COURSE DESCRIPTION CARD - SYLLABUS

Course name

STRUCTURAL BIOINFORMATICS: CURRENT CHALLENGES AND FUTURE PERSPECTIVES

Course

Proposed by Discipline

Information and communication technology

Type of studies

Doctoral School

Form of study

full-time

Year/Semester

II/4, III/6

Course offered in

English

Requirements

elective

Number of hours

Lecture	Tutorials	Projects/seminars
4		

Number of credit points

1

Lecturers

Responsible for the course/lecturer:

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Faculty of Computing and Telecommunications

Poznan University of Technology

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Responsible for the course/lecturer:

Prerequisites

Knowledge: Basic knowledge and skills in algorithm design, software development with Python, and statistics. Basic knowledge of bioinformatics or biology is welcome although not required.

Skills: ability to search information in sources of various kind, often in English, and transfer learned patterns between research domains.

Social competencies: honesty, perseverance, creativity, open-mindedness, and respect for other people.

Course objective

The course objective is to present the latest methodological developments of artificial intelligence (AI) in structural bioinformatics, to discuss the opportunities and challenges of AI methods bring to life science. The course focuses mainly on data-driven machine learning (ML) techniques.

Course-related learning outcomes

Knowledge

A PhD student who graduated from doctoral school knows and understands:

1) breakthrough achievements and their theoretical foundations as well as guidelines for designing AI models solving problems originated from structural bioinformatics field, [P8S_WG/SzD_W01]
2) future development perspectives related to AI applications in structural bioinformatics. [P8S_WG/SzD_W02]

Skills

A PhD student who graduated from doctoral school can:

1) explore literature, select the promising AI-based models/techniques, and creatively apply them to solve complex biologically-inspired problems, [P8S_UW/SzD_U01]
2) critically analyze and assess the usefulness of scientific results for solving selected challenges of structural bioinformatics, together with their contribution to knowledge development. [P8S_UW/SzD_U02]

Social competencies

A PhD student who graduated from doctoral school is ready to:

1. acknowledge the importance of AI models/techniques in solving problems originated from structural bioinformatics. [P8S_KK/SzD_K03]

Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

PQF code	Methods for verification of learning outcomes	Assessment criteria
W01, W02	A test covering the lecture at the end of the course.	Over 50% of points to pass.
U01, U02	A test covering the lecture at the end of the course.	Over 50% of points to pass.
K03	A test covering the lecture at the end of the course.	Over 50% of points to pass.

Programme content

The lecture presents successful applications of ML-based models for solving structural bioinformatics challenges. We focus also on the most important opportunities and risks in processing multimodal biological data.

Course topics

The course covers the following topics:

1. An application of ML-based techniques for integration and comprehensive analysis of multimodal biological data.
2. A review and analysis of AI methods for solving selected challenges in the field of structural bioinformatics with particular emphasis on:
   a) modeling and quality assessment of tertiary structures of biological molecules,
   b) discovery and classification of molecular interactions crucial for drug design.
3. An impact of AI on further development of structural bioinformatics (opportunities and risks).

Teaching methods

Lecture: multimedia presentation including illustrations and examples.

Bibliography

Basic

1. S. Mitra, S. Datta, T. Perkins, G. Michailidis, "Introduction to Machine Learning and Bioinformatics".
2. P. Baldi, S. Brunak, "Bioinformatics: The Machine Learning Approach".

Additional

1. D. Baxevanis, G. D. Bader, D. S. Wishart, "Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins".
2. P. Compeau, P. Pevzner, "Bioinformatics Algorithms".

Breakdown of average student's workload

	Hours	ECTS
Total workload	25	1,0
Classes requiring direct contact with the teacher	4	0
Doctoral student's own work (literature studies, preparation for tutorials, project preparation) [1]	21	1,0

[1] delete or add other activities as appropriate