



COURSE DESCRIPTION CARD - SYLLABUS

Course name

Bioinformatics [S1Inf1>BIO]

Course

Field of study

Computing

Year/Semester

3/6

Area of study (specialization)

–

Profile of study

general academic

Level of study

first-cycle

Course offered in

Polish

Form of study

full-time

Requirements

elective

Number of hours

Lecture

24

Laboratory classes

16

Other

0

Tutorials

0

Projects/seminars

0

Number of credit points

3,00

Coordinators

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Lecturers

Prerequisites

The student starting this module should have knowledge of algorithms, data structures, computational complexity and combinatorial optimization. He/she should be able to program in C/C++. The student should also understand the need to expand his/her competences and be ready to cooperate in a team.

Course objective

Providing basic knowledge of bioinformatics, mainly on how to use combinatorial models and methods to solve selected biological problems. Developing students' skills in solving problems arising in the field of biological sciences, mainly molecular biology, using combinatorial optimization methods. Developing teamwork skills by working in 2-person groups during laboratory classes.

Course-related learning outcomes

Knowledge

Upon completion of the course, a student:

1. has systematic and theoretically founded knowledge of selected issues of bioinformatics.
2. knows development trends and some important achievements in bioinformatics.
- 2
3. knows basic methods, techniques and tools of computer science applied for solving simple bioinformatics tasks.

Skills

Upon completion of the course, a student:

1. can obtain information from literature, databases and other sources in order to expand his knowledge of bioinformatics.
2. can apply analytical and experimental methods to formulate and solve bioinformatics tasks.
3. is able to communicate using notions and terms of bioinformatics.
4. can cooperate in a team in order to solve a posed problem

Social competences

Upon completion of the course, a student:

1. understands that in bioinformatics knowledge and skills can quickly become obsolete.
2. is aware of the importance of knowledge of computer science in solving biological problems

Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

Verification of the assumed learning outcomes related to lectures is realized by evaluation of acquired knowledge on the basis of a written test. The test is composed of 12 questions rated in the range 0–1 points; the test is passed with at least 6 points. Regular attendance in lectures is taken into account. Verification of the assumed learning outcomes related to laboratory classes is realized by evaluation of progress in the implementation of tasks and by evaluation and defence of finished laboratory tasks and reports. On-time realization of laboratory tasks is taken into account.

Programme content

During lectures students learn about basic problems arising in the field of biological sciences and algorithmic methods for solving them. The first part of the lectures is focused on problems associated with recognizing and analyzing one-dimensional structure of DNA, i.e., sequences of nucleotides. The second part of the lectures is focused on analysis of more complex biological structures and systems. Among others, combinatorial problems related to the analysis of peptide chains and smaller molecules are discussed. Methods of modeling and analysis of complex biological systems are presented, in particular methods based on Petri nets. In addition, the idea of the so-called DNA computers is discussed, where DNA molecules are involved in performing computation.

Course topics

The subject matter of the lectures is as follows.

- Lecture 1: introduction
- Lecture 2: sequencing part 1
- Lecture 3: sequencing part 2
- Lecture 4: sequence alignment
- Lecture 5: search for motifs
- Lecture 6: sequence assembly
- Lecture 7: mapping
- Lecture 8: phylogenetic trees
- Lecture 9: 3D structures
- Lecture 10: complex biological systems part 1
- Lecture 11: complex biological systems part 2
- Lecture 12: DNA computing

During laboratory classes students solve one bioinformatics problem on the theoretical and practical grounds. They design and implement algorithms and verify them in tests, among others, on data from real biological experiments. Because such a problem is computationally hard, the development of an algorithm effective both in terms of quality of obtained results and computation time is a challenge. Subsequent

stages of the laboratory task are described in reports, with emphasis put on theoretical analysis of the problem, originality of the proposed solution, optimization of the algorithm, and conclusions based on tests on various instances. This content is partially realized as students' own work.

Teaching methods

Lectures: presentation illustrated with examples presented on a blackboard, solving exercises. Laboratory classes: design and implementation of algorithms, performing computational experiments, discussion.

Bibliography

Basic

1. Podstawy bioinformatyki, Jin Xiong, Wydawnictwo Uniwersytetu Warszawskiego, Warszawa, 2011.
2. Bioinformatyka i ewolucja molekularna, Paul G. Higgs, Teresa K. Attwood, Wydawnictwo Naukowe PWN, Warszawa, 2012.
3. Wybrane algorytmy i modele grafowe w bioinformatyce, Marta Kasprzak, Wydawnictwo Politechniki Poznańskiej, Poznań, 2013.

Additional

1. Computational Molecular Biology: an Algorithmic Approach, Pavel A. Pevzner, MIT Press, Cambridge, MA, 2000.
2. Systems Biology: a Textbook, Edda Klipp, Wolfram Liebermeister, Christoph Wierling, Axel Kowald, Wiley, 2016.
3. Analysis of Biological Networks, Björn H. Junker, Falk Schreiber (Eds.), Wiley-Interscience 2008.
4. Modeling in Systems Biology. The Petri Net Approach, Ina Koch, Wolfgang Reisig, Falk Schreiber (Eds.), Springer, 2011.
5. Introduction to the Modeling and Analysis of Complex Systems, Hiroki Sayama, Open SUNY Textbooks, 2015.
6. Hemojuvelin-hepcidine axis modeled and analyzed using Petri nets, Dorota Formanowicz, Adam Kozak, Tomasz Głowacki, Marcin Radom, Piotr Formanowicz, Journal of Biomedical Informatics, 2013, 46, 1030-1043.
7. DNA computing, Piotr Formanowicz, Computational Methods in Science and Technology, 2005, 11, 11-20.

Breakdown of average student's workload

	Hours	ECTS
Total workload	75	3,00
Classes requiring direct contact with the teacher	40	1,50
Student's own work (literature studies, preparation for laboratory classes/ tutorials, preparation for tests/exam, project preparation)	35	1,50