

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)	Plant genomics and transcriptomics Genomica și transcriptomica plantelor						
2.2 Course coordinator	Assoc. Prof. Podar Dorina, PhD						
2.3 Seminar coordinator	Iosip Anda, PhD						
2.4. Year of study	2	2.5 Semester	2	2.6. Type of evaluation	E	2.7 Type of discipline	Optional
2.8 Code of the discipline	BME1133						

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	<ul style="list-style-type: none"> • R programming for data analysis and visualisation • Genomics and functional genomics • (Fundamentals of programming)
4.2. competencies	<ul style="list-style-type: none"> • Beginner programming skills (bash and R)

5. Conditions (if necessary)

5.1. for the course	<ul style="list-style-type: none"> • Videoprojector
5.2. for the seminar /lab activities	<ul style="list-style-type: none"> • Computers, specific development environment

6. Specific competencies acquired

Professional competencies	<ul style="list-style-type: none"> • Understand key steps in plant genome and transcriptome assembly • Understand basic methods used in plant comparative genomics • Apply plant genome and transcriptome analysis methods: differential expression analysis, building and visualizing transcription factor networks, inferring orthology and paralogy, building and visualising gene trees • Using online databases, tools and resources for plant genomes and transcriptomes exploration: Plant genome databases, Genome browsers, Plant expression tools, Genomic repositories and stress-related databases, Biotic stress databases
Transversal competencies	<ul style="list-style-type: none"> • Development of empathic capacity through helping and collaborating in small groups • 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	<ul style="list-style-type: none"> • The aim of the course is to make students become familiar with genomics and transcriptomics advances in plant sciences
7.2 Specific objective of the discipline	<ul style="list-style-type: none"> • The students will learn independently using hands-on approach various plant genomic and transcriptomic data analysis methods and techniques as well as explore online databases, tools and resources for plant genomes and transcriptomes.

8. Content

8.1 Course	Teaching methods	Remarks		
1. - 2. Introduction to Plant Genomics. Why Are Plant Genomes Special?	<ul style="list-style-type: none"> • Interactive exposure • Presentation • Explanation • Practical examples • Case-study discussions 			
3. Current Sequencing Technologies Used for Plant Genomics and Transcriptomics				
4. Brief Introduction to Algorithms Used in Genomic Data Science				
5. - 6. Genome Assembly and Annotation Steps. Confounding Factors for Plant Genome Assembly				
7. - 9. Exploring Plant Genomes: GWAS (Genome Wide Association Studies), WGA (Whole Genome Alignment), Repetitive Elements, Orthology and Paralogy.				
10. Introduction to Plant Transcriptomics				
11. <i>De novo</i> Transcriptome Assembly Steps				
12. - 13. Exploring Plant Transcriptomes: Differential Gene Expression Analysis, Isoforms and Splice Variant Analysis, Transcription Factor Network Analysis, Analysing Different Types of RNAs				
14. The Importance of Plant Genomics and Transcriptomics in a Changing Climate. Exploring Genomic Repositories and Stress-related Databases.				
Bibliography:				
1. Poltronieri, P., Burbulis, N., & Fogher, C. (Eds.). (2013). <i>From plant genomics to plant biotechnology</i> . Elsevier.				
2. Edwards, D., & Batley, J. (Eds.). (2016). <i>Plant genomics and climate change</i> . Springer.				

<ol style="list-style-type: none"> 3. Hakeem, K. R., Shaik, N. A., Banaganapalli, B., & Elango, R. (Eds.). (2019). <i>Essentials of Bioinformatics</i>, Volume III: In Silico Life Sciences: Agriculture. Springer International Publishing. 4. Kim, J. H. (2019). <i>Genome data analysis</i>. Springer. 5. Anisimova, M. (2019). <i>Evolutionary genomics: statistical and computational methods</i>. Humana. 6. Singh, R. L., Mondal, S., Parihar, A., & Singh, P. K. (2023). <i>Plant Genomics for Sustainable Agriculture</i>. Genomics. 7. Husen, A., & Ahmad, A. (2023). <i>Genomics, Transcriptomics, Proteomics and Metabolomics of Crop Plants</i>. Academic Press. 				
8.2 Seminar / laboratory	Teaching methods	Remarks		
1. Exploring Genome Visualisation and Plant Expression Data Tools	<ul style="list-style-type: none"> • Interactive exposure • Explanation • Conversation • Didactical demonstration • Hands-on case-study 			
2. Running Differential Expression Analysis on Case-study				
3. Functional Annotation and Functional Enrichment Analysis using GO-terms and MapMan				
4. Transcription Factors Identification of Differentially Expressed Genes (obtained in previous step, using plant transcription factor databases)				
5.- 7. Transcription Factor Network Analysis. Transcription Factor Motif Search and Target Genes Identification				
8. Using Online Gene Network Exploration Tools				
9. - 13. Finding Orthogroups. Visualizing Orthogroup Trees for Genes of Interest (<i>i.e.</i> transcription factors identified in earlier analysis)				
14. Results Interpretation and Discussion				
Bibliography:				
<ol style="list-style-type: none"> 1. Claros, M. G., Bautista, R., Guerrero-Fernández, D., Benzerki, H., Seoane, P., & Fernández-Pozo, N. (2012). Why assembling plant genome sequences is so challenging. <i>Biology</i>, <i>1</i>(2), 439-459. 2. Bailey, T. L., Johnson, J., Grant, C. E., & Noble, W. S. (2015). The MEME suite. <i>Nucleic acids research</i>, <i>43</i>(W1), W39-W49. 3. Schwacke, R., Ponce-Soto, G. Y., Krause, K., Bolger, A. M., Arsova, B., Hallab, A., ... & Usadel, B. (2019). MapMan4: a refined protein classification and annotation framework applicable to multi-omics data analysis. <i>Molecular plant</i>, <i>12</i>(6), 879-892. 4. Jung, H., Ventura, T., Chung, J. S., Kim, W. J., Nam, B. H., Kong, H. J., ... & Eyun, S. I. (2020). Twelve quick steps for genome assembly and annotation in the classroom. <i>PLoS computational biology</i>, <i>16</i>(11), e1008325. 5. Lim, P. K., Zheng, X., Goh, J. C., & Mutwil, M. (2022). Exploiting plant transcriptomic databases: Resources, tools, and approaches. <i>Plant Communications</i>, <i>3</i>(4). 6. Szklarczyk, D., Kirsch, R., Koutrouli, M., Nastou, K., Mehryary, F., Hachilif, R., ... & Von Mering, C. (2023). The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest. <i>Nucleic acids research</i>, <i>51</i>(D1), D638-D646. 7. Letunic, I., & Bork, P. (2024). Interactive Tree of Life (iTOL) v6: recent updates to the phylogenetic tree display and annotation tool. <i>Nucleic Acids Research</i>, gkae268. 				

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

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| <ul style="list-style-type: none"> • The course exists in the curriculum of many universities in the world. |
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10. Evaluation

Type of activity	10.1 Evaluation criteria	10.2 Evaluation methods	10.3 Share in the grade (%)
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10.4 Course	Know concepts and methods for genome as well as transcriptome assembly and exploration	Written or oral examination on one of the topics discussed during the course	50%
10.5 Seminar/lab activities	Apply genome and transcriptome analysis methods	Oral presentation of workflow and results obtained during seminar	50%
10.6 Minimum performance standards			
Each student should be graded at least 5 for the assessment of both course and seminar/lab activities. 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

10.07.2024

Signature of course coordinator

Assoc. Prof. Dorina Podar, PhD

Signature of seminar coordinator

Iosip Anda, PhD

Date of approval

16.07.2024

Signature of the head of department

Assoc. Prof. Beatrice Kelemen, PhD