przypisanego do zajęć/*the content of the effect assigned to the course:*	Odniesienie do efektu kierunkowego /*Relation to the course outcomes*	Siła dla ef. kier* /*Impact on the course outcomes* *
Wiedza (absolwent zna i rozumie) /*Knowledge*: (the graduate knows and understands)	W1	knows and skilfully uses the basic databases of biological sequences and scientific literature	K_W04 K_W05 K_W07 K_W13	3 3 3 3
Umiejętności (absolwent potrafi) /*Skills*: (the graduate is able to)	U1	skilfully uses basic databases of biological sequences and scientific literature	K_U17 K_U15 K_U22	3 3 3
	U2	edits and describes newly sequenced nucleic acid molecules, as well as the sequence of nucleic acid and proteins from the database, and designs primers for PCR reactions	K_U15 K_U17 K_U22	3 3 3
	U3	deduces the putative function of an unknown biological sequence from personally made comparisons to other sequences in the databases	K_U12 K_U17 K_U18 K_U22	3 3 3 3

Kompetencje (absolwent jest gotów do) /Competences: (The graduate is ready to)	K1	is ready to solve simple bioinfromatic problems and expand knowledge on the basis of databases	K_K01	1

Treści programowe zapewniające uzyskanie efektów uczenia się: /Program contents ensuring the achievement of the learning outcomes:	Concepts related to the analysis of rapidly increasing sequential, structural and functional data. Compare and analyze your own results in the context of other genome data (transcriptomes, proteomes, metabolomes). Databases and computer programs. The use of appropriate bioinformatics tools and the interpretation of the obtained results.
Sposób weryfikacji efektów uczenia się/ *Methods of the verification of the learning outcomes:*	credit - theory test and practical tests,
Szczegóły dotyczące sposobów weryfikacji i form dokumentacji osiąganych efektów uczenia się /Details on the verification methods and of the ways of documenting the learning outcomes:	Name list of students' grades, assessed tests and final tasks, possibilities of using distance education when necessary
Elementy i wagi mające wpływ na ocenę końcową/*Elements and weights influencing the final grade:*	Written test, completing tasks and commenting on the results
Miejsce realizacji zajęć/ *Teaching place:*	Bioinformatics laboratory

Literature / *Literarture:*
Addresses of the applications used and documentation on them are available at: http://marcin_filipecki.users.sggw.pl/filipecki_links.htm; Auxiliary materials prepared by the lecturers available at: http://marcin_filipecki.users.sggw.pl/bioinformatyka.htm http://grzegorz_bartoszewski.users.sggw.pl/; Baxevanis AD, Ouellette BFF (ed.) "Bioinformatics. A textbook for gene and protein analysis. " (2004) PWN; Plant biotechnology 2009, new edition, edited by S. Malepszy, Polish Scientific Publishers PWN

UWAGI/*ANNOTATIONS*
The following scale is used to calculate the final score: 100-91% points - 5.0; 90-81% points - 4.5, 80-71% points - 4.0; 70-61% points - 3.5; 60-51% points - 3.0

*) 3 – zaawansowany i szczegółowy, 2 – znaczący, 1 – podstawowy/ *3 – significant and detailed, 2 – considerable, 1 – basic,*

Wskaźniki ilościowe charakteryzujące moduł/przedmiot/*Quantitative summary of the course:*

Szacunkowa sumaryczna liczba godzin pracy studenta (kontaktowych i pracy własnej) niezbędna dla osiągnięcia zakładanych dla zajęć efektów uczenia się - na tej podstawie należy wypełnić pole ECTS /*Estimated number of work hours per student (contact and self-study) essential to achieve the presumed learning outcomes - basis for the calculation of ECTS credits:*	99 h
Łączna liczba punktów ECTS, którą student uzyskuje na zajęciach wymagających bezpośredniego udziału nauczycieli akademickich lub innych osób prowadzących zajęcia/ *Total number of ECTS credits accumulated by the student during contact learning:*	1.8 ECTS