SYLLABUS

Transcriptomics

Academic year 2025-2026

1. Information regarding the programme

1.1. Higher education institution	Babeș-Bolyai University
1.2. Faculty	Faculty of Biology and Geology
1.3. Department	Department of Molecular Biology and Biotechnology
1.4. Field of study	Biology
1.5. Study cycle	Master, 4 semesters
1.6. Study programme/Qualification	Bioinformatics Applied in Life Sciences (English)/ Biologist
1.7. Form of education	Full-time

2. Information regarding the discipline

2.1. Name of the dis	cipli	ne Structura	Structural and functional genomics				Discipline code	BME 1121	
2.2. Course coordinator				Assoc. Prof. Dorina Podar, PhD					
2.3. Seminar coordinator					An	ıda Ios	ip, PhD		
2.4. Year of study	1	2.5. Semester	2	2.6. Type of evaluation E		2.7. Dis	cipline regime	Optional	

3. Total estimated time (hours/semester of teaching activities)

3.1. Hours per week	4	of which: 3.2 course	4	3.3 seminar/laboratory	4
3.4. Total hours in the curriculum	56	of which: 3.5 course	28	3.6 seminar/laborator	28
Time allotment for individual study (ID) and self-study activities (SA)					hours
Learning using manual, course support, bibliography, course notes (SA)					
Additional documentation (in libraries,	on electro	nic platforms, field docu	mentatio	n)	18
Preparation for seminars/labs, homework, papers, portfolios and essays					14
Tutorship					8
Evaluations					4
Other activities: two-way communication with the course holder / tutor				2	
3.7. Total individual study hours 70					
3.8. Total hours per semester 126					
3.9. Number of ECTS credits	3.9. Number of ECTS credits 5				

4. Prerequisites (if necessary)

4.1. curriculum	Genetics, Biochemistry, Cell and molecular biology
4.2. competencies	Computer skills Ability to analyze, evaluate, and synthesize information in order to make informed decisions and solve problems logically and reasoned

5. Conditions (if necessary)

E 1 for the course	Online meeting platform
5.1. Ior the course	Beamer, projection screen
5.2. for the seminar / lab activities	Attendance of a minimum of 90% of seminar classes is mandatory for granting the participation at the written exam. Computers, specific environment for developing and implementing bioinformatic pipelines/tools

6.1. Specific competencies acquired ¹

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Professional/essential competencies	 Ability to analyze and interpret transcriptomic data to discover gene expression patterns and correlate these patterns with biological functions. Skills in quality control of raw sequencing data, aligning reads with the reference genome, quantifying reads, and analyzing differential gene expression. Competence in using bioinformatics tools to visualize data and interpret results, facilitating the understanding of the biological impact of gene expression variations.
Transversal competencies	 Ability to clearly and convincingly communicate scientific results appropriate to the audience's level of understanding (specialists, the general public, or decision-makers). Application of theoretical concepts to solve practical problems. Ability to analyze and interpret scientific data and formulate relevant conclusions based on it. Understanding the ethical aspects and implications of biological and biomedical scientific research

6.2. Learning outcomes

	The student knows:
wledge	• the molecular and technological principles of transcriptomics, including the differences between gene expression profiling methods (RNA-Seq, microarray, scRNA-Seq) and their applications in molecular biology and biomedicine.
Kno	• the stages of the transcriptomic data analysis workflow, from sequence preprocessing (quality control, trimming) to gene expression quantification and differential analysis, along with the associated statistical and computational foundations.
	The student is able to:
aills	• apply specialized bioinformatics algorithms and tools (e.g., STAR, HISAT2, DESeq2, edgeR) for RNA-Seq read alignment, expression quantification, and identification of differentially expressed genes in a given
S	 critically interpret transcriptomic results by integrating gene information, signaling pathways, and functional databases (e.g., Gene Ontology, KEGG) to formulate relevant biological hypotheses.
Responsibility and autonomy:	 The student has the ability to work independently to obtain: develop and implement an individual transcriptomic analysis project, integrating advanced bioinformatics methods; document, interpret, and communicate the results of transcriptomic analyses through the writing of scientific reports and presentations.

7. Objectives of the discipline (outcome of the acquired competencies)

7.1 General objective of the discipline	• The general goal of this course is to teach techniques for RNA sequencing data analysis, starting from raw data up to the analysis of differential gene expression. Students will learn these methods individually, in a practical and active manner.
7.2 Specific objective of the discipline	 Providing theoretical knowledge on the biological principles, experimental technologies, and computational paradigms used in transcriptome analysis. Developing practical skills in the use of bioinformatics tools for processing, analyzing, and interpreting RNA-Seq and scRNA-Seq data. Cultivating the ability to integrate transcriptomic data into biological and biomedical contexts, for the purpose of formulating scientific hypotheses and drawing relevant conclusions.

¹ One can choose either competences or learning outcomes, or both. If only one option is chosen, the row related to the other option will be deleted, and the kept one will be numbered 6.

8. Content

8.1 Course	Teaching methods	Remarks	
1. Introduction to transcriptomics. experimental design for RNA-seq data	Interactive		
analysis	exposure		
2. Short introduction to major current RNA technologies: microarray and	 Presentation 		
RNA-seq	Explanation		
3. Reads quality control and pre-processing	Practical examples		
4. Introduction to genome structure. RNA types and their structures			
5. Aligning reads to reference genome – Concepts, algorithms and tools	Case-study		
6. Quantification of gene expression – concepts and tools	discussions		
7. – 9. RNA-seq analysis framework in R (Introduction to packages used for			
differential expression analysis)			
10. Navigating useful transcriptomics databases			
11. Data visualization tools for gene expression analysis			
12. – 13. Functional gene annotation (GO-term, KEGG pathway, MapMan)			
14. Results data interpretation and discussion			
 Alessandro Cenerino, M. S. (2016). Transcriptome Analysis. Infoduction Edizioni della Normale. Bernot, A. (2004). Genome Transcriptome and Proteome Analysis. John Brown, T. A. (2017). Genomes 4. Garland Science: 4 edition. 	Wiley & Sons.	eurosciences.	
8.2 Seminar / Jaboratory	Teaching methods	Remarks	
1. – 2. Getting started. Establishing the workflow and pipeline	• Interactive exposure		
3. Raw Reads quality check	• Explanation		
4. Pre-processing: genome indexing	· Conversation		
5. Reads mapping to reference genome	• Didactical		
6. Reads counting	demonstration		
7. – 11 Differential expression analysis using R: DEseq2 Package, PCA Plots,	• Group work		
MA Plots, Sample Correlation Plots, Venn Diagrams, UpSet Plot	 Hands-on case-study 		
12. – 13. Gene Ontology (GO-term) enrichment analysis			
14. Results presentation and discussion			
Bibliography			
1. Eija Korpelainen, J. T. (2014). RNA-seq Data Analysis: A Practical Approach. Chapman and Hall/CRC; 1 edition .			
2. Nalini Raghavachari, N. GR. (2019). Gene Expression Analysis: Methods and Protocols. Springer New York.			

3. Yejun Wang, M.-a. S. (2018). Transcriptome Data Analysis: Methods and Protocols. Springer New York.

9. Corroborating the content of the discipline with the expectations of the epistemic community, professional associations and representative employers within the field of the program

- The course enables the acquisition of theoretical and practical skills necessary for a career in the research and development field within academic entities, as well as in R&D units of private companies.
- The course is included in the curricula of similar specializations at universities both Romanian and foreign.

10. Evaluation

Activity type	10.1 Evaluation criteria	10.2 Evaluation methods	10.3 Percentage of final grade		
	Knowledge of information from the topics of the course	Written exam	50 %		
10.4 Course	Accuracy, coherence, and organization of responses. The ability to analyze and interpret.				
	Skills to understand and synthesize scientific information.				
10.5 Seminar/laboratory	Accuracy, coherence, and organization of responses.	Written colloquium	50%		
	Skills for presenting/ communicating scientific information				
10.6 Minimum standard of performance					
• Obtaining a minimum grade of 5.00 (five) both on the written exam and in the final average for the course.					
Completion and sub- established require	 Completion and submission of at least one assigned task during the course, in accordance with the established requirements. 				

established requirements.

11. Labels ODD (Sustainable Development Goals)²

3 GOOD HEALTH AND WELL-BEING	DG 3. Health and well-being				
Date: 08.01.2025	Signature of course coordinatorSignature of seminar coordinatorAssoc. Prof Dorina Podar, PhDAnda Iosip, PhD				

Date of approval:

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Signature of the head of department

Assoc. Prof. Beatrice Kelemen, PhD

² Keep only the labels that, according to the *Procedure for applying ODD labels in the academic process*, suit the discipline and delete the others, including the general one for Sustainable Development - if not applicable. If no label describes the discipline, delete them all and write "Not applicable.".