

Course: Bioinformatics

Code: L6

Type of the course: obligatory

Level of the course: first cycle

Year: III

Semester: 6

ECTS: 4

Lecturer: Joanna Szyda, PhD

Aim of the course:

1. Learning outcomes:

Students learn content and structure of the most important public data bases of DNA and protein sequences, gene functions, single nucleotide polymorphism and research papers. At the same time, students obtain practical knowledge on how to use those data bases as well as how to utilise data bases contents in practical tasks involving sequence alignment, phylogenetic analysis and gene mapping. Additionally, students learn how to solve complex problems working in a team.

2. Competences:

The completion of this course allows students for using public data bases, visualization and processing the information on nucleotide and amino acid sequences. The skills can be further used for their bachelor or master thesis, as well as in jobs involving research, genetic counseling, molecular biology and software development for molecular biology.

3. Prerequisites:

elements of computer science, general genetics, cell biology, molecular biology

4. Course contents:

data bases, nucleotide sequences, amino acid sequences, protein structure, nucleotide polymorphism

Recommended literature:

- Baxevanis, A.D., Ouellette, B.F. (2005) Bioinformatyka. Wydawnictwo Naukowe PWN.;
- Lesk, A.M. (2002) Introduction to Bioinformatics, Oxford University Press;
- Barnes, M.R., Gray, I.C. (2003) Bioinformatics for Geneticists. John Wiley & Sons;
- <http://www.ncbi.nlm.nih.gov/About/index.html>

Form: lectures – 15 h., computer lab -30 h. self study -15 h.

Assessment: completion of the computer lab is based on grades, which are granted during the semester (minimum average grade to pass 2.51), completion of the lecture part requires the completion of the computer lab and of the exam (minimum 60% of knowledge required to pass).

Language of instruction: Polish or English (upon request)