

Course title: DIGITIZATION TECHNOLOGIES FOR BIOLOGICAL DATA

ECTS credit allocation (and other scores): 2

Semester: autumn

Level of study: ISCED-7 - second-cycle programmes (EQF-7)

Branch of science: Natural sciences

Language: English

Number of hours per semester: 40 h.

Course coordinator/ Department and e-mail: Jan Paweł Jastrzębski; Department of Plant Genetics, Physiology and Biotechnology; jan.jastrzebski@uwm.edu.pl

Type of classes: classes and lectures

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#### Substantive content

**CLASSES:** operating the system from the command line, installing and operating software; programming basics in R, performing basic statistical analysis and processing biological data in a programming environment; writing functions and creating executable scripts

**LECTURES:** Basics of operating systems, including, digitizing biological data, digital processing and analysis of biological data in digital form, analyzing and drawing biological conclusions from digital data; data processing is implemented in selected most popular systems (macOS/Linux/Windows) and algorithm creation, basic analysis techniques in python and R, operation of programs for editing and analyzing molecular data (including NCBI Workbench, UGene).

#### LEARNING PURPOSE:

Presentation of the possibilities and technologies for entering biological data into digital systems, their processing, collection, analysis and inference based on digital data about the properties and characteristics of biological and biotechnological systems. Acquire basic programming skills.

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On completion of the study programme the graduate will gain:

**KNOWLEDGE:** The student is familiar with computer tools for digitizing biological data; basic digital formats of biological data; basic commands for operating the operating system from the command list; the need for continuous exploration in the field of digitizing biological data.

**SKILLS:** The student knows how to select and collect biological data in digital form; apply computer techniques and tools for digitizing biological data, navigate operating systems at the command line level perform basic biological data analysis in a professional software environment; create and apply a simple algorithm for data analysis.

**SOCIAL COMPETENCIES:** The student is aware of the use of in silico techniques. He works in a group on a joint project. He is creative in the search for new applications of known tools in solving a biological problem

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#### Basic literature:

1.) Maria Doyle, Jessica Chung, Vicky Perreau. "Introduction to R for Biologists", 14 July 2023 ([https://melbournebioinformatics.github.io/r-intro-biologists/intro\\_r\\_biologists.html](https://melbournebioinformatics.github.io/r-intro-biologists/intro_r_biologists.html))

2.) Orchestrating high-throughput genomic analysis with Bioconductor. W. Huber, V.J. Carey, R. Gentleman, ..., M. Morgan *Nature Methods*, 2015:12, 115. (<https://www.bioconductor.org>)

3.) Michael I. Love, Simon Anders, and Wolfgang Huber. "Analyzing RNA-seq data with DESeq2". 24 July 2024  
<https://bioconductor.org/packages/devel/bioc/vignettes/DESeq2/inst/doc/DESeq2.html>

4.) <https://master.bioconductor.org/packages/release/workflows/html/rnaseqGene.html>

5.) Love MI, Anders S, Kim V, Huber W (2016). "RNA-Seq workflow: gene-level exploratory analysis and differential expression." *F1000Research*. doi:10.12688/f1000research.7035.2.

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The allocated number of ECTS points consists of:

Contact hours with an academic teacher: 42 h.

Student's independent work: 18 h.