



## COURSE DESCRIPTION CARD - SYLLABUS

Course name

Bioinformatics

### Course

Field of study

Education in Technology and Informatics

Area of study (specialization)

Level of study

Second-cycle studies

Form of study

full-time

Year/Semester

1/2

Profile of study

general academic

Course offered in

polish

Requirements

compulsory

### Number of hours

Lecture

15

Laboratory classes

15

Other (e.g. online)

Tutorials

Projects/seminars

### Number of credit points

3

### Lecturers

Responsible for the course/lecturer:

dr Luiza Handschuh

Responsible for the course/lecturer:

luizahan@ibch.poznan.pl

### Prerequisites

Basics of biology (high school level), basic IT skills, basics of programming, willingness to go beyond the boundaries of one's own field of study, the ability to think creatively.

### Course objective

Introducing the student to the basic issues in the field of bioinformatics, the possible applications of IT methods to solve biological problems and presenting the challenges faced by bioinformatics in the face of the dynamic growth of large data sets.

### Course-related learning outcomes

Knowledge

After completing the course, the student will have basic, systematic knowledge in the field of bioinformatics, will know the most important biological databases, data formats and tools for biological data analysis.

Skills

The student will be able to search biological databases in order to find information about specific genes,



proteins and biological processes, will also be able to use basic tools for processing and visualization of biological data. He will know how to independently expand his knowledge and practical skills in the field of bioinformatics.

#### Social competences

The student will be aware that bioinformatics is a field with great potential, dynamically developing and will know the possible applications of IT knowledge and skills in biology and medicine. They will also be aware that solving biological problems requires not only knowledge and ability to use tools, but also a creative approach and discussion with specialists representing various fields of science.

#### Methods for verifying learning outcomes and assessment criteria

Learning outcomes presented above are verified as follows:

The issues discussed during the lectures will be verified during the laboratory classes by performing tasks that require the ability to search biological databases and use IT tools for the analysis and visualization of biological data. Participation in the lectures will be rewarded, as will active work during the laboratory classes. The basis for passing the laboratories will be the preparation of a project on a given topic, using databases and tools learned during the classes (it will be possible to work in groups of 2-3). The exam will be practical - the student will be able to use a computer and any available Internet resources to solve the exam tasks.

#### Programme content

The expression of genetic information, basics of genomics, genome sequencing, biological databases, challenges and examples of bioinformatics applications, big data processing methods, data formats, tools for DNA sequence analysis and prediction of RNA and protein structures, basics of statistics and work in the R Bioconductor environment. Particular issues will be discussed based on the examples from the field of human genomics, biomedicine, oncology and epidemiology.

#### Teaching methods

The lectures will take the form of a presentation richly illustrated with examples of bioinformatics applications. Practical skills in using the presented content will be trained during the laboratory classes, when students will have the opportunity to independently explore databases and use various methods of biological data analysis in order to solve specific problems. Both during the lectures and the laboratories, it will be possible to interact with the lecturer in the form of discussions on the issues presented.

#### Bibliography

Basic

"Introduction to bioinformatics", Arthur Lesk, Oxford University Press, 2021

"Essential Bioinformatics", Jin Xiong, Cambridge University Press, 2012 or 2006

"Bioinformatics and Molecular Evolution", Paul G. Higgs, Teresa K. Attwood, Blackwell Publishing Ltd., 2005



"Introduction to bioinformatics", Magdalena Tkacz, Tadeusz Wilczok, Institute of Computer Science University of Silesia, 2009

Additional

"Bioinformatics and functional genomics", Jonathan Pevsner, Wiley-Blackwell, 2015

"Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins", ed.by. A. D. Baxevanisa i B. F. F. Ouellette'a, John Wiley & Sons, 2005

"Przewodnik po pakiecie R", Przemysław Biecek, GIS, 2017 or earlier (up to 2008)

### Breakdown of average student's workload

	Hours	ECTS
Total workload	45	3.0
Classes requiring direct contact with the teacher	30	2,0
Student's own work (literature studies, preparation for laboratory classes/tutorials, preparation for tests/exam, project preparation) <sup>1</sup>	15	1.0

<sup>1</sup> delete or add other activities as appropriate