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| Module name | **Bioinformatics – Analysis of DNA and Protein Structure** |
| Module code | B-BTO.071 |
| ISCED code | 0511: Biology |
| Study cycle | IIo |
| Semester | summer |
| Responsible for this module | Dr Michał Kalita, Department of Genetics and Microbiology, michal.kalita@umcs.pl  Dr Przemysław Grela, Department of Molecular Biology,  przemek@hektor.umcs.lublin.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  Total number of hours with an academic teacher – 45  Number of ECTS points with an academic teacher – 1.5 Non-contact hours (students' own work) – 45  Total number of non-contact hours **–** 45  Number of ECTS points for non-contact hours **–** 1.5  **Total number of ECTS points for the module - 3** |
| Educational outcomes verification methods | Continuous evaluation of the computer classes |
| 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. |
| Reading list | 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 |
| 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  - understands the advantages and disadvantages of different techniques used in bioinformatics  **SKILLS**  A student is able to:  - use well-established and widely used bioinformatics tools and platforms  - 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.  - A recognition of the need for, and an ability to engage   in lifelong learning.  - Understand social, legal, and privacy implications of electronic storage and sharing of biological information |
| Practice | - |

**Information about classes in the cycle**

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| Website | - |
| Educational outcomes verification methods | Continuous evaluation of the computer classes |
| Comments | - |
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| A list of topics | 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. Gene and promoter prediction. Restriction analysis using bioinformatics tools. Use of bioinformatics tools for PCR primer design. |
| 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. |