

# Warsaw University of Technology | Doctoral School No. 3

Course offered in the Doctoral School No. 3  
– Spring semester of the 2021/2022 academic year

TITLE
Seminars on Bioinformatics and Computational Genomics
CONDUCTING UNIT
Doctoral School No. 3
SCIENTIFIC DISCIPLINE
Information and communication technology
IMPLEMENTING UNIT
112000 - Faculty of Mathematics and Information Science
SUMMARY DESCRIPTION
<p>The aim of the seminars is to familiarize students with the advanced theoretical ideas in bioinformatics and computational genomics, with particular emphasis on mathematical, physical, 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 the Laboratory of Bioinformatics and Computational Genomics and other Laboratories united within the Genomics Platform of Warsaw University of Technology will present the results of their most recent work. The topics of the student's presentations will be related to the protein, RNA, and DNA sequence, the 3D structure of biomolecules; their biological function and interactions; genomic medicine, epigenomics, functional studies, structural genomics, the higher-order organization 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.</p>
FULL DESCRIPTION
<p>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 applies not only to simple chemical entities, heteropolymer molecules such as proteins, RNA molecules but also to the very blueprint of Life: genome, which is the most complex information-carrying biomolecule known up to date.</p> <p>The genome is often seen as a simple, linear DNA sequence used for the 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</p>

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 the 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 bioinformatics and genomics. The novel massive data provided by the newest experiments bring 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 PhD 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.

## LITERATURE

1. Bioinformatics in the Post-Genomic Era: Genome, Transcriptome, Proteome, and Information-Based Medicine. By: Jeffrey Augen, Edition: 1st edition, August 2004, Publisher: Addison-Wesley
2. 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: Routledge.
3. Introduction to Bioinformatics. By: Arthur M. Lesk, Edition: 1st edition, September 2002, Publisher: Oxford University Press.
4. Introduction to Bioinformatics. By: Teresa K. Attwood, David Parry-Smith, Edition: 1st edition, May 2001, Publisher: Pearson Education.
5. The Ten Most Wanted Solutions in Protein Bioinformatics. By: Anna Tramontano, Edition: 1st edition, May 2005, Publisher: CRC Press.
6. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. By: Andreas D. Baxevanis (Ed), B. F. Francis Ouellette (Ed), Edition: 3rd edition, October 2004, Publisher: Wiley, John & Sons, Incorporated.
7. Genomes. By T.A. Brown Oxford: Wiley-Liss; 2002.
8. Bioinformatics, The Machine Learning Approach. By Pierre Baldi and Søren Brunak, MIT Press; 2001.
9. An Introduction to Bioinformatics Algorithms (Computational Molecular Biology). By Neil C. Jones and Pavel Pevzner, 1st Edition, MIT Press, 2004.
10. A Primer of Genome Science 3rd Edition. By Greg Gibson, Spencer V. Muse, Sinauer Associates, Inc; 3rd edition (January 1, 2009).
11. M. Kasahara i S. Morishita, Large-scale Genome sequence processing, Imperial College Press, 2006.
12. Higgs Paul G., Attword Teresa K., "Bioinformatics and Molecular Evolution", John Wiley & Sons, 2005.
13. Bioinformatics and Functional Genomics. By Jonathan Pevsner, 3rd Edition, Wiley-Blackwell, 2015.

## LEARNING OUTCOMES

W01 Zna metody komputerowe wykorzystywane do zarządzania ogromnymi ilościami danych, zawartymi w biologicznych i medycznych bazach danych oraz algorytmy bioinformatyczne wykorzystywane do przeszukiwania, eksploracji i klasyfikacji tak przechowywanych danych I.P7S\_WG

SI\_W11, CC\_W11 ocena aktywności podczas zajęć, prezentacja

W02 Zna algorytmy przewidywania i badania złożonych oddziaływań występujących w systemach biologicznych oraz w poszczególnych cząsteczkach biologicznych (w szczególności w białkach) I.P7S\_WG

SI\_W11, CC\_W11 ocena aktywności podczas zajęć, prezentacja

W03 Zna podstawowe algorytmy modelowania molekularnego oraz techniki wizualizacji cząstek molekularnych I.P7S\_WG

SI\_W11, CC\_W11 ocena aktywności podczas zajęć, prezentacja

## UMIEJĘTNOŚCI / SKILLS

U01 Potrafi dokonać klasyfikacji problemu bioinformatycznego i znaleźć jego przybliżone rozwiązanie I.P7S\_UW

SI\_U01-, CC\_U01-, SI\_U09-, CC\_U09- ocena aktywności podczas zajęć, prezentacja

## KOMPETENCJE SPOŁECZNE / SOCIAL COMPETENCE

K01 Ma świadomość wpływu i zastosowania technik komputerowych w różnych dziedzinach nauki i życia I.P7S\_KK

SI\_K06, CC\_K06 prezentacja

## ASSESSMENT METHODS AND CITERIA; COURSE COMPLETION FORM

Case study, individual preparation of at least two, or more (depending on the number of participants) thematic minimum 45 minutes long presentations based on own experience or articles in peer-reviewed journals.

Guest speakers' presentations.

## LANGUAGE OF THE COURSE

## ECTS CREDITS

English

2

## TYPE OF CLASSES

## NUMBER OF HOURS

## COURSE INSTRUCTOR

Seminar

30

Dariusz Plewczyński,  
prof. dr hab.