POZNAN UNIVERSITY OF TECHNOLOGY

EUROPEAN CREDIT TRANSFER AND ACCUMULATION SYSTEM (ECTS)

pl. M. Skłodowskiej-Curie 5, 60-965 Poznań

# COURSE DESCRIPTION CARD - SYLLABUS

Course name
**Combinatorial Algorithms in Bioinformatics**

## Course

| Field of study | Year/Semester |
|---|---|
| Bioinformatics | 2/3 |
| Area of study (specialization) | Profile of study |
| | general academic |
| Level of study | Course offered in |
| First-cycle studies | Polish |
| Form of study | Requirements |
| full-time | compulsory |

### Number of hours

| Lecture | Laboratory classes | Other (e.g. online) |
|---|---|---|
| 15 | 30 | |
| Tutorials | Projects/seminars | |

### Number of credit points

4

### Lecturers

| Responsible for the course/lecturer: | Responsible for the course/lecturer: |
|---|---|
| Prof. Marta Kasprzak | |
| Faculty of Computing and Telecommunications | |

### Prerequisites

The student starting this module should have knowledge about issues of the course Algorithms and data structures. He/she should be able to program in C or C++.

### Course objective

Providing the knowledge of selected combinatorial problems and algorithms used in bioinformatics. Developing students' skills in viewing biological problems in algorithmic terms. Developing students' skills in selecting appropriate algorithmic approach to solve a biological problem.

### Course-related learning outcomes

Knowledge

Upon completion of the course a student:

1. has knowledge of discrete mathematics and combinatorial optimization useful to formulate and solve simple bioinformatic tasks.

2. has systematic and thorough knowledge of modeling biological problems on the combinatorial ground.

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3. knows basic methods, techniques and tools of computer science applied for solving simple bioinformatic tasks concerning analysis of biological sequences.

Skills

Upon completion of the course a student:

1. integrates and interprets data, draws conclusions, formulates and justifies his/her opinions while solving laboratory tasks.

2. performs simple computational experiments and interprets their results.

3. applies basic techniques and tools of computer science for solving biological problems, is able to assess their usefulness.

4. designs and implements computer software according to a provided specification, using appropriate methods, techniques, and tools.

Social competences

Upon completion of the course a student:

1. correctly identifies and resolves ethical dilemmas associated with the profession, especially by obeying rules of proper use of other people's work.

2. is aware of responsibility for his/her decisions, because delay in the realization of laboratory tasks or improper use of other people's work has considerable impact on final assessment.

## Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

Verification of assumed learning objectives related to lectures is realized by evaluation of acquired knowledge on the basis of a written test. With every lecture (1–7) one question is associated and the answer for it gets 0–2 points (with step 0.5); the test is passed with at least 7.5 points. Regular attendance in lectures is taken into account. Verification of assumed learning objectives related to laboratory classes is realized by evaluation and defence of finished laboratory tasks and reports and evaluation how advanced the realization of laboratory tasks is. On-time realization of laboratory tasks is taken into account. The final assessment is determined by getting together grades obtained for four laboratory tasks and calculating the average one; all grades must be positive (at least 3.0) to pass the classes.

## Programme content

The course includes the following contents related to problems connected with recognizing and analyzing one-dimensional structure of DNA.

- Modeling of biological problems with the use of known combinatorial problems
- Graphs as data structures commonly used for encoding instances of problems in bioinformatics
- Examples of the influence of the presence of experimental errors in instances on the computational complexity of related problems
- Examples of the use of known combinatorial algorithms for solving biological problems
- Examples of new algorithms dedicated to biological problems, based on graph structures
- String processing algorithms

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The subject matter of the lectures is the following.

- Lecture 1: introduction
- Lecture 2: sequencing part 1
- Lecture 3: sequencing part 2
- Lecture 4: sequence alignment, search for motifs
- Lecture 5: sequence assembly
- Lecture 6: mapping
- Lecture 7: phylogenetic trees
- Lecture 8: conclusions

Laboratory classes (15 × 2 hours) take place in a computer laboratory. At the first meeting students get to know rules of work during the classes. During laboratory classes students apply knowledge from the lectures to the construction of algorithms for bioinformatic problems. Every student works individually on his/her tasks.

## Teaching methods

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

## Bibliography

### Basic

1. Wybrane algorytmy i modele grafowe w bioinformatyce, Marta Kasprzak, Wydawnictwo Politechniki Poznańskiej, Poznań, 2013

### Additional

1. Introduction to Computational Biology. Maps, Sequences, and Genomes, Michael S. Waterman, Chapman & Hall, London, 1995
2. Introduction to Computational Molecular Biology, Joao Setubal, Joao Meidanis, PWS Publishing Company, Boston, MA, 1997
3. Computational Molecular Biology: an Algorithmic Approach, Pavel A. Pevzner, MIT Press, Cambridge, MA, 2000
4. Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology, Dan Gusfield, Cambridge University Press, Cambridge, MA, 1997
5. Graphs and Hypergraphs, Claude Berge, North-Holland Publishing Company, London, 1973
6. Combinatorial Optimization: Networks and Matroids, Eugene L. Lawler, Holt, Rinehart and Winston, New York, 1976
7. Combinatorial Optimization: Algorithms and Complexity, Christos H. Papadimitriou, Kenneth Steiglitz, Prentice Hall, Englewood Cliffs, 1982
8. Computers and Intractability. A Guide to the Theory of NP-Completeness, Michael R. Garey, David S. Johnson, W.H. Freeman & Co., San Francisco, 1979
9. Złożoność obliczeniowa problemów kombinatorycznych, Jacek Błażewicz, WNT, Warszawa, 1988

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**Breakdown of average student's workload**

|  | Hours | ECTS |
|---|---|---|
| Total workload | 100 | 4,0 |
| Classes requiring direct contact with the teacher | 45 | 2,0 |
| Student's own work (literature studies, preparation for laboratory classes, preparation for the final test) [1] | 55 | 2,0 |

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[1] delete or add other activities as appropriate