SYLLABUS

1. Information regarding the programme

1.1 Higher education institution	**Babeş 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**
1.6 Study programme / Qualification	**Bioinformatics applied in life sciences**

2. Information regarding the discipline

2.1 Name of the discipline (en) (ro)	**Transcriptomics** **Transcriptomică**						
2.2 Course coordinator	**Conf. Dr. Podar Dorina**						
2.3 Seminar coordinator	**Conf. Dr. Podar Dorina**						
2.4. Year of study	**I**	2.5 Semester	**2**	2.6. Type of evaluation	**C**	2.7 Type of discipline	**Opţional**
2.8 Code of the discipline	**BME1127**						

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

3.1 Hours per week	**4**	Of which: 3.2 course	**2**	3.3 seminar/laboratory	**2**
3.4 Total hours in the curriculum	**56**	Of which: 3.5 course	**28**	3.6 seminar/laboratory	**28**

Time allotment:	hours
Learning using manual, course support, bibliography, course notes	24
Additional documentation (in libraries, on electronic platforms, field documentation)	18
Preparation for seminars/labs, homework, papers, portfolios and essays	16
Tutorship	8
Evaluations	4
Other activities:	

3.7 Total individual study hours	70
3.8 Total hours per semester	126
3.9 Number of ECTS credits	5

4. Prerequisites (if necessary)

4.1. curriculum	• R programming for data analysis and visualisation • (Fundamentals of programming)
4.2. competencies	• Beginner programming skills (bash and R)

5. Conditions (if necessary)

5.1. for the course	• Video projector
5.2. for the seminar /lab activities	• Computers (with Linux operating system), specific development environment • High-performance compute cluster

6. Specific competencies acquired

Professional competencies	• Understanding how transcriptomes can be used to explore gene expression and function • Applying general methods used for RNA-seq data analysis using case-study (reads quality control, reads mapping to reference genome, quantification, deferential expression analysis) • RNA-seq data results visualization and understanding • Visualization and interpretation of gene expression results of the case-study
Transversal competencies	• Development of empathic capacity through helping and collaborationg in small groups according to the principles and rules of professional ethics • Acquiring oral presentation skills • Development of communication in a widely used foreign language • Development of abilities for knowledge exploration • Data foraging skills

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

7.1 General objective of the discipline	• The aim of this course is to teach students how to perform gene expression analysis starting from raw RNA-seq data by using hands-on approach
7.2 Specific objective of the discipline	• At the end of the course, the students will be able to manipulate raw RNA-seq data and perform the following analysis: differential expression analysis, intersection analysis of differentially expressed genes, GO-term enrichment analysis, pathways analysis of differentially expressed genes. The students will also know how to visualize the results using specific charts and plots in R.

8. Content

8.1 Course	Teaching methods	Remarks
1. Introduction to Transcriptomics. Experimental Design for RNA-seq Data Analysis	• Interactive exposure • Presentation • Explanation • Practical examples • Case-study discussions	
2. Short Introduction to Major Current RNA-seq Technologies and Applications		
3. Reads Quality Control and Pre-processing		
4. Short Introduction to Genome Structure. RNA Types and Their Structure		
5. Aligning Reads to Reference Genome – Concepts, Algorithms and Tools		
6. Quantification of Gene Expression – Concepts and Tools		
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. Seminar Results Data Interpretation and Discussion		
Bibliography 1. Alessandro Cellerino, M. S. (2018). Transcriptome Analysis: Introduction and Examples from the Neurosciences. Edizioni della Normale.		

2. Bernot, A. (2004). Genome Transcriptome and Proteome Analysis. John Wiley & Sons.
3. Brown, T. A. (2017). Genomes 4. Garland Science; 4 edition.

8.2 Seminar / laboratory	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 demonstration	
6. Reads Counting		
7. – 11 Differential Expression Analysis Using R: DEseq2 Package, PCA Plots, MA Plots, Sample Correlation Plots, Venn Diagrams, UpSet Plot	• Group work • 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. G.-R. (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 exists in the curriculum of many universities in the world.

10. Evaluation

Type of activity	10.1 Evaluation criteria	10.2 Evaluation methods	10.3 Share in the grade (%)
10.4 Course	Know concepts and methods for RNA-seq data analysis	Oral presentation of results obtained during the seminar	30%
10.5 Seminar/lab activities	Apply differential expression analysis methods. Visualise and interpret results.	Written protocol about the methods and results obtained during the seminar	70%
10.6 Minimum performance standards			
Each student should obtain minimum 5 for the research report and for the final grade. In order to obtain the minimum grade 5, the student must demonstrate the mastery of the basic concepts of data preparation in order to analyse them.			

Date	Signature of course coordinator	Signature of seminar coordinator
16.01.2023	**Assoc. Prof. Dorina Podar**	**Assoc. Prof. Dorina Podar**

Date of approval	Signature of the head of department
20.01.2023	**Assoc. Prof. Beatrice Kelemen**