Module name	**Bioinformatics – analysis of DNA and protein structure**
Module code	B-BTO.071
ISCED code	0511: Biology
Study cycle	II^{o}
Semester	Winter
Responsible for this module	Dr Przemysław Grela, Department of Molecular Biology, przemek@hektor.umcs.lublin.pl Dr Michał Kalita, Department of Genetics and Microbiology, michal.kalita@umcs.pl
Language of instruction	English
Website	
Prerequisites	Basic knowledge of genetics and molecular biology
ECTS	3
ECTS points hour equivalents	Contact hours (work with an academic teacher) – 30 - computer labs: 30 Non-contact hours (students' own work) – 45 - preparation for the exam: 15 - preparation for labs: 15 - preparation of reports from laboratory exercises: 10 - literature study: 5 **Total number of ECTS points for the module - 3**
Learning outcomes verification methods	Continuous evaluation of the computer classes, reports from computer laboratories, written examination
Course full description	Protein structure and methods of structure determination will be presented as well as the use of protein databases and software for visualizing proteins. Methods for secondary and tertiary protein structure prediction will be discussed as well as methods for modeling small/molecule-protein interactions and protein-protein interactions. Finally, students will be introduced to experimental and computational aspects of mapping protein interaction networks. Computational methods for study of biological DNA sequence data in comparative biology and evolution. Analysis of genome DNA content and organization. Techniques for searching sequence databases, pairwise and multiple sequence alignment, phylogenetic methods, and methods for pattern recognition and functional inference from sequence data.
Bibliography	1. Baxevanis, A.D., Ouellette, B.F.F. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. (2004) Wiley-Interscience 2. Higgs P.G., Attwood T.K. Bioinformatics and Molecular Evolution (2005) Wiley-Blackwell 3. Jin Xiong, Essential Bioinformatics (2006) Cambridge University Press
Learning outcomes	**KNOWLEDGE**

	W1: Student knows and understands professional terms and terminology used in bioinformatics
	W2: Student knows and understands the theory and statistical background of commonly available bioinformatics tools
	W3: Student knows and understands the advantages and disadvantages of different techniques used in bioinformatics
	W4: Student recognizes the role of bioinfomatics methods in modern biosciences
	SKILLS
	U1: Student is able to use well-established and widely used bioinformatics tools and platforms
	U2: Student is able to navigate through internet-based biological databases
	U3: Student is able to manipulate DNA and protein sequences using stand-alone PC programs and online tools; find homologues, analyse sequences, construct and interpret evolutionary trees
	U4: Student is able to analyse protein sequences, identify proteins, and retrieve protein structures from databases.
	SOCIAL COMPETENCIES
	K1: Student recognizes the need for, and an ability to engage in lifelong learning.
	K2: Student understands social, legal, and privacy implications of electronic storage and sharing of biological information
Practice	-
Teaching methods	Discussion, computer exercises, multimedia presentations.