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-EngGme**	
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: **Lecture, 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.**

	Learning outcomes:	Outcome symbols:
15.	• Student understands and knows the idea of genomic databases and algorithms applied in bioinformatics software related to genomics. • Student knows principles of molecular evolution, understands the idea of phylogenetic analyses and is able to give examples of evolution at the molecular level.	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: **open test**
18.	Conditions of earning credits: **Attendance, passing test and practical colloquia**

	Student's workload:	
	Activity	Number of hours for the activity
19.	Hours of instruction (as stipulated in study programme): • lecture	30 hours
	Student's own work • preparing for lecture test	30 hours
	Total number of hours:	**60 hours**
	Number of ECTS:	**3 ECTS**