COURSE/MODULE DESCRIPTION (SYLLABUS)

1.	Course: **Genomics and Molecular Evolution**
2.	Language of instruction: **English**
3.	Faculty: **Faculty of Biotechnology**
4.	Course/module code: **29-BT-S2-E2-EngGmec**
5.	Course/module type (*mandatory* or *elective*): **Mandatory**
6.	Programme: **Medical Biotechnology**
7.	Study cycle: **2nd cycle**
8.	Year: **1st**
9.	Semester *(autumn* or *spring):* **Spring**
10.	Form of tuition and number of hours: **Computer laboratory, 30 h**
11.	Name, Surname, academic title: **Paweł MACKIEWICZ, Prof.**
12.	Initial requirements (knowledge, skills, social competences) regarding the course/module and its completion: **Basic computer skills. Genetics and molecular biology. Bioinformatics.**
13.	Objectives: **Understanding the basic issues in the field of genomics and related databases; knowing the idea of algorithms and computer methods used in genome analysis; learning the basics of transcriptomics: bioinformatic analysis of the expression profile, examples of microarray applications in biology and medicine; knowing the organization of genomes, methods for their analysis and genomic databases; understanding New Generation Sequencing (NGS);** **Understanding the principles of molecular evolution; understanding the methods of molecular phylogenetics: collecting homologous sequences and preparing alignments for phylogenetic analyses; determining the substitution model, constructing a phylogenetic tree, analysis and evaluation of phylogenetic tree, testing phylogenetic hypotheses; getting to know examples of the evolution of genes, proteins and**

	genomes and the inferring phylogeny of groups of organisms; understanding the idea of molecular clock and molecular dating.	
14.	Content: **Basic issues in the field of genomics and related databases; basics of transcriptomics: bioinformatic analysis of the expression profile, examples of microarray applications in biology and medicine; organization of genomes, methods for their analysis and genomic databases; New Generation Sequencing (NGS);** **Principles of molecular evolution; types of homologous sequences (orthologs, paralogs and xenologs); alignments suitable for phylogenetic analyses; types of substitution model; variation of substitution rate in and between sequences; methods of phylogenetic tree construction (UPGMA, NJ, ME, LS/FM, MP, ML, Bayesian); analysis and evaluation of phylogenetic tree, bootstrap method; testing phylogenetic hypotheses; evolution of genes, proteins and genomes; molecular clock and molecular dating.**	
15.	Learning outcomes: - Student is able to search appropriate genomic databases and apply suitable bioinformatics software to specific problems and tasks related to genomics. - Student is able to carry out phylogenetic analyses and interpret their results.	Outcome symbols: K_W01, K_W03, K_W04, K_W06 K_U01, K_U03, K_U05, K_U07 K_K01, K_K05
16.	Recommended literature: - **Lesk. Introduction to Genomics. Oxford University Press. 2017.** - **G. Hall. Phylogenetic Trees Made Easy. A How-To Manual. Oxford University Press. 2017** - **P.G. Higgs, T.K. Attwood Bioinformatics and Molecular Evolution, Blackwell Publishing, 2005**	
17.	Methods of verification of the assumed learning outcomes: - **practical colloquium using computer every second lesson for mark**	
18.	Conditions of earning credits: - **attendance, passing practical colloquia**	

Section 19 — Student's workload:

Activity	Number of hours for the activity
Hours of instruction (as stipulated in study programme): - computer laboratory	30 hours
Student's own work - preparing for classes	30 hours
Total number of hours:	**60 hours**
Number of ECTS:	**3 ECTS**