COURSE OFFERED IN THE DOCTORAL SCHOOL

Code of the course	4606-ES-0000CDK-0028	Name of the course	Polish	Konwersatorium Bioinformatyki
			English	Seminars on Bioinformatics

Type of the course	specialty		
Course coordinator	Prof. dr hab. Dariusz Plewczyński		
Implementing unit	MINI WUT	Scientific discipline / disciplines*	Information and communication technology, biomedical engineering, chemical sciences, biotechnology
Level of education	PhD students	Semester	winter
Language of the course	English		

Type of assessment:	Graded credit	Number of hours in a semester	30	ECTS credits	2
Minimum number of participants	10	Maximum number of participants	30	Available for students (BSc, MSc)	Yes/~~No~~

Type of classes		Lecture	Auditory classes	Project classes	Laboratory	Seminar
Number of hours	in a week					2
	in a semester					30

* does not apply to the Researcher's Workshop

1. Prerequisites

The basic knowledge of programming, molecular biology and bioinformatics

2. Course objectives

The aim of the seminars is to familiarize students with the advanced theoretical ideas in bioinformatics, with particular emphasis on mathematical and computer algorithms. The students will individually present the most recent discoveries in the field (based on their own experience or on the peer-reviewed articles from international journals). Additionally, guest speakers from Laboratory of Bioinformatics and Computational Genomics and other Laboratories will present the results of their most recent work. The topics of the students' presentations will be related to proteins sequences, the three-dimensional structure of proteins and their complexes with other proteins or ligands, and the biological function of the biomolecules (proteins, RNA) in a cell. We will discuss the fundamental question: the link between sequence, structure and function of biopolymers at the scale of evolutionary processes.

3. Course content (separate for each type of classes)

Seminar

The seminar will be focused on the fundamental paradigm of bioinformatics: biopolymer' sequence defines its three-dimensional structure, and the spatial conformation embodies a biological function. We will discuss how this paradigm apply not only to simple chemical entities, heteropolymer molecules such as proteins, RNA molecules.

The course will therefore concentrate on the most recent findings in the field of bioinformatics. The novel massive data provided by the newest experiments brings new algorithms needed for their computational analysis. Each student will be presenting various discoveries either completed by his or her own analysis (e.g., in their MSc research), or published in peer-reviewed scientific journals (Nature, Science, Cell, Genome Research, Genome Biology, Nucleic Acids Research). The accepted presentations can cover bioinformatics databases and computational algorithms used in modern bioinformatics, and their linkage between types of data. The course will also include guest speakers from the Laboratory of Bioinformatics and Computational Genomics and other Laboratories presenting the original and up-to-date work.

Laboratory

4. Learning outcomes

	Learning outcomes description	Reference to the learning outcomes of the WUT DS	Learning outcomes verification methods*
Knowledge			
K01	Knows computer methods used to manage huge amounts of data contained in biological and medical databases and bioinformatics algorithms used for searching, exploring and classifying data stored in such a way	SD_W2 SD_W3	assessment of activity during classes, presentation
K02	Knows the algorithms for predicting and studying complex interactions occurring in biological systems and in individual biological molecules (in particular in proteins)	SD_W2 SD_W3	assessment of activity during classes, presentation
K03	He knows the basic molecular modeling and machine learning algorithms and molecular biomolecules visualization techniques	SD_W2 SD_W3	assessment of activity during classes, presentation
Skills			
S01	He can classify a bioinformatics problem and find its approximate solution	SD_U1	assessment of activity during classes, presentation
Social competences			
SC01	Is aware of the impact and application of computer techniques in various fields of science and life	SD_K1 SD_K2	presentation

*Allowed learning outcomes verification methods: exam; oral exam; written test; oral test; project evaluation; report evaluation; presentation evaluation; active participation during classes; homework; tests

5. Assessment criteria

Completion of the course is based on the presentations grade and activity during the seminars.

6. Literature

Basic literature:

1. Introduction to Bioinformatics. By: Arthur M. Lesk, Edition: 1st edition, September 2002, Publisher: Oxford University Press.

2. Bioinformatics and Functional Genomics. By Jonathan Pevsner, 3rd Edition, WileyBlackwell, 2015.

3. Bioinformatics, The Machine Learning Approach. By Pierre Baldi and Søren Brunak, MIT Press; 2001.

Additional literature:

4. Bioinformatics in the Post-Genomic Era: Genome, Transcriptome, Proteome, and Information-Based Medicine. By: Jeffrey Augen, Edition: 1st edition, August 2004, Publisher: Addison-Wesley

5. Bioinformatics: Genes, Proteins and Computers. By: C. A. Orengo, D. T. Jones, J. M. Thornton (Ed), D. T. Jones (Ed). Edition: 1st edition, May 2003, Publisher: Roultledge.

6. Introduction to Bioinformatics. By: Teresa K. Attwood, David Parry-Smith, Edition: 1st edition, May 2001, Publisher: Pearson Education.

7. The Ten Most Wanted Solutions in Protein Bioinformatics. By: Anna Tramontano, Edition: 1st edition, May 2005, Publisher: CRC Press.

8. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. By: Andreas D. Baxevanis (Ed), B. F. Francis Ouellette (Ed), Edition: 3nd edition, October 2004, Publisher: Wiley, John & Sons, Incorporated.

9. An Introduction to Bioinformatics Algorithims (Computational Molecular Biology). By Neil C. Jones and Pavel Pevzner, 1st Edition, MIT Press, 2004.

10. Higgs Paul G., Attword Teresa K., "Bioinformatics and Molecular Evolution", John Wiley & Sons, 2005.

7. PhD student's workload necessary to achieve the learning outcomes**		
No.	Description	Number of hours
1	Hours of scheduled instruction given by the academic teacher in the classroom	30h
2	Hours of consultations with the academic teacher, exams, tests, etc.	
3	Amount of time devoted to the preparation for classes, preparation of presentations, reports, projects, homework	30h
4	Amount of time devoted to the preparation for exams, test, assessments	
	Total number of hours	60h
	ECTS credits	2

** 1 ECTS = 25-30 hours of the PhD students work (2 ECTS = 60 hours; 4 ECTS = 110 hours, etc.)