|  |  |
| --- | --- |
| Module name | **Bioinformatics** |
| Module code | B-BTM.052 |
| ISCED code | 0511: Biology |
| Study cycle | IIo |
| Semester | winter or summer |
| Responsible for this module  | Dr Przemysław Grela, Department of Molecular Biology,przemek@hektor.umcs.lublin.plDr 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 | 1 |
| ECTS points hour equivalents | Contact hours (work with an academic teacher) – 10Total number of hours with an academic teacher – 15 Number of ECTS points with an academic teacher – 0.5Non-contact hours (students' own work) – 15 Total number of non-contact hours **–** 15 Number of ECTS points for non-contact hours **–** 0.5**Total number of ECTS points for the module - 1** |
| Educational outcomes verification methods | Continuous evaluation of the computer classes |
| Description | The course will familiarize students with the bioinformatics tools for searching DNA/ protein sequence databases and principles of DNA/protein structural bioinformatics. This course provides students with an overview of protein bioinformatics including computational and experimental approaches. It will introduce DNA, amino acid and protein physical properties as well as the alignment and evolution of DNA/protein sequences.  |
| Reading list | 1. Baxevanis, A.D., Ouellette, B.F.F. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. (2004) Wiley-Interscience2. Higgs P.G., Attwood T.K. Bioinformatics and Molecular Evolution (2005) Wiley-Blackwell3. Jin Xiong, Essential Bioinformatics (2006) Cambridge University Press |
| Educational outcomes | **KNOWLEDGE**A student:- understands the theory and statistical background of commonly available bioinformatics tools- recognizes the role of bioinfomatics methods in modern biosciences**SKILLS**A student is able to:- navigate through internet-based biological databases- manipulate DNA and protein sequences using stand-alone PC programs and online tools- find homologues, analyse sequences, construct and interpret evolutionary trees- analyse protein sequences, identify proteins, and retrieve protein structures from databases. View and interpret these structures.**ATTITUDES**- The broad education necessary to understand the impact of bioinformatics in a global, and societal context.- Understand social, legal, and privacy implications of electronic storage and sharing of biological information |
| Practice | - |

**Information about classes in the cycle**

|  |  |
| --- | --- |
| Website | - |
| Educational outcomes verification methods | Continuous evaluation of the computer classes |
| Comments | - |
| Reading list | 1. Baxevanis, A.D., Ouellette, B.F.F. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. (2004) Wiley-Interscience2. Higgs P.G., Attwood T.K. Bioinformatics and Molecular Evolution (2005) Wiley-Blackwell3. Jin Xiong, Essential Bioinformatics (2006) Cambridge University Press |
| Educational outcomes | **KNOWLEDGE**A student:- understands the theory and statistical background of commonly available bioinformatics tools- recognizes the role of bioinfomatics methods in modern biosciences**SKILLS**A student is able to:- navigate through internet-based biological databases- manipulate DNA and protein sequences using stand-alone PC programs and online tools- find homologues, analyse sequences, construct and interpret evolutionary trees- analyse protein sequences, identify proteins, and retrieve protein structures from databases. View and interpret these structures.**ATTITUDES**- The broad education necessary to understand the impact of bioinformatics in a global, and societal context.- Understand social, legal, and privacy implications of electronic storage and sharing of biological information |
| A list of topics | Introduction to usage of DNA/protein databases. Techniques for searching DNA/protein sequence databases. Pairwise and multiple sequence alignment, phylogenetic methods, constructing of phylogenetic trees, methods for pattern recognition and functional inference from sequence data. Basics of protein structure and methods of structure determination will be presented as well as the software for visualizing 3D structures of 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.  |
| Teaching methods | The teaching is given in the form of lectures, seminars and computer exercises. |
| Assessment methods | Assessment will be by a combination of computer assignments, a written report and an examination. |