COURSE OFFERED IN THE DOCTORAL SCHOOL

Code of the course	4606-ES-0000CDK-0101	Name of the course	Polish	**Konwersatorium Genomiki Obliczeniowej**	
			English	**Seminars on Computational Genomics**	
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	summer		
Language of the course	english				
Type of assessment:	Graded credit	Number of hours in a semester	30h	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, bioinformatics and computational methods in genomics

2. Course objectives

The aim of the seminars is to familiarize students with the advanced theoretical ideas in computational genomics, 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 the DNA sequence, the three-dimensional structure of chromatin, and the biological function of the genome in a cell. We will discuss the fundamental question: how biological information is stored, processed, and changed in living organisms 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 genomics: DNA sequence defines its three-dimensional structure, and the spatial conformation embodies a biological function. We will discuss how this paradigm apply to the very blueprint of Life: genome, which is the most complex information carrying biomolecule known up to date.

The genome is often seen as a simple, linear DNA sequence used for digital recording of biological information by living organisms. However, it turns out that the spatial structure of the genome is of great importance for its biological function. In the case of the human genome, we know that genes close together are either all "on" or all "off" at the same time. It is also often the case that genes located in completely different locations on DNA sequence approach each other to be able to act together. In recent years, experimental methods have been developed that allow you to learn about the three-dimensional structure of chromatin and its dynamics. Based on this data, it is possible to reproduce the higher form of spatial organization of chromosomes in the cell nucleus.

The seminar will allow us to discuss the complexity of DNA sequence across the Tree of Life, the dynamical nature of the three-dimensional structure of chromatin, and the universe of biological functions implemented by the genome in a cell. We will focus on the fundamental question: how biological information is stored, processed and changed in living organisms at the scale of evolutionary processes.

The course will therefore concentrate on the most recent findings in the field of genomics. 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 genomic databases and computational genomics algorithms

used in modern mammalian genomics, 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 Genomics. By: Arthur M. Lesk, Publisher: Oxford University Press.
2. Bioinformatics and Functional Genomics. By Jonathan Pevsner, 3rd Edition, Wiley-Blackwell, 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. Genomes. By T.A. Brown Oxford: Wiley-Liss; 2002.
7. A Primer of Genome Science 3rd Edition. By Greg Gibson, Spencer V. Muse, Sinauer Associates, Inc; 3rd edition (January 1, 2009).
8. M. Kasahara i S. Morishita, Large-scale Genome sequence processing, Imperial College Press, 2006.
9. 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.)