

## MODULE DESCRIPTION (SYLLABUS)

1.	Module:  <b>Bioinformatics</b>
2.	Language of instruction:  <b>English</b>
3.	Faculty:  <b>Faculty of Biotechnology</b>
4.	Course/module code:  <b>29-BT-S1-E4-EnBin</b> <b>29-BT-S1-E4-EnBinc</b>
5.	Course/module type ( <i>mandatory or elective</i> ):  <b>mandatory</b>
6.	Programme:  <b>Biotechnology</b>
7.	Study cycle ( <i>1st/2nd</i> ):  <b>1st cycle</b>
8.	Year:  <b>2nd</b>
9.	Semester ( <i>autumn or spring</i> ):  <b>spring</b>
10.	Form of tuition and number of hours: Lecture: <b>15 h</b> Computer laboratory: <b>30 h</b>
11.	Coordinator(s):  <b>Paweł Mackiewicz, Prof.</b>
12.	Initial requirements ( <i>knowledge, skills, social competences</i> ):  <b>Basic computer skills.</b>
13.	Objectives:  <b>The main objective of this course is to teach students about theoretical and practical aspects of different bioinformatics and genomics studies such as: searching biological databases, recognition of coding sequences, genome analyses, making sequence alignment, searching databases for homologous sequences, motifs and patterns searching, analyses of amino acid sequences and protein structure prediction, phylogenetic analyses.</b>
14.	Content:  <ul style="list-style-type: none"> <li>• <b>Subject and levels of genomics and bioinformatics analyses.</b></li> </ul>

	<ul style="list-style-type: none"> <li>• <b>Types of biological databases.</b></li> <li>• <b>Problems in the databases.</b></li> <li>• <b>Computational methods in recognition of protein coding sequences in Prokaryota and Eukaryota.</b></li> <li>• <b>Structure and organization of genomes, genome analyses, comparative genomics.</b></li> <li>• <b>Computational analyses of RNA sequences.</b></li> <li>• <b>Alignment of pair of sequences and multiple sequence alignment.</b></li> <li>• <b>Searching databases for similar sequences (FASTA and BLAST algorithms).</b></li> <li>• <b>Motifs and patterns in sequences.</b></li> <li>• <b>Computational analyses of protein sequences, analysis of basic physicochemical properties, recognition of transmembrane regions, motifs and domains in proteins, determination of secondary structure.</b></li> <li>• <b>Databases of structures, methods predicting tertiary structure, structural classification of proteins.</b></li> <li>• <b>Phylogenetics and molecular evolution, construction and evaluation of phylogenetic trees, phylogenomics.</b></li> <li>• <b>System biology.</b></li> </ul>	
1.	<p>Learning outcomes:</p> <p>Student is able to:</p> <ul style="list-style-type: none"> <li>• <b>search appropriate databases and apply suitable bioinformatics software to specific problems and tasks related to analyses of biological data on the nucleotide and amino acid as well as genomic levels;</b></li> <li>• <b>can perform basic phylogenetic analyses.</b></li> </ul>	<p>Outcome symbols:</p> <p>K1_W02, K1_W07, K1_U06, K1_U12, K1_K01</p>
2.	<p>Obligatory and recommended literature:</p> <ul style="list-style-type: none"> <li>• <b>J.-M. Claverie, C. Notredame, <u>Bioinformatics For Dummies</u>. 2nd Edition. Wiley Publishing, Inc. 2006.</b></li> <li>• <b>P.G. Higgs, T.K. Attwood, <u>Bioinformatics and Molecular Evolution</u>, Blackwell Publishing, 2005.</b></li> <li>• <b>J. Xiong, <u>Essential Bioinformatics</u>, Cambridge University, 2006.</b></li> </ul>	
3.	<p>Methods of verification of the assumed learning outcomes:</p> <ul style="list-style-type: none"> <li>• <b>Lect.: open test;</b></li> <li>• <b>Comp. Lab.: practical colloquium using computer every second lesson for mark.</b></li> </ul>	
4.	<p>Conditions of earning credits:</p> <ul style="list-style-type: none"> <li>• <b>Lect.: positive test result;</b></li> <li>• <b>Comp. Lab.: active participation in classes, positive result of the practical tests.</b></li> </ul>	
5.	Student's workload:	
	Activity	Number of hours for the activity
	Hours of instruction (as stipulated in study programme):	45 h

	<ul style="list-style-type: none"> <li>• Lect.: <b>15 h</b></li> <li>• Comp. Lab.: <b>30 h</b></li> </ul>	
	Student's own work: <ul style="list-style-type: none"> <li>• preparation before classes</li> <li>• preparing for the lecture test</li> </ul>	45 h
	Total number of hours:	<b>90 h</b>
	Number of ECTS: <ul style="list-style-type: none"> <li>• Lect.: <b>2 ECTS</b></li> <li>• Comp. Lab.: <b>2 ECTS</b></li> </ul>	<b>4 ECTS</b>